

Lys	Asn	Pro	Ala	Phe	Pro	Leu	Asp	Ser	Leu	Val	Ala	Met	Thr	Glu	Gly
				85					90					95	
Ser	Ile	Gly	Phe	Trp	Leu	Lys	Asn	Ala	Leu	Gln	Asn	Ala	Leu	Leu	Asp
			100				105						110		
Glu	Gly	Ile	Glu	Lys	Asn	Val	Ala	Ser	Val	Val	Thr	Gln	Val	Ile	Val
		115				120						125			
Asp	Lys	Asn	Asp	Pro	Ala	Phe	Val	Asn	Leu	Ser	Lys	Pro	Ile	Gly	Pro
	130					135					140				
Phe	Tyr	Ser	Glu	Glu	Glu	Ala	Lys	Ala	Glu	Ala	Glu	Lys	Ser	Gly	Ala
145					150					155					160
Thr	Phe	Lys	Glu	Asp	Ala	Gly	Arg	Gly	Trp	Arg	Lys	Val	Val	Ala	Ser
				165				170						175	
Pro	Lys	Pro	Val	Asp	Ile	Lys	Glu	Ile	Glu	Thr	Ile	Arg	Thr	Leu	Leu
			180				185						190		
Asn	Asn	Gly	Gln	Val	Val	Val	Ala	Ala	Gly	Gly	Gly	Gly	Ile	Pro	Val
		195					200					205			
Val	Lys	Glu	Asn	Asn	Gly	His	Leu	Thr	Gly	Val	Glu	Ala	Val	Ile	Asp
	210					215					220				
Lys	Asp	Phe	Ala	Ser	Gln	Arg	Leu	Ala	Glu	Leu	Val	Asp	Ala	Asp	Leu
225					230					235					240
Phe	Ile	Val	Leu	Thr	Gly	Val	Asp	Tyr	Val	Phe	Val	Asn	Tyr	Asn	Lys
				245				250						255	
Pro	Asn	Gln	Glu	Lys	Leu	Glu	His	Val	Asn	Val	Ala	Gln	Leu	Glu	Glu
			260					265					270		
Tyr	Ile	Lys	Gln	Asp	Gln	Phe	Ala	Pro	Gly	Ser	Met	Leu	Pro	Lys	Val
		275				280						285			
Glu	Ala	Ala	Ile	Ala	Phe	Val	Asn	Gly	Arg	Pro	Glu	Gly	Lys	Ala	Val
	290					295					300				
Ile	Thr	Ser	Leu	Glu	Asn	Leu	Gly	Ala	Leu	Ile	Glu	Ser	Glu	Ser	Gly
305					310					315					320
Thr	Ile	Ile	Glu	Lys	Gly										
				325											

(2) INFORMATION FOR SEQ ID NO:4568:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...71
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4568:

Cys	Phe	Ser	Ile	Ile	His	Ile	Leu	Pro	Phe	Ser	Cys	Lys	Arg	Phe	Leu
1				5					10					15	
Cys	Phe	Tyr	Tyr	Thr	Thr	Phe	Leu	Glu	Lys	Ile	Gln	Val	Asn	Tyr	Tyr
		20						25					30		

Thr	Ser	Leu	Ile	Ile	Leu	Lys	Ile	Tyr	Asn	Lys	Phe	Thr	Tyr	Ser	Phe
		35					40					45			
Asn	Cys	Lys	Ser	Ile	Phe	Phe	Gln	Lys	Ile	Ala	Lys	Thr	Pro	Phe	Phe
	50					55					60				
Phe	Tyr	Tyr	Ser	Glu	Met	Lys									
65					70										

(2) INFORMATION FOR SEQ ID NO:4569:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...74
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4569:

Phe	Gln	Ser	Ile	Ile	Ser	Ile	Met	His	Thr	Thr	Ile	Gly	Ser	Asn	Lys
1				5					10					15	
Asn	His	Asn	Lys	Phe	Ile	His	Arg	Trp	Leu	Pro	Gln	Gly	Thr	Lys	Lys
		20					25					30			
Thr	Thr	Thr	Lys	Glu	Val	Ala	Phe	Ile	Glu	Lys	Trp	Ile	Asn	Asn	Tyr
		35				40					45				
Pro	Lys	Lys	Cys	Leu	Asn	Tyr	Lys	Ser	Pro	Arg	Glu	Asp	Phe	Trp	Met
	50				55						60				
Thr	Asn	Leu	Asn	Leu	Lys	Phe	Ser	Asn	Asn						
65					70										

(2) INFORMATION FOR SEQ ID NO:4570:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 237 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...237
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4570:


```

Ile Met Ser Ile His Ile Ala Ala Gln Gln Gly Glu Ile Ala Asp Lys
1      5      10      15
Ile Leu Leu Pro Gly Asp Pro Leu Arg Ala Lys Phe Ile Ala Glu Asn
20     25     30
Phe Leu Gly Asp Ala Val Cys Phe Asn Glu Val Arg Asn Met Phe Gly
35     40     45
Tyr Thr Gly Thr Tyr Lys Gly His Arg Val Ser Val Met Gly Thr Gly
50     55     60
Met Gly Met Pro Ser Ile Ser Ile Tyr Ala Arg Glu Leu Ile Val Asp
65     70     75     80
Tyr Gly Val Lys Lys Leu Ile Arg Val Gly Thr Ala Gly Ser Leu Asn
85     90     95
Glu Glu Val His Val Arg Glu Leu Val Leu Ala Gln Ala Ala Ala Thr
100    105    110
Asn Ser Asn Ile Val Arg Asn Asp Trp Pro Gln Tyr Asp Phe Pro Gln
115    120    125
Ile Ala Ser Phe Asp Leu Leu Asp Lys Ala Tyr His Ile Ala Lys Glu
130    135    140
Leu Gly Met Thr Thr His Val Gly Asn Val Leu Ser Ser Asp Val Phe
145    150    155    160
Tyr Ser Asn Tyr Phe Glu Lys Asn Ile Glu Leu Gly Lys Trp Gly Val
165    170    175
Lys Ala Val Glu Met Glu Ala Ala Ala Leu Tyr Tyr Leu Ala Ala Gln
180    185    190
Tyr His Val Asp Ala Leu Ala Ile Met Thr Ile Ser Asp Ser Leu Val
195    200    205
Asn Pro Asp Glu Asp Thr Thr Ala Glu Glu Arg Gln Asn Thr Phe Thr
210    215    220
Asp Met Met Lys Val Gly Leu Glu Thr Leu Ile Ala Glu
225    230    235

```

(2) INFORMATION FOR SEQ ID NO:4571:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 497 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...497

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4571:

```

Leu Trp Ser Ile Glu Arg Lys Asp Met Tyr Gln Tyr Leu Thr Tyr Pro
1      5      10      15
Arg Asp Gly Tyr Asp Glu Gly Ser Leu Lys Lys Asp Leu Ile Tyr Lys
20     25     30
Leu Ile Thr Ile His Asn Thr Glu Ser Ser Arg Leu Lys Asn Leu Lys

```

		35				40				45					
Ser	Tyr	Tyr	Met	Gly	Asp	His	Ala	Ile	Leu	Asn	His	Lys	Arg	Arg	Asn
50						55					60				
Val	Asn	Ala	Pro	Asn	Tyr	Lys	Thr	Val	Ala	Asn	His	Ala	Lys	Asp	Ile
65					70					75					80
Ala	Asp	Thr	Ala	Thr	Gly	Tyr	Phe	Met	Gly	Asn	Pro	Ile	Lys	Tyr	Asn
				85					90					95	
Asn	Thr	Ala	Asp	Gly	Asp	Ile	Asp	Glu	Leu	Leu	Thr	Ala	Phe	Asp	Gly
			100					105					110		
Ala	Glu	Ile	Asp	Gln	Val	Asp	Ala	Gln	Asn	Ala	Leu	Asn	Met	Ala	Ile
		115					120					125			
Tyr	Gly	Arg	Ala	Tyr	Glu	Tyr	Ile	Tyr	Ala	Lys	Glu	Gly	Met	Thr	Glu
	130					135					140				
Leu	Asp	Ser	Thr	Ser	Ile	Asp	Pro	Glu	Asn	Thr	Phe	Met	Val	Tyr	Asp
145					150					155					160
Asp	Ser	Ile	Glu	Arg	Lys	Pro	Leu	Phe	Ala	Val	Tyr	Tyr	Tyr	Glu	Val
				165					170					175	
Lys	Asp	Asp	Thr	Lys	Asp	Thr	Thr	Lys	His	Gln	Ala	Glu	Val	Phe	Thr
			180					185					190		
Glu	Asn	Leu	His	Tyr	His	Met	Val	Leu	Arg	Ser	Thr	Asp	Ser	Gly	Thr
	195						200					205			
Thr	Gln	Ser	Glu	Glu	Ala	Thr	Pro	His	Asn	Leu	Gly	Gln	Ile	Pro	Ile
	210					215					220				
Ile	Glu	Tyr	Arg	Asn	Asn	His	Phe	Ala	Ile	Gly	Asp	Tyr	Glu	Gln	Gln
225				230						235					240
Ile	Ser	Leu	Ile	Asp	Ala	Tyr	Asn	Ser	Leu	Met	Gly	Asn	Arg	Val	Asn
				245					250					255	
Asp	Lys	Glu	Gln	Ala	Val	Glu	Ser	Ile	Leu	Val	Leu	Tyr	Gly	Thr	Gln
			260					265					270		
Leu	Ala	Asp	Thr	Pro	Glu	Asp	Ala	Lys	Val	Ala	Met	Lys	Ile	Leu	Ser
		275					280					285			
Glu	Glu	Gly	Leu	Leu	Glu	Leu	Pro	Gly	Asp	Ser	Ala	Arg	Ala	Glu	Phe
	290					295					300				
Leu	Lys	Asn	Thr	Leu	Asp	Glu	Ser	Ala	Thr	Glu	Ile	Leu	Arg	Thr	Ala
305					310					315					320
Leu	Lys	Glu	Asp	Ile	Tyr	Thr	Phe	Ser	His	Val	Pro	Asn	Leu	Thr	Asp
				325					330					335	
Glu	Asn	Phe	Ala	Gly	Asn	Thr	Ser	Gly	Val	Ala	Met	Glu	Phe	Lys	Leu
		340						345					350		
Met	Gly	Leu	Glu	Met	Ile	Thr	Lys	Thr	Lys	Glu	Ala	Asn	Tyr	Lys	Arg
		355					360					365			
Gly	Leu	Arg	Gln	Arg	Ile	Ala	Ile	Phe	Ala	His	Tyr	Leu	Gly	Met	Lys
	370					375					380				
Gln	Ile	Ala	Leu	Glu	Ser	His	Ser	Ile	Val	Pro	Gln	Phe	Ser	Arg	Gly
385					390					395					400
Leu	Pro	Lys	Asn	Leu	Leu	Glu	Ile	Ser	Gln	Ile	Val	Asn	Asn	Leu	Glu
			405						410					415	
Gly	Lys	Val	Thr	Asn	Arg	Gln	Leu	Ile	Ser	Leu	Leu	Pro	Phe	Val	Glu
			420					425					430		
Asp	Pro	Asp	Ala	Glu	Leu	Glu	Ala	Leu	Glu	Glu	Glu	Lys	Lys	Lys	Asn
		435					440					445			
Met	Glu	Asp	Met	Pro	Met	Phe	Asn	Lys	Asp	Asn	Thr	Lys	Pro	Glu	Asp
	450					455					460				
Glu	Val	Glu	Asp	Glu	Glu	Ser	Gly	Val	Leu	Gly	Glu	Glu	Glu	Ser	Gln
465					470					475					480
Ser	Asp	Leu	Pro	Ala	Asp	Gly	Gln	Gly	Arg	Lys	Ala	Gly	Arg	Pro	Val
				485					490					495	

Arg

(2) INFORMATION FOR SEQ ID NO:4572:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 370 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...370

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4572:

Gly	Val	Pro	Met	Ala	Lys	Thr	Ile	Tyr	Ile	Ala	Gly	Leu	Gly	Leu	Ile
1				5				10						15	
Gly	Ala	Ser	Met	Ala	Leu	Gly	Ile	Lys	Arg	Asp	His	Pro	Asp	Tyr	Glu
			20					25					30		
Ile	Leu	Gly	Tyr	Asn	Arg	Ser	Gln	Ala	Ser	Arg	Asp	Ile	Ala	Leu	Lys
		35					40					45			
Glu	Gly	Met	Ile	Asp	Arg	Ala	Thr	Asp	Asp	Phe	Ala	Ser	Phe	Ala	Pro
	50					55				60					
Leu	Ala	Asp	Val	Ile	Ile	Leu	Ser	Leu	Pro	Ile	Lys	Gln	Thr	Ile	Ala
65					70					75					80
Phe	Ile	Lys	Glu	Leu	Ala	Asn	Leu	Asp	Leu	Arg	Glu	Gly	Val	Ile	Ile
				85					90					95	
Ser	Asp	Ala	Gly	Ser	Thr	Lys	Ser	Thr	Ile	Val	Asp	Ala	Ala	Glu	Gln
		100						105					110		
Tyr	Leu	Ala	Gly	Lys	Ser	Val	Arg	Phe	Val	Gly	Ala	His	Pro	Met	Ala
	115						120					125			
Gly	Ser	His	Lys	Thr	Gly	Ala	Ala	Ser	Ala	Asp	Val	Asn	Leu	Phe	Glu
	130				135						140				
Asn	Ala	Tyr	Tyr	Ile	Phe	Thr	Pro	Ser	Ser	Leu	Thr	Ser	Gln	Asp	Thr
145					150					155					160
Leu	Lys	Glu	Met	Lys	Asp	Leu	Leu	Ser	Gly	Leu	His	Ala	Arg	Phe	Ile
				165					170					175	
Glu	Ile	Asp	Ala	Lys	Glu	His	Asp	Arg	Val	Thr	Ser	Gln	Ile	Ser	His
		180						185					190		
Phe	Pro	His	Ile	Leu	Ala	Ser	Ser	Leu	Met	Glu	Gln	Thr	Ala	Val	Tyr
	195						200						205		
Ala	Gln	Glu	His	Glu	Met	Ala	Arg	Arg	Phe	Ala	Ala	Gly	Gly	Phe	Arg
	210					215					220				
Asp	Met	Thr	Arg	Ile	Ala	Glu	Ser	Glu	Pro	Gly	Met	Trp	Thr	Ser	Ile
225					230					235					240
Leu	Leu	Ser	Asn	Ser	Glu	Thr	Ile	Leu	Asp	Arg	Ile	Glu	Asp	Phe	Lys
			245						250					255	
Glu	Arg	Leu	Glu	Ala	Ile	Gly	Gln	Ala	Ile	Ser	Lys	Gly	Asp	Glu	Glu
			260					265						270	

Gln	Ile	Trp	Asn	Phe	Phe	Asn	Gln	Ala	Arg	Glu	Gln	Arg	Gln	Thr	Met
		275					280					285			
Glu	Ile	His	Lys	Arg	Gly	Gly	Val	Asp	Ser	Ser	Tyr	Asp	Leu	Tyr	Val
		290				295					300				
Asp	Val	Pro	Asp	Glu	Glu	Asp	Val	Ile	Leu	Arg	Ile	Leu	Glu	Leu	Leu
305					310					315					320
Arg	Gly	Thr	Ser	Leu	Val	Asn	Ile	His	Ile	Asn	Glu	Glu	Asn	Arg	Glu
				325					330					335	
Asp	Ile	His	Gly	Ile	Leu	Gln	Ile	Ser	Phe	Lys	Asn	Ala	Gln	Asp	Leu
			340					345					350		
Glu	Arg	Ala	Glu	His	Leu	Ile	Thr	Glu	Asn	Thr	Asp	Tyr	Thr	Val	Val
		355					360					365			
Ile	Lys														
	370														

(2) INFORMATION FOR SEQ ID NO:4573:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 204 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...204

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4573:

Gln	Val	Pro	Met	Ser	Leu	Arg	Glu	Lys	Ser	Met	Ser	Glu	Tyr	Lys	Leu
1				5				10						15	
Ser	Glu	Asn	Asn	Trp	Thr	Arg	Val	Ala	Val	Phe	Ala	Gly	Gly	Asn	Arg
		20						25					30		
Gly	His	Tyr	Arg	Thr	Asp	Phe	Asp	Ala	Phe	Val	Gly	Val	Asp	Arg	Gly
		35				40						45			
Ser	Leu	Trp	Val	Leu	Glu	Glu	Asp	Leu	Pro	Leu	Ala	Leu	Ala	Val	Gly
	50					55				60					
Asp	Phe	Asp	Ser	Val	Thr	Glu	Glu	Glu	Arg	Gln	Val	Ile	Gln	Lys	Arg
65					70					75					80
Ala	Gln	Tyr	Phe	Val	Gln	Ala	Arg	Pro	Glu	Lys	Asp	Asp	Thr	Asp	Leu
				85					90					95	
Glu	Leu	Ala	Leu	Leu	Thr	Ile	Phe	Glu	Lys	Asn	Pro	Gln	Ala	Gln	Val
			100					105					110		
Thr	Ile	Phe	Gly	Ala	Leu	Gly	Gly	Arg	Ile	Asp	His	Met	Leu	Ala	Asn
		115					120					125			
Val	Phe	Leu	Pro	Ser	Asn	Pro	Lys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
		130				135						140			
Xaa	Xaa	Xaa	Xaa	Xaa	Lys	Lys	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
145					150					155					160
Gly	Xaa	Xaa	Gly	Xaa	Gly	Xaa	Xaa	Gly	Gly	Gly	Gly	Gly	Gly	Gly	Xaa
				165					170						175

Gly Gly Gly Gly Gly Gly Gly Gly Xaa Gly Xaa Gly Gly Gly Gly Xaa
 180 185 190
 Gly Gly Gly Gly Gly Xaa Gly Gly Gly Gly Gly
 195 200

(2) INFORMATION FOR SEQ ID NO:4574:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4574:

Lys Tyr Pro Met Tyr Asn Asp Val Ile Glu Arg Ile Ser Leu Tyr Glu
 1 5 10 15
 Phe Ile Gly Asp Ile Phe Tyr Ser Lys Ile Ile Ser Cys Cys Ile Val
 20 25 30
 Ala Ser Asp Leu Ser Lys Asn Thr Met Lys Leu Asp Val Ile Phe Phe
 35 40 45
 Glu Asp Lys Asn Lys Arg Ser Ala Val Leu Gly Leu Arg Arg Asp Lys
 50 55 60
 Ser Gly Val Phe Lys Pro Val Thr Leu His Phe Thr Ser Ala Lys Lys
 65 70 75 80
 Tyr Ala Lys Val Arg Lys Thr Asp Val Lys Glu Met Lys Trp Leu
 85 90 95

(2) INFORMATION FOR SEQ ID NO:4575:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 85 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...85

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4575:

Asn	Val	Phe	Phe	Asn	Val	Thr	Met	Asn	Cys	Lys	Ile	Ser	Leu	Leu	Ser
1				5				10						15	
Leu	Val	Trp	Met	Ser	Phe	Leu	Met	Lys	Lys	Arg	Pro	Trp	Leu	Leu	Ala
		20						25					30		
Pro	Val	Val	Ser	Ser	Ser	Ser	Cys	His	Lys	Thr	Ser	Thr	Leu	Arg	Asn
		35					40					45			
Asn	Leu	Leu	Val	Ser	Gln	Val	Leu	Met	Phe	Gln	Leu	Leu	Lys	Leu	Tyr
	50					55					60				
Val	Ala	Leu	Arg	Lys	Ser	Leu	Met	Val	Asn	Thr	Thr	Thr	Cys	Gln	Lys
65					70					75					80
Met	Pro	Ser	Val	Val											
				85											

(2) INFORMATION FOR SEQ ID NO:4576:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...63
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4576:

Ile	Glu	Pro	Ile	Leu	Ser	Gln	Asn	Ile	Arg	Glu	Ser	Tyr	Val	Gly	Phe
1				5				10						15	
Gln	Lys	Asn	Thr	Phe	Asn	Thr	Leu	Arg	Lys	Ser	Leu	Gln	Thr	Thr	Ser
		20						25				30			
Val	Leu	Ser	Ala	Thr	Ser	Lys	Leu	Cys	Phe	Glu	Gln	Pro	Ala	Ala	Ser
		35					40					45			
Phe	Leu	Val	Cys	Ser	Leu	Ile	Phe	Ile	Glu	Tyr	Asn	Ser	Lys	Lys	
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:4577:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 222 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4577:

Glu	Val	Thr	Met	Glu	Ser	Ile	Leu	Glu	Ile	Leu	Thr	Pro	Asp	Asn	Leu
1				5				10						15	
Val	Phe	Ile	Phe	Lys	Gly	Phe	Gly	Leu	Thr	Leu	Tyr	Ile	Ser	Leu	Ile
			20					25					30		
Ala	Ile	Ile	Leu	Ser	Thr	Ile	Ile	Gly	Thr	Val	Leu	Ala	Val	Met	Arg
			35					40					45		
Asn	Gly	Lys	Asn	Pro	Ile	Leu	Arg	Ile	Ile	Ser	Ser	Ile	Tyr	Ile	Glu
			50				55				60				
Phe	Val	Arg	Asn	Val	Pro	Asn	Leu	Leu	Trp	Ile	Phe	Thr	Ile	Phe	Leu
65					70					75					80
Val	Phe	Lys	Met	Lys	Ser	Thr	Pro	Ala	Gly	Ile	Thr	Ala	Phe	Thr	Leu
				85					90					95	
Phe	Thr	Ser	Ala	Ala	Leu	Ala	Glu	Ile	Ile	Arg	Gly	Gly	Leu	Asn	Ala
			100					105					110		
Val	Asn	Lys	Gly	Gln	Tyr	Glu	Ala	Gly	Met	Ser	Gln	Gly	Phe	Thr	Ser
		115					120					125			
Ala	Gln	Ile	Leu	Tyr	Tyr	Ile	Ile	Leu	Pro	Gln	Ala	Ile	Arg	Lys	Met
		130					135				140				
Leu	Pro	Ala	Ile	Ile	Ser	Gln	Phe	Val	Thr	Val	Ile	Lys	Asp	Thr	Ser
145					150					155					160
Leu	Leu	Tyr	Ser	Val	Ile	Ala	Leu	Gln	Glu	Leu	Phe	Gly	Ala	Ser	Gln
				165					170					175	
Ile	Leu	Met	Gly	Arg	Tyr	Phe	Glu	Pro	Glu	Gln	Val	Phe	Ser	Leu	Tyr
			180					185					190		
Ile	Leu	Ile	Ala	Leu	Ile	Tyr	Phe	Ser	Phe	Asn	Leu	Ala	Ile	Ser	Asn
		195					200					205			
Leu	Ser	His	Met	Leu	Ala	Lys	Arg	Trp	Gln	Gln	Ala	Ala	Glu		
		210					215					220			

(2) INFORMATION FOR SEQ ID NO:4578:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 61 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4578:

His	Tyr	Thr	Ile	Pro	Ala	Ala	Gly	Val	Glu	Pro	Ala	Arg	Pro	Cys	Gly
1				5				10						15	

His	Trp	Ile	Leu	Ser	Pro	Ala	Arg	Leu	Pro	Ile	Pro	Pro	Arg	Arg	Gln
			20					25					30		
Ile	Val	Thr	Gly	Val	Ala	Gly	Phe	Glu	Pro	Thr	His	Glu	Gly	Val	Lys
		35				40						45			
Val	Pro	Cys	Leu	Thr	Ala	Trp	Leu	Tyr	Pro	Asn	Ile	Lys			
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:4579:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 563 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...563

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4579:

Tyr	Asn	Thr	Met	Glu	Tyr	Asn	His	Lys	Glu	Arg	Thr	Met	Ser	Phe	Asp
1				5					10					15	
Gly	Phe	Phe	Leu	His	His	Ile	Val	Glu	Glu	Leu	Arg	Ser	Glu	Leu	Val
			20					25					30		
Asn	Gly	Arg	Ile	Gln	Lys	Ile	Asn	Gln	Pro	Phe	Glu	Gln	Glu	Leu	Val
		35				40					45				
Leu	Gln	Ile	Arg	Ser	Asn	Arg	Gln	Ser	His	Arg	Leu	Leu	Leu	Ser	Ala
	50					55					60				
His	Pro	Val	Phe	Gly	Arg	Ile	Gln	Leu	Thr	Gln	Thr	Thr	Phe	Glu	Asn
65					70					75				80	
Pro	Ala	Gln	Pro	Ser	Thr	Phe	Ile	Met	Val	Leu	Arg	Lys	Tyr	Leu	Gln
			85						90					95	
Gly	Ala	Leu	Ile	Glu	Ser	Ile	Glu	Gln	Val	Glu	Asn	Asp	Arg	Ile	Val
		100					105					110			
Glu	Ile	Thr	Val	Ser	Asn	Lys	Asn	Glu	Ile	Gly	Asp	His	Ile	Gln	Ala
	115					120					125				
Thr	Leu	Ile	Ile	Glu	Ile	Met	Gly	Lys	His	Ser	Asn	Ile	Leu	Leu	Val
	130					135					140				
Asp	Lys	Ser	Ser	His	Lys	Ile	Leu	Glu	Val	Ile	Lys	His	Val	Gly	Phe
145					150					155					160
Ser	Gln	Asn	Ser	Tyr	Arg	Thr	Leu	Leu	Pro	Gly	Ser	Thr	Tyr	Ile	Ala
			165						170					175	
Pro	Pro	Ser	Thr	Glu	Ser	Leu	Asn	Pro	Phe	Thr	Ile	Lys	Asp	Glu	Lys
			180				185						190		
Leu	Phe	Glu	Ile	Leu	Gln	Thr	Gln	Glu	Leu	Thr	Ala	Lys	Asn	Leu	Gln
		195				200					205				
Ser	Leu	Phe	Gln	Gly	Leu	Gly	Arg	Asp	Thr	Ala	Asn	Glu	Leu	Glu	Arg
	210					215					220				
Ile	Leu	Val	Ser	Glu	Lys	Leu	Ser	Ala	Phe	Arg	Asn	Phe	Phe	Asn	Gln

225		230		235		240
Glu Thr Lys Pro Cys	Leu Thr Glu Thr Ser Phe Ser Pro Val	Pro Phe				
	245	250	255			
Ala Asn Gln Val Gly	Glu Pro Phe Ala Asn Leu Ser Asp Leu Leu Asp					
	260	265	270			
Thr Tyr Tyr Lys Asp Lys	Ala Glu Arg Asp Arg Val Lys Gln Gln Ala					
	275	280	285			
Ser Glu Leu Ile Arg Arg	Val Glu Asn Glu Leu Gln Lys Asn Arg His					
	290	295	300			
Lys Leu Lys Lys Gln	Glu Lys Glu Leu Leu Ala Thr Asp Asn Ala Glu					
305	310	315	320			
Glu Phe Arg Gln Lys	Gly Glu Leu Leu Thr Thr Phe Leu His Gln Val					
	325	330	335			
Pro Asn Asp Gln Asp	Gln Val Ile Leu Asp Asn Tyr Tyr Thr Asn Gln					
	340	345	350			
Pro Ile Met Ile Ala	Leu Asp Lys Ala Leu Thr Pro Asn Gln Asn Ala					
	355	360	365			
Gln Arg Tyr Phe Lys	Arg Tyr Gln Lys Leu Lys Glu Ala Val Lys Tyr					
	370	375	380			
Leu Thr Asp Leu Ile	Glu Glu Thr Lys Ala Thr Ile Leu Tyr Leu Glu					
385	390	395	400			
Ser Val Glu Thr Val	Leu Asn Gln Ala Gly Leu Glu Glu Ile Ala Glu					
	405	410	415			
Ile Arg Glu Glu Leu	Ile Gln Thr Gly Phe Ile Arg Arg Arg Gln Arg					
	420	425	430			
Glu Lys Ile Gln Lys	Arg Lys Lys Leu Glu Gln Tyr Leu Ala Ser Asp					
	435	440	445			
Gly Lys Thr Ile Ile	Tyr Val Gly Arg Asn Asn Leu Gln Asn Glu Glu					
	450	455	460			
Leu Thr Phe Lys Met	Ala Arg Lys Glu Glu Leu Trp Phe His Ala Lys					
465	470	475	480			
Asp Ile Pro Gly Ser	His Val Val Ile Ser Gly Asn Leu Asp Pro Ser					
	485	490	495			
Asp Ala Val Lys Thr	Asp Ala Ala Glu Leu Ala Ala Tyr Phe Ser Gln					
	500	505	510			
Gly Arg Leu Ser Asn	Leu Val Gln Val Asp Met Ile Glu Val Lys Lys					
	515	520	525			
Leu Asn Lys Pro Thr	Gly Gly Lys Pro Gly Phe Val Thr Tyr Thr Gly					
	530	535	540			
Gln Lys Thr Leu Arg	Val Thr Pro Asp Ser Lys Lys Ile Ala Ser Met					
545	550	555	560			
Lys Lys Ser						

(2) INFORMATION FOR SEQ ID NO:4580:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 149 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...149

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4580:

```
Arg Cys Thr Ile Leu Val Ser Ile Tyr Tyr Lys Ile Gly Leu Ser Ser
1          5          10          15
Ser Gly Val Tyr Lys Ala Val Ala Asp Gly Glu Met Thr Val Gly Leu
          20          25          30
Ser Tyr Glu Asp Pro Ala Val Lys Leu Leu Asn Asp Gly Ala Asn Ile
          35          40          45
Lys Val Val Tyr Pro Lys Glu Gly Thr Val Phe Leu Pro Ala Ser Ala
          50          55          60
Ala Ile Val Lys Lys Ser Lys Asn Met Glu Asn Ala Lys Lys Phe Ile
65          70          75          80
Asp Phe Ile Ile Ser Gln Glu Val Gln Asp Thr Leu Gly Thr Thr Thr
          85          90          95
Thr Asn Arg Pro Val Arg Lys Asn Ala Lys Thr Ser Glu Asn Met Lys
          100         105         110
Pro Ile Asp Lys Ile Lys Thr Leu Thr Glu Asp Tyr Asp Tyr Val Ile
          115         120         125
Lys Asn Lys Ser Asp Ile Val Lys Lys Tyr Asn Glu Val Phe Thr Asp
          130         135         140
Ile Gln Ser Lys Gln
145
```

(2) INFORMATION FOR SEQ ID NO:4581:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 79 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4581:

```
Arg Cys Thr Ile Leu Val Ser Ile Tyr Tyr Ile Met Asp Asn Ala Arg
1          5          10          15
Phe His Arg Met Gly Lys Leu Glu Leu Leu Cys Glu Glu Phe Gly His
          20          25          30
Lys Leu Leu Pro Leu Leu Pro Tyr Ser Pro Glu Tyr Asn Pro Ile Glu
          35          40          45
Lys Thr Trp Ala His Ile Lys Lys Asn Leu Lys Lys Val Leu Pro Arg
          50          55          60
```

Cys His Thr Phe Tyr Glu Ala Leu Leu Ser Cys Ser Cys Phe Asn
65 70 75

(2) INFORMATION FOR SEQ ID NO:4582:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4582:

Arg	Cys	Thr	Ile	Leu	Val	Ser	Ile	Tyr	Tyr	Ile	Met	Asp	Asn	Ala	Arg
1				5				10						15	
Phe	His	Arg	Met	Gly	Lys	Leu	Glu	Leu	Cys	Glu	Glu	Phe	Gly	His	
			20				25					30			
Lys	Leu	Leu	Pro	Leu	Pro	Pro	Tyr	Ser	Ser	Glu	Tyr	Ile	Leu	Leu	Arg
			35				40					45			
Lys	His	Gly	Leu	Ile	Ser	Lys	Ser	Thr	Ser	Lys	Arg				
			50			55					60				

(2) INFORMATION FOR SEQ ID NO:4583:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...81

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4583:

Asn	Thr	Thr	Ile	Ile	Ser	Ile	Ser	Ser	Cys	Phe	Ser	Thr	Leu	Phe	Lys
1				5				10						15	
Thr	Phe	Leu	Lys	Asp	Lys	Glu	Lys	Ile	Val	Asn	Ala	Leu	Gln	Leu	Pro
			20				25					30			
Tyr	Ser	Asn	Ala	Lys	Leu	Glu	Ala	Thr	Asn	Asn	Leu	Ile	Lys	Leu	Ile

		35				40				45					
Lys	His	Asn	Ala	Phe	Gly	Phe	Arg	Asn	Phe	Glu	Asn	Phe	Lys	Lys	Glu
	50					55				60					
Arg	Thr	Lys	Phe	Val	Leu	Ser	Arg	Ser	Ser	Leu	Ser	Ser	Thr	His	Tyr
65					70					75					80
Ser															

(2) INFORMATION FOR SEQ ID NO:4584:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...98

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4584:

Phe	Glu	Thr	Ile	Tyr	Leu	Phe	Arg	Thr	Lys	Glu	Lys	Asp	Leu	Lys	Gln
1				5					10					15	
Thr	Ser	Gln	Ile	Leu	Cys	Ile	Ala	Cys	Phe	Ile	Ala	Leu	Phe	Gln	Leu
		20					25					30			
Asp	Gly	Ser	Asn	Ala	Leu	Leu	Val	Ile	Leu	Ile	Ser	Asp	Tyr	Gly	Leu
		35				40					45				
Leu	Leu	Glu	Lys	Thr	Ile	Thr	Asp	Ser	Ser	Gln	Leu	Phe	Pro	Cys	Ser
	50					55				60					
Ser	Gly	Thr	Thr	Ala	Ser	Val	Phe	Pro	Arg	Leu	Ala	Arg	Thr	Phe	Lys
65				70					75					80	
Thr	Val	Ser	Asn	Cys	Gly	Leu	Val	Leu	Pro	Val	Ser	Ile	Leu	Ala	Ile
			85					90						95	
Thr	Gly														

(2) INFORMATION FOR SEQ ID NO:4585:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 547 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...547

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4585:

Val	Glu	Thr	Met	Thr	Glu	Ile	Val	Lys	Ala	Ser	Leu	Glu	Asn	Gly	Ile
1				5					10					15	
Gln	Lys	Ile	Arg	Ile	Arg	Ala	Glu	Lys	Gly	Tyr	His	Pro	Ala	His	Ile
			20					25					30		
Gln	Leu	Gln	Lys	Gly	Ile	Pro	Ala	Glu	Ile	Thr	Phe	His	Arg	Ala	Thr
		35					40					45			
Pro	Ser	Asn	Cys	Tyr	Lys	Glu	Ile	Leu	Phe	Glu	Glu	Glu	Gly	Ile	Leu
	50					55				60					
Glu	Pro	Ile	Gly	Val	Asp	Glu	Glu	Lys	Val	Ile	Arg	Phe	Thr	Pro	Gln
65					70					75					80
Glu	Leu	Gly	Arg	His	Glu	Phe	Ser	Cys	Gly	Met	Lys	Met	Gln	Lys	Gly
				85					90					95	
Ser	Tyr	Ile	Val	Val	Glu	Lys	Thr	Arg	Lys	Ser	Leu	Ser	Leu	Leu	Gln
			100					105					110		
Arg	Phe	Trp	Ile	Thr	Ser	Ile	Phe	Thr	Val	Pro	Leu	Val	Ile	Leu	Met
	115						120					125			
Ile	Gly	Met	Leu	Thr	Gly	Ser	Ile	Ser	His	Gln	Val	Met	His	Trp	Gly
	130					135					140				
Thr	Phe	Leu	Ala	Thr	Thr	Pro	Ile	Met	Leu	Val	Ala	Gly	Lys	Pro	Tyr
145					150					155					160
Ile	Gln	Ser	Ala	Trp	Ala	Ser	Phe	Lys	Lys	His	Asn	Ala	Asn	Met	Asp
				165					170					175	
Thr	Leu	Val	Ala	Leu	Gly	Thr	Leu	Val	Ala	Tyr	Phe	Tyr	Ser	Leu	Val
			180					185					190		
Ala	Leu	Phe	Ala	Gly	Leu	Pro	Val	Tyr	Phe	Glu	Ser	Ala	Gly	Phe	Ile
	195					200						205			
Leu	Phe	Phe	Val	Leu	Leu	Gly	Ala	Val	Phe	Glu	Glu	Lys	Met	Arg	Lys
	210					215				220					
Asn	Thr	Ser	Gln	Ala	Val	Glu	Lys	Leu	Leu	Asp	Leu	Gln	Ala	Lys	Thr
225					230					235					240
Ala	Glu	Val	Leu	Ser	Asp	Asp	Ser	Tyr	Val	Gln	Val	Pro	Leu	Glu	Gln
				245					250					255	
Val	Lys	Val	Gly	Asp	Leu	Ile	Arg	Val	Arg	Pro	Gly	Glu	Lys	Ile	Ala
			260					265					270		
Val	Asp	Gly	Val	Val	Val	Glu	Gly	Val	Ser	Ser	Ile	Asp	Glu	Ser	Met
	275						280					285			
Val	Thr	Gly	Glu	Ser	Leu	Pro	Val	Asp	Lys	Thr	Val	Gly	Asp	Thr	Val
	290					295					300				
Ile	Gly	Ser	Thr	Ile	Asn	His	Ser	Gly	Thr	Leu	Val	Phe	Arg	Ala	Glu
305					310					315					320
Lys	Val	Gly	Ser	Glu	Thr	Val	Leu	Ala	Gln	Ile	Val	Asp	Phe	Val	Lys
				325					330					335	
Lys	Ala	Gln	Thr	Ser	Arg	Ala	Pro	Ile	Gln	Asp	Leu	Thr	Asp	Lys	Ile
			340					345					350		
Ser	Gly	Ile	Phe	Val	Pro	Val	Val	Val	Ile	Leu	Gly	Ile	Met	Thr	Phe
	355						360					365			
Trp	Val	Trp	Phe	Val	Leu	Leu	Arg	Asp	Ser	Val	Val	Val	Leu	Gly	Ala
	370					375					380				
Ser	Phe	Val	Ser	Ser	Leu	Leu	Tyr	Gly	Val	Ala	Val	Leu	Ile	Ile	Ala
385					390					395					400
Cys	Pro	Cys	Ala	Leu	Gly	Leu	Ala	Thr	Pro	Thr	Ala	Leu	Met	Val	Gly

```

          405          410          415
Thr Gly Arg Ser Ala Lys Met Gly Val Leu Leu Lys Asn Gly Thr Val
          420          425          430
Leu Gln Glu Ile Gln Lys Val Gln Thr Leu Val Phe Asp Lys Thr Gly
          435          440          445
Thr Leu Thr Glu Gly Lys Pro Val Val Thr Asp Ile Ile Gly Asp Glu
          450          455          460
Val Glu Val Phe Gly Leu Ala Ala Ser Leu Glu Asp Ala Ser Gln His
465          470          475          480
Pro Leu Ala Glu Ala Ile Val Lys Arg Ala Ser Glu Ala Gly Leu Glu
          485          490          495
Phe Lys Thr Val Glu Asn Phe Gln Ala Leu His Gly Lys Gly Val Ser
          500          505          510
Gly Arg Ile Asn Gly Lys Gln Val Leu Leu Gly Asn Ala Lys Met Leu
          515          520          525
Asp Gly Met Asp Ile Ser Asn Thr Tyr Arg Asp Lys Leu Glu Glu Leu
          530          535          540
Glu Lys Gly
545

```

(2) INFORMATION FOR SEQ ID NO:4586:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 98 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...98

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4586:

```

Gly Val Ala Met Lys Leu Ser Asn Leu Leu Leu Phe Ala Gly Ala Ala
1          5          10          15
Ala Gly Ser Tyr Leu Val Thr Lys Asn Arg Gln Thr Ile Thr Asp Glu
          20          25          30
Val Leu Asn Thr Thr Asp Arg Val Gln Ala Ile Lys Asp Asp Val Asp
          35          40          45
Ile Ile Gln Asn Ser Leu Gln Ile Ile Asp Gln Gln Lys Glu Leu Ile
          50          55          60
Lys Glu Tyr Gln Glu Asp Leu Thr Tyr Lys Phe Lys Val Leu Glu Lys
65          70          75          80
Asp Ile Gln Thr Arg Leu Ala Val Ile Lys Glu Met Gln Gly Thr Glu
          85          90          95
Asp Lys

```

(2) INFORMATION FOR SEQ ID NO:4587:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 194 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...194
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4587:

```

Lys Asn Ala Ile Met Lys Gly Met Lys Tyr His Asp Tyr Ile Trp Asp
1      5      10      15
Leu Gly Gly Thr Leu Leu Asp Asn Tyr Glu Thr Ser Thr Ala Ala Phe
      20      25      30
Val Glu Thr Leu Ala Leu Tyr Gly Ile Thr Gln Asp His Asp Ser Val
      35      40      45
Tyr Gln Ala Leu Lys Val Ser Thr Pro Phe Ala Ile Glu Thr Phe Ala
      50      55      60
Pro Asn Leu Glu Asn Phe Leu Glu Lys Tyr Lys Glu Asn Glu Ala Arg
65      70      75      80
Glu Leu Glu His Pro Ile Leu Phe Glu Gly Val Ser Asp Leu Leu Glu
      85      90      95
Val Ile Ser Asn Gln Gly Gly Arg His Phe Leu Val Ser His Arg Asn
      100     105     110
Asp Gln Val Leu Glu Ile Leu Glu Lys Thr Ser Ile Ala Ala Tyr Phe
      115     120     125
Thr Glu Val Val Thr Ser Ser Ser Gly Phe Lys Arg Lys Pro Asn Pro
      130     135     140
Glu Ser Met Leu Tyr Leu Arg Glu Lys Tyr Gln Ile Ser Ser Gly Leu
145     150     155     160
Val Ile Gly Asp Arg Pro Ile Asp Ile Glu Ala Gly Gln Ala Ala Gly
      165     170     175
Leu Asp Thr His Leu Phe Thr Ser Ile Val Asn Leu Arg Gln Val Leu
      180     185     190
Asp Ile

```

(2) INFORMATION FOR SEQ ID NO:4588:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 355 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4588:

Lys	Asn	Ala	Ile	Ile	Glu	Arg	Thr	Ile	Ser	Lys	Glu	Asn	Lys	Met	Thr
1				5					10					15	
Lys	Pro	Ile	Ile	Leu	Thr	Gly	Asp	Arg	Pro	Thr	Gly	Lys	Leu	His	Ile
			20					25					30		
Gly	His	Tyr	Val	Gly	Ser	Leu	Lys	Asn	Arg	Val	Leu	Leu	Gln	Glu	Glu
		35					40					45			
Asp	Lys	Tyr	Asp	Met	Phe	Val	Phe	Leu	Ala	Asp	Gln	Gln	Ala	Leu	Thr
	50					55					60				
Asp	His	Ala	Lys	Asp	Pro	Gln	Thr	Ile	Val	Glu	Ser	Ile	Gly	Asn	Val
65					70					75					80
Ala	Leu	Asp	Tyr	Leu	Ala	Val	Gly	Leu	Asp	Pro	Asn	Lys	Ser	Thr	Ile
			85						90					95	
Phe	Ile	Gln	Ser	Gln	Ile	Pro	Glu	Leu	Ala	Glu	Leu	Ser	Met	Tyr	Tyr
			100					105					110		
Met	Asn	Leu	Val	Ser	Leu	Ala	Arg	Leu	Glu	Arg	Asn	Pro	Thr	Val	Lys
		115					120					125			
Thr	Glu	Ile	Ser	Gln	Lys	Gly	Phe	Gly	Glu	Ser	Ile	Pro	Thr	Gly	Phe
	130					135						140			
Leu	Val	Tyr	Pro	Ile	Ala	Gln	Ala	Ala	Asp	Ile	Thr	Ala	Phe	Lys	Ala
145					150					155					160
Asn	Tyr	Val	Pro	Val	Gly	Thr	Asp	Gln	Lys	Pro	Met	Ile	Glu	Gln	Thr
				165					170					175	
Arg	Glu	Ile	Val	Arg	Ser	Phe	Asn	Asn	Ala	Tyr	Asn	Cys	Asp	Val	Leu
			180					185					190		
Val	Glu	Pro	Glu	Gly	Ile	Tyr	Pro	Asp	Asn	Glu	Arg	Ala	Gly	Arg	Leu
		195					200					205			
Pro	Gly	Leu	Asp	Gly	Asn	Ala	Lys	Met	Ser	Lys	Ser	Leu	Asn	Asn	Gly
	210					215						220			
Ile	Tyr	Leu	Ala	Asp	Asp	Ala	Asp	Thr	Leu	Arg	Lys	Lys	Val	Met	Ser
225					230					235					240
Met	Tyr	Thr	Asp	Pro	Asp	His	Ile	Arg	Val	Glu	Asp	Pro	Gly	Lys	Ile
			245						250					255	
Glu	Gly	Asn	Met	Val	Phe	His	Tyr	Leu	Asp	Val	Phe	Gly	Arg	Pro	Glu
		260						265					270		
Asp	Ala	Gln	Glu	Ile	Ala	Asp	Met	Lys	Glu	Arg	Tyr	Gln	Arg	Gly	Gly
	275						280					285			
Leu	Gly	Asp	Val	Lys	Thr	Lys	Arg	Tyr	Leu	Leu	Glu	Ile	Leu	Glu	Arg
	290					295					300				
Glu	Leu	Gly	Pro	Ile	Arg	Glu	Arg	Arg	Ile	Glu	Phe	Ala	Lys	Asp	Met
305					310					315					320
Gly	Glu	Val	Tyr	Asn	Met	Ile	Gln	Lys	Gly	Ser	Glu	Arg	Ala	Arg	Glu
			325						330					335	
Val	Ala	Gly	Gln	Thr	Leu	Ser	Glu	Val	Lys	Gly	Ala	Met	Gly	Leu	His
		340						345					350		
Tyr	Phe	Asn													
		355													

(2) INFORMATION FOR SEQ ID NO:4589:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 146 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...146
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4589:

```

Lys Cys Ala Ile Ile Glu Gly Gly Lys Gly Gly Phe Ser Asp Ile Arg
1      5      10      15
Val Ser Ala Gln Leu Met Ile Cys Gln Phe Ile Arg Asp Met Leu Asp
      20      25      30
Leu Pro Ala Lys Asn Val Thr Ile Leu Glu Gly Ser Asn Ile His Val
      35      40      45
Leu Pro Ser Met Pro Tyr Ser Ala Gln Asp Phe Tyr Thr Ser Ile Asp
      50      55      60
Val Leu Ala Glu Leu Asp Asn Gly Ile Gln Val Ile Ile Glu Ile Gln
65      70      75      80
Val His His Gln Asn Phe Phe Ile Asn Arg Leu Trp Ala Tyr Leu Cys
      85      90      95
Ser Gln Val Asn Gln Asn Leu Glu Lys Ile Arg Gln Arg Glu Gly Asp
      100     105     110
Thr His Gln Ser Tyr Lys Gln Ile Ala Pro Val Tyr Ala Ile Ala Ile
      115     120     125
Val Asp Ser Asn Tyr Phe Ser Asp Asp Leu Ala Phe His Ser Phe Ile
130      135      140
Val Lys
145

```

(2) INFORMATION FOR SEQ ID NO:4590:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 163 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4590:

Tyr	Asn	Ala	Ile	Gln	Val	Gly	Phe	Asp	Asp	Lys	Arg	Glu	Val	Leu	Ser
1			5					10						15	
Asn	Lys	Pro	Ala	Lys	Gly	His	Val	Ala	Lys	Ala	Asn	Thr	Ala	Pro	Lys
		20					25					30			
Arg	Phe	Ile	Arg	Glu	Phe	Lys	Asn	Val	Glu	Gly	Leu	Glu	Val	Gly	Ala
	35					40						45			
Glu	Ile	Thr	Val	Glu	Thr	Phe	Ala	Ala	Gly	Asp	Val	Val	Asp	Val	Thr
	50					55				60					
Gly	Thr	Ser	Lys	Gly	Lys	Gly	Phe	Gln	Gly	Val	Ile	Lys	Arg	His	Gly
65				70					75					80	
Gln	Ser	Arg	Gly	Pro	Met	Ala	His	Gly	Ser	Arg	Tyr	His	Arg	Arg	Pro
		85						90					95		
Gly	Ser	Met	Gly	Pro	Val	Ala	Pro	Asn	Arg	Val	Phe	Lys	Gly	Lys	Asn
		100						105					110		
Leu	Ala	Gly	Arg	Met	Gly	Gly	Asp	Arg	Val	Thr	Ile	Gln	Asn	Leu	Glu
	115					120						125			
Val	Val	Gln	Val	Val	Pro	Glu	Lys	Asn	Val	Ile	Leu	Ile	Lys	Gly	Asn
	130					135					140				
Val	Pro	Gly	Ala	Lys	Lys	Ser	Leu	Ile	Thr	Ile	Lys	Ser	Ala	Val	Lys
145				150						155					160
Ala	Gly	Lys													

(2) INFORMATION FOR SEQ ID NO:4591:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4591:

Asn	Leu	Ile	Leu	Tyr	Ser	Ser	Lys	Ile	Ser	Ser	Ser	His	Val	Ser	Ile
1			5					10						15	
Ala	Leu	Pro	Tyr	Val	Trp	Leu	Leu	Thr	Ser	Ser	Val	Ser	Ser	Thr	Thr
		20					25					30			
Ser	Lys	Gln	Cys	Phe	Glu	Gln	Pro	Ala	Ala	Ser	Phe	Leu	Val	Cys	Ser
	35					40					45				
Leu	Ile	Leu	Ser	Ile	Arg	Phe	Thr	Gln	Asn	Gln	Gly	Phe			
	50				55						60				

(2) INFORMATION FOR SEQ ID NO:4592:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 567 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...567
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4592:

```

Lys Asn Tyr Ile Glu Val Asn Thr Met Ser Lys Glu Lys Ile Lys Val
1      5      10      15
Tyr Leu Tyr Thr Arg Val Ser Thr Ser Ile Gln Ile Glu Gly Tyr Ser
20      25      30
Leu Glu Ala Gln Lys Ser Arg Met Lys Ala Phe Ala Ile Tyr Asn Asp
35      40      45
Tyr Glu Ile Val Gly Glu Tyr Glu Asp Ala Gly Lys Ser Gly Lys Ser
50      55      60
Ile Glu Gly Arg Ile Gln Phe Asn Arg Met Met Glu Asp Ile Lys Ser
65      70      75      80
Gly Lys Asp Gly Val Ser Phe Val Leu Val Phe Lys Leu Ser Arg Phe
85      90      95
Ala Arg Asn Ala Ala Asp Val Leu Ser Thr Leu Gln Ile Met Gln Asp
100     105     110
Tyr Gly Val Asn Leu Ile Cys Val Glu Asp Gly Ile Asp Ser Ser Lys
115     120     125
Asp Ala Gly Lys Leu Met Ile Ser Val Leu Ser Ala Val Ala Glu Ile
130     135     140
Glu Arg Glu Asn Ile Arg Ile Gln Thr Met Glu Gly Arg Ile Gln Lys
145     150     155     160
Ala Arg Glu Gly Lys Trp Asn Gly Gly Phe Ala Pro Tyr Gly Tyr Lys
165     170     175
Leu Glu Asp Gly Lys Leu Phe Ile Asn Glu Glu Glu Ala Val Ala Ile
180     185     190
Arg Thr Ile Phe Asp Gln Tyr Val Asn Thr Thr Ile Gly Ala Asn Gly
195     200     205

Ile Ser Lys Tyr Leu Glu Asn His Gly Ile Arg Lys Ile Pro Arg Gln
210     215     220
Asn Gly Lys Asn Pro Leu Phe Asp Ala Gly Leu Ile Arg Lys Ile Leu
225     230     235     240
Lys Asn Pro Val Tyr Asn Gly Lys Ile Ala Phe Gly Arg Arg Thr Leu
245     250     255
Glu Lys Val His Gly Thr Arg Asn Glu Tyr Lys Gln Val Glu Gln Asp
260     265     270
Glu Tyr Leu Ile Ser Glu Gly Ile His Glu Ala Ile Val Ser Asp Glu
275     280     285
Val Trp Gln Ala Ala Gln Val Lys Leu Lys Ser Gln Ala Lys Lys Tyr

```

290		295		300
Glu His Val Asn Lys	Gly Lys Asp Thr Arg	Thr His Leu Leu Ser Gly		
305	310	315		320
Ile Val Lys Cys Pro	Ile Cys Gly Val Gly	Met Phe Gly Asn Lys Cys		
	325	330		335
Ile Lys Lys Lys Lys	Asp Gly Thr Lys Tyr	Lys Asp Phe Tyr Tyr Tyr		
	340	345		350
Gly Cys Lys His Arg	Gln Met Ile Arg Gly	His Lys Cys Thr Phe Ser		
	355	360		365
Lys Gln Ile Arg Glu	Glu Leu Leu Asp Asp	Ala Val Ala Glu Val Ile		
	370	375		380
Val Lys Ile Val Ser	Asn Pro Lys Phe Ala	Ser Met Met Gln Glu Lys		
385	390	395		400
Ile Asn Met Lys Val	Asp Thr Ser Glu Ile	Glu Lys Glu Ile Asp Asn		
	405	410		415
Tyr Gln Lys Glu Leu	Arg Lys Ser His Ser	Thr Lys Phe Lys Leu Ile		
	420	425		430
Glu Glu Ile Asp Asn	Leu Asp Val Glu Asp	Lys His Tyr Lys Arg Arg		
	435	440		445
Lys Gln Asp Leu Asp	Asp Arg Leu Tyr Arg	Met Tyr Asp Lys Ile Asp		
	450	455		460
Glu Leu Glu Ser Ser	Leu Ile Asp Ala Lys	Ala Lys Lys Gln Thr Ile		
465	470	475		480
Glu Ala Glu Lys Leu	Thr Gly Asp Asn Ile	Tyr Lys Val Leu Ile Tyr		
	485	490		495
Phe Asp Lys Leu Tyr	Lys Val Met Asn Asp	Val Glu Arg Arg Gln Leu		
	500	505		510
Ile Ser Ala Leu Ile	Ser Glu Ile Gln Val	Tyr Glu Glu Lys Gln Ser		
	515	520		525
Asn Gly Gln Trp Leu	Lys Ser Ile Thr Phe	Lys Leu Pro Ile Ile Glu		
530	535	540		
Glu Asn Leu Asn Ile	Gly Leu Asp Asn Asp	Glu Gln Val Glu Cys Val		
545	550	555		560
Ser Leu Leu Glu Lys	Arg Ser			
	565			

(2) INFORMATION FOR SEQ ID NO:4593:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 62 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...62

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4593:

Pro	Val	Leu	Phe	Ile	Ile	Pro	Gln	Asn	Asn	Lys	His	Lys	Ala	Asp	Ser
1				5					10					15	
Lys	Ile	Lys	Ile	Lys	Val	His	Ile	Leu	Ile	Phe	Phe	Ile	Asp	Phe	Leu
			20					25					30		
Ser	Ser	Val	Leu	Gly	Ser	Leu	Ser	Phe	Ser	Lys	Asn	Phe	Ile	Phe	Asn
		35					40					45			
Leu	Leu	Ser	Lys	Ile	Ser	Thr	Ile	Lys	Lys	Pro	Thr	Phe	Gln		
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:4594:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4594:

Cys	Ser	Tyr	Ile	Ile	Ser	Lys	Phe	Ser	Thr	Val	Glu	Val	Asp	Phe	Met
1				5					10					15	
Ser	Asp	Cys	Ile	Phe	Cys	Lys	Ile	Ile	Ala	Gly	Glu	Ile	Ala	Ala	Ser
			20					25					30		
Glu	Val	Tyr	Glu	Asp	Glu	Gln	Val	Leu	Ala	Phe	Leu	Asp	Ile	Ser	Gln
		35				40						45			
Val	Thr	Leu	Gly	His	Thr	Leu	Val	Val	Pro	Lys	Glu	His	Tyr	Arg	Asn
	50					55					60				
Leu	Leu	Glu	Met	Asn	Ala	Thr	Ser	Ala	Ser	Gln	Leu	Phe	Ala	Gln	Val
65				70					75					80	
Pro	Lys	Val	Ala	Gln	Lys	Val	Met	Lys	Val	Thr	Lys	Ala	Ala	Gly	Met
			85					90						95	
Asn	Ile	Ile	Ser	Asn	Cys	Glu	Glu	Val	Ala	Gly	Gln	Thr	Val	Phe	His
			100					105					110		
Thr	His	Val	His	Leu	Val	Pro	Arg	Tyr	Ser	Ala	Asp	Asp	Asp	Leu	Lys
	115					120					125				
Ile	Asp	Phe	Ile	Ala	His	Glu	Pro	Asp	Phe	Asp	Lys	Leu	Ala	Gln	Val
	130					135					140				
Ala	Glu	Thr	Ile	Lys	Asn	Ala									
145						150									

(2) INFORMATION FOR SEQ ID NO:4595:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 659 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...659

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4595:

Glu	Glu	Tyr	Met	Ser	Leu	Gln	Ser	Val	Asn	Ala	Ile	Arg	Phe	Leu	Gly
1				5					10					15	
Val	Asp	Ala	Ile	Asn	Lys	Ser	Asn	Ser	Gly	His	Pro	Gly	Ile	Val	Met
			20					25					30		
Gly	Ala	Ala	Pro	Met	Ala	Tyr	Ser	Leu	Phe	Thr	Lys	His	Leu	Arg	Ile
			35				40					45			
Thr	Pro	Glu	Gln	Pro	Asn	Trp	Ile	Asn	Arg	Asp	Arg	Phe	Ile	Leu	Ser
	50				55					60					
Ala	Gly	His	Gly	Ser	Met	Leu	Leu	Tyr	Ala	Leu	Leu	His	Leu	Thr	Gly
65					70				75						80
Tyr	Lys	Asp	Val	Ser	Met	Asp	Glu	Ile	Lys	Asn	Phe	Arg	Gln	Trp	Gly
				85					90					95	
Ser	Lys	Thr	Pro	Gly	His	Pro	Glu	Val	Thr	His	Thr	Ser	Gly	Val	Asp
			100					105					110		
Ala	Thr	Ser	Gly	Pro	Leu	Gly	Gln	Gly	Ile	Ser	Thr	Ala	Val	Gly	Phe
			115				120					125			
Ala	Gln	Ala	Glu	Arg	Phe	Leu	Ala	Ala	Lys	Tyr	Asn	Lys	Asp	Gly	Phe
	130					135					140				
Pro	Ile	Phe	Asp	His	Tyr	Thr	Tyr	Val	Ile	Ala	Gly	Asp	Gly	Asp	Phe
145					150					155					160
Met	Glu	Gly	Val	Ser	Ala	Glu	Ala	Ala	Ser	Tyr	Ala	Gly	His	Gln	Ala
				165					170					175	
Leu	Asp	Lys	Leu	Ile	Val	Leu	Tyr	Asp	Ser	Asn	Asp	Ile	Cys	Leu	Asp
			180					185					190		
Gly	Glu	Thr	Lys	Asp	Thr	Phe	Ser	Glu	Asn	Val	Arg	Ala	Arg	Tyr	Asp
			195				200					205			
Ala	Tyr	Gly	Trp	His	Thr	Val	Leu	Val	Glu	Asp	Gly	Thr	Asp	Leu	Ala
	210					215					220				
Ala	Ile	Ser	Thr	Ala	Ile	Glu	Thr	Ala	Lys	Phe	Ser	Gly	Lys	Pro	Ser
225					230					235					240
Leu	Ile	Glu	Val	Lys	Thr	Val	Ile	Gly	Tyr	Gly	Ser	Pro	Asn	Lys	Ser
				245					250					255	
Gly	Thr	Asn	Ala	Val	His	Gly	Ala	Pro	Leu	Gly	Ala	Glu	Glu	Thr	Gly
			260					265					270		
Ala	Thr	Arg	Lys	Phe	Leu	Gly	Trp	Asp	Tyr	Asp	Pro	Phe	Glu	Val	Pro
			275				280					285			
Glu	Glu	Val	Tyr	Ser	Asp	Phe	Lys	Thr	Asn	Val	Ala	Asp	Arg	Gly	Gln
	290					295					300				
Glu	Ala	Tyr	Asp	Ala	Trp	Ala	Ser	Leu	Val	Ser	Asp	Tyr	Lys	Val	Ala
305					310					315					320
Tyr	Pro	Glu	Val	Ala	Ser	Glu	Ile	Asp	Ala	Ile	Val	Ala	Gly	Lys	Ser
				325					330				335		
Pro	Val	Thr	Ile	Thr	Glu	Lys	Asp	Phe	Pro	Val	Tyr	Glu	Asn	Gly	Phe
			340					345					350		

Ser	Gln	Ala	Thr	Arg	Asn	Ser	Ser	Gln	Asp	Ala	Ile	Asn	Thr	Ala	Ala
		355					360					365			
Ala	Val	Leu	Pro	Thr	Phe	Leu	Gly	Gly	Ser	Ala	Asp	Leu	Ala	His	Ser
	370					375					380				
Asn	Met	Thr	Tyr	Ile	Lys	Ala	Asp	Gly	Leu	Gln	Asp	Lys	Tyr	Asn	Pro
385					390					395					400
Leu	Asn	Arg	Asn	Ile	Gln	Phe	Gly	Val	Arg	Glu	Phe	Ala	Met	Gly	Thr
			405						410					415	
Ile	Leu	Asn	Gly	Met	Ala	Leu	His	Gly	Gly	Leu	Arg	Val	Tyr	Gly	Gly
		420						425					430		
Thr	Phe	Phe	Val	Phe	Ser	Asp	Tyr	Val	Lys	Ala	Ala	Ile	Arg	Leu	Ser
	435					440						445			
Ala	Ile	Gln	Glu	Leu	Pro	Val	Thr	Tyr	Val	Phe	Thr	His	Asp	Ser	Ile
	450					455					460				
Ala	Val	Gly	Glu	Asp	Gly	Pro	Thr	His	Glu	Pro	Val	Glu	His	Leu	Ala
465					470					475					480
Gly	Leu	Arg	Ser	Met	Pro	Asn	Leu	Thr	Val	Ile	Arg	Pro	Ala	Asp	Ala
			485						490					495	
Arg	Glu	Thr	Gln	Ala	Ala	Trp	His	His	Ala	Leu	Thr	Ser	Thr	Thr	Thr
		500						505					510		
Pro	Thr	Val	Ile	Val	Leu	Thr	Arg	Gln	Asn	Leu	Val	Val	Glu	Glu	Gly
	515					520						525			
Thr	Asp	Phe	Gly	Lys	Val	Ala	Lys	Gly	Ala	Tyr	Val	Val	Tyr	Asp	Thr
	530					535					540				
Pro	Gly	Phe	Asp	Thr	Ile	Ile	Ala	Thr	Gly	Ser	Glu	Val	Asn	Leu	
545					550				555					560	
Ala	Ile	Lys	Ala	Ala	Lys	Glu	Leu	Val	Leu	Gln	Gly	Gly	Lys	Val	Arg
			565						570					575	
Val	Val	Ser	Met	Pro	Ser	Thr	Glu	Leu	Phe	Asp	Ala	Gln	Asp	Ala	Thr
		580						585					590		
Tyr	Lys	Glu	Asp	Ile	Leu	Pro	Ser	Lys	Thr	Arg	Arg	Arg	Val	Ala	Ile
	595					600						605			
Glu	Met	Ala	Ala	Thr	Gln	Ser	Trp	Tyr	Lys	Tyr	Val	Gly	Leu	Asp	Gly
	610					615					620				
Ala	Val	Ile	Gly	Ile	Asp	Ile	Phe	Gly	Ala	Ser	Ala	Pro	Ala	Gln	Thr
625					630					635					640
Val	Ile	Asp	Asn	Tyr	Gly	Phe	Thr	Val	Glu	Asn	Ile	Val	Ala	Gln	Val
			645						650					655	
Lys	Ser	Leu													

(2) INFORMATION FOR SEQ ID NO:4596:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 617 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4596:

Gln	Leu	His	Ile	Asn	Pro	Ala	Gln	Pro	Asn	Trp	Ile	Asn	Arg	Asp	Arg
1				5					10					15	
Phe	Ile	Leu	Ser	Ala	Gly	His	Gly	Ser	Met	Leu	Leu	Tyr	Ala	Leu	Leu
			20					25					30		
His	Leu	Ser	Gly	Phe	Glu	Asp	Val	Ser	Met	Asp	Glu	Ile	Lys	Ser	Phe
		35					40					45			
Arg	Gln	Trp	Gly	Ser	Lys	Thr	Pro	Gly	His	Pro	Glu	Phe	Gly	His	Thr
	50					55					60				
Ala	Gly	Ile	Asp	Ala	Thr	Thr	Gly	Pro	Leu	Gly	Gln	Gly	Ile	Ser	Thr
65					70					75					80
Ala	Thr	Gly	Phe	Ala	Gln	Ala	Glu	Arg	Phe	Leu	Ala	Ala	Lys	Tyr	Asn
				85					90					95	
Arg	Glu	Gly	Tyr	Asn	Ile	Phe	Asp	His	Tyr	Thr	Tyr	Val	Ile	Cys	Gly
			100					105					110		
Asp	Gly	Asp	Leu	Met	Glu	Gly	Val	Ser	Ser	Glu	Ala	Ala	Ser	Tyr	Ala
		115					120					125			
Gly	Leu	Gln	Lys	Leu	Asp	Lys	Leu	Val	Val	Leu	Tyr	Asp	Ser	Asn	Asp
	130					135					140				
Ile	Asn	Leu	Asp	Gly	Glu	Thr	Lys	Asp	Ser	Phe	Thr	Glu	Ser	Val	Arg
145					150					155					160
Asp	Arg	Tyr	Asn	Ala	Tyr	Gly	Trp	His	Thr	Ala	Leu	Val	Glu	Asn	Gly
			165						170					175	
Thr	Asp	Leu	Glu	Ala	Ile	His	Ala	Ala	Ile	Glu	Thr	Ala	Lys	Ala	Ser
		180						185					190		
Gly	Lys	Pro	Ser	Leu	Ile	Glu	Val	Lys	Thr	Val	Ile	Gly	Tyr	Gly	Ser
		195					200					205			
Pro	Asn	Lys	Gln	Gly	Thr	Asn	Ala	Val	His	Gly	Ala	Pro	Leu	Gly	Ala
	210					215					220				
Asp	Glu	Thr	Ala	Ser	Thr	Arg	Gln	Ala	Leu	Gly	Trp	Asp	Tyr	Glu	Pro
225					230					235					240
Phe	Glu	Ile	Pro	Glu	Gln	Val	Tyr	Ala	Asp	Phe	Lys	Glu	His	Val	Ala
				245					250					255	
Asp	Arg	Gly	Ala	Ser	Ala	Tyr	Gln	Ala	Trp	Thr	Lys	Leu	Val	Ala	Asp
		260						265					270		
Tyr	Lys	Glu	Ala	His	Pro	Glu	Leu	Ala	Ala	Glu	Val	Glu	Ala	Ile	Ile
		275					280					285			
Asp	Gly	Arg	Asp	Pro	Val	Glu	Val	Thr	Pro	Ala	Asp	Phe	Pro	Ala	Leu
	290					295					300				
Glu	Asn	Gly	Phe	Ser	Gln	Ala	Thr	Arg	Asn	Ser	Ser	Gln	Asp	Ala	Leu
305					310					315					320
Asn	Val	Val	Ala	Ala	Lys	Leu	Pro	Thr	Phe	Leu	Gly	Gly	Ser	Ala	Asp
			325						330					335	
Leu	Ala	His	Ser	Asn	Met	Thr	Tyr	Ile	Lys	Thr	Asp	Gly	Leu	Gln	Asp
		340						345					350		
Asp	Ala	Asn	Arg	Leu	Asn	Arg	Asn	Ile	Gln	Phe	Gly	Val	Arg	Glu	Phe
		355					360					365			
Ala	Met	Gly	Thr	Ile	Leu	Asn	Gly	Met	Ala	Leu	His	Gly	Gly	Leu	Arg
	370					375					380				
Val	Tyr	Gly	Gly	Thr	Phe	Phe	Val	Phe	Ser	Asp	Tyr	Val	Lys	Ala	Ala
385					390					395					400
Val	Arg	Leu	Ser	Ala	Leu	Gln	Gly	Leu	Pro	Val	Thr	Tyr	Val	Phe	Thr
			405						410					415	
His	Asp	Ser	Ile	Ala	Val	Gly	Glu	Asp	Gly	Pro	Thr	His	Glu	Pro	Val

		420				425				430					
Glu	His	Leu	Ala	Gly	Leu	Arg	Ala	Met	Pro	Asn	Leu	Asn	Val	Phe	Arg
		435					440					445			
Pro	Ala	Asp	Ala	Arg	Glu	Thr	Gln	Ala	Ala	Trp	Tyr	Leu	Ala	Val	Thr
		450					455					460			
Ser	Glu	Lys	Thr	Pro	Thr	Ala	Leu	Val	Leu	Thr	Arg	Gln	Asn	Leu	Thr
465						470					475				480
Val	Glu	Asp	Gly	Thr	Asp	Phe	Asp	Lys	Val	Ala	Lys	Gly	Ala	Tyr	Val
			485						490					495	
Val	Tyr	Glu	Asn	Ala	Ala	Asp	Phe	Asp	Thr	Ile	Leu	Ile	Ala	Thr	Gly
			500					505					510		
Ser	Glu	Val	Asn	Leu	Ala	Val	Ser	Ala	Ala	Lys	Glu	Leu	Ala	Ser	Gln
		515					520					525			
Gly	Glu	Lys	Ile	Arg	Val	Val	Ser	Met	Pro	Ser	Thr	Asp	Val	Phe	Asp
		530				535					540				
Lys	Gln	Asp	Ala	Ala	Tyr	Lys	Glu	Glu	Ile	Leu	Pro	Asn	Ala	Val	Arg
545					550					555					560
Arg	Arg	Val	Ala	Val	Glu	Met	Gly	Ala	Ser	Gln	Asn	Trp	Tyr	Lys	Tyr
			565					570						575	
Val	Gly	Leu	Asp	Gly	Ala	Val	Leu	Gly	Ile	Asp	Thr	Phe	Gly	Ala	Ser
		580					585					590			
Ala	Pro	Ala	Pro	Lys	Val	Leu	Ala	Glu	Tyr	Gly	Phe	Thr	Val	Glu	Asn
		595				600					605				
Leu	Val	Lys	Ile	Val	Arg	Asn	Leu	Lys							
		610				615									

(2) INFORMATION FOR SEQ ID NO:4597:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 107 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4597:

Glu	Val	His	Met	Asn	Gln	Glu	Glu	Leu	Gln	Val	Ala	Ala	Phe	Glu	Ile
1				5				10					15		
Ile	Leu	His	Ser	Gly	Asn	Ala	Arg	Ser	Glu	Ile	His	Glu	Ala	Phe	Ala
			20				25					30			
Lys	Met	Arg	Glu	Gly	Ser	Phe	Asp	Asp	Ala	Glu	Ser	Lys	Leu	Asn	Gln
		35				40					45				
Ser	Asn	Glu	Ile	Ile	Leu	Glu	Ala	His	His	Ala	Gln	Thr	Lys	Leu	Leu
		50			55					60					
Gln	Glu	Tyr	Ala	Ser	Gly	Val	Glu	Ile	Lys	Ile	Glu	Ile	Ile	Met	Val
65				70				75						80	
His	Ala	Gln	Asp	His	Leu	Met	Thr	Thr	Met	Thr	Leu	Leu	Glu	Val	Ala

	85	90	95
Lys	Glu	Met	Leu
	Ala	Leu	Tyr
		Lys	Lys
		Val	Asn
	100	105	

(2) INFORMATION FOR SEQ ID NO:4598:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 112 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...112
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4598:

Thr	Cys	His	Ile	Glu	Ile	Leu	Pro	Phe	His	Phe	Ile	Arg	Ser	Thr	Asp
1				5					10					15	
Phe	Asp	Leu	Ser	Leu	Ser	Phe	Val	Lys	Lys	Phe	Phe	Ser	Phe	Thr	Leu
		20						25					30		
Asn	Asp	Leu	Tyr	Ser	Met	Lys	Ile	Lys	Glu	Gln	Thr	Arg	Lys	Leu	Thr
		35					40					45			
Ala	Asp	Cys	Ser	Lys	His	Cys	Phe	Glu	Pro	Val	Asp	Lys	Thr	Asp	Glu
		50					55				60				
Val	Ser	Ser	Lys	His	Cys	Phe	Glu	Val	Val	Asp	Arg	Thr	Asp	Glu	Val
65				70						75				80	
Ser	Asn	His	Thr	Tyr	Gly	Lys	Val	Lys	Leu	Thr	Trp	Phe	Glu	Glu	Ile
			85						90				95		
Phe	Glu	Glu	Tyr	Tyr	Leu	Ile	Lys	Phe	Val	Asn	Ile	Met	Ser	Leu	Leu
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:4599:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 360 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4599:

Asn	Ser	His	Met	Lys	Arg	Ile	Gln	Leu	Asn	Met	Asn	Glu	Thr	Lys	Lys	
1				5					10					15		
Tyr	Leu	Val	Ile	Lys	Ala	Ile	Ala	Gln	Gly	Lys	Lys	Thr	Lys	Lys	Arg	
				20				25					30			
Ala	Cys	Val	Glu	Leu	Asn	Leu	Ser	Glu	Arg	Gln	Ile	Asn	Arg	Leu	Leu	
				35			40					45				
Leu	Ala	Tyr	Gln	Gln	Lys	Glu	Lys	Glu	Ala	Phe	Arg	His	Gly	Asn	Arg	
						55					60					
Asn	Arg	Lys	Pro	Lys	His	Ala	Ile	Pro	Asp	Glu	Ile	Lys	Glu	Arg	Ile	
65					70				75						80	
Leu	Lys	Lys	Tyr	Leu	Ser	Tyr	Gln	Thr	Tyr	Lys	Pro	Asn	Val	Arg	His	
				85					90					95		
Phe	Cys	Glu	Leu	Leu	Ala	Glu	Glu	Glu	Gly	Ile	Gln	Leu	Ser	Asp	Thr	
				100				105					110			
Thr	Val	Arg	Lys	Ile	Leu	Tyr	Lys	Lys	Asn	Ile	Leu	Ser	Pro	Lys	Ser	
				115			120						125			
His	Arg	Lys	Thr	Lys	Lys	Arg	Val	Arg	Lys	Gln	Ala	Lys	Leu	Asn	Pro	
						135					140					
Lys	Gln	Pro	Leu	Asp	Asn	Pro	Ile	Leu	Pro	Thr	Ala	Glu	Asn	Phe	Leu	
145					150					155					160	
Glu	Asp	Pro	Lys	Lys	Val	His	Pro	Ser	Arg	Pro	Arg	Lys	Lys	Phe	Ala	
				165					170					175		
Gly	Glu	Leu	Ile	Gln	Met	Asp	Ala	Ser	Pro	His	Ala	Trp	Phe	Gly	Val	
			180					185					190			
Glu	Thr	Ser	Asn	Leu	His	Leu	Ala	Ile	Asp	Asp	Ala	Ser	Gly	Asn	Ile	
				195				200					205			
Leu	Gly	Ala	Tyr	Phe	Asp	Lys	Gln	Glu	Thr	Leu	Asn	Ala	Tyr	Tyr	His	
	210					215					220					
Val	Leu	Glu	Gln	Ile	Leu	Ala	Asn	His	Gly	Ile	Pro	Leu	Gln	Ile	Lys	
225					230					235					240	
Thr	Asp	Lys	Arg	Thr	Val	Phe	Thr	Tyr	Gln	Ala	Ser	Asn	Ser	Lys	Lys	
				245					250					255		
Met	Glu	Asp	Asp	Thr	His	Thr	Gln	Phe	Gly	Tyr	Ala	Cys	His	Gln	Leu	
			260					265					270			
Gly	Ile	Leu	Leu	Glu	Thr	Thr	Ser	Ile	Pro	Gln	Ala	Lys	Gly	Arg	Val	
		275					280					285				
Glu	Arg	Leu	Asn	Gln	Thr	Leu	Gln	Ser	Arg	Leu	Pro	Ile	Glu	Leu	Glu	
	290					295					300					
Arg	Asn	Asn	Ile	His	Thr	Leu	Glu	Glu	Ala	Asn	Thr	Phe	Leu	Pro	Ser	
305					310					315					320	
Tyr	Ile	Gln	Thr	Phe	Asn	Glu	Gln	Phe	Gly	Asn	Lys	Thr	Lys	Leu	Ser	
				325					330					335		
Val	Phe	Glu	Glu	Ala	Pro	Lys	Pro	Ser	Glu	Arg	Asn	Leu	Ile	Leu	Ala	
				340				345					350			
Arg	Leu	Ala	Gly	Glu	Ser	Arg	Arg									
			355				360									

(2) INFORMATION FOR SEQ ID NO:4600:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 400 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...400

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4600:

Phe	Lys	His	Met	Glu	Ala	Asn	Met	Lys	His	Leu	Lys	Thr	Phe	Tyr	Lys
1				5				10						15	
Lys	Trp	Phe	Gln	Leu	Leu	Val	Val	Ile	Val	Ile	Ser	Phe	Phe	Ser	Gly
			20					25					30		
Ala	Leu	Gly	Ser	Phe	Ser	Ile	Thr	Gln	Leu	Thr	Gln	Lys	Ser	Ser	Val
		35					40					45			
Asn	Asn	Ser	Asn	Asn	Asn	Ser	Thr	Ile	Thr	Gln	Thr	Ala	Tyr	Lys	Asn
	50					55					60				
Glu	Asn	Ser	Thr	Thr	Gln	Ala	Val	Asn	Lys	Val	Lys	Asp	Ala	Val	Val
65					70					75					80
Ser	Val	Ile	Thr	Tyr	Ser	Ala	Asn	Arg	Gln	Asn	Ser	Val	Phe	Gly	Asn
			85					90						95	
Asp	Asp	Thr	Asp	Thr	Asp	Ser	Gln	Arg	Ile	Ser	Ser	Glu	Gly	Ser	Gly
		100						105					110		
Val	Ile	Tyr	Lys	Lys	Asn	Asp	Lys	Glu	Ala	Tyr	Ile	Val	Thr	Asn	Asn
		115					120					125			
His	Val	Ile	Asn	Gly	Ala	Ser	Lys	Val	Asp	Ile	Arg	Leu	Ser	Asp	Gly
	130					135					140				
Thr	Lys	Val	Pro	Gly	Glu	Ile	Val	Gly	Ala	Asp	Thr	Phe	Ser	Asp	Ile
145					150					155					160
Ala	Val	Val	Lys	Ile	Ser	Ser	Glu	Lys	Val	Thr	Thr	Val	Ala	Glu	Phe
			165					170						175	
Gly	Asp	Ser	Ser	Lys	Leu	Thr	Val	Gly	Glu	Thr	Ala	Ile	Ala	Ile	Gly
		180						185					190		
Ser	Pro	Leu	Gly	Ser	Glu	Tyr	Ala	Asn	Thr	Val	Thr	Gln	Gly	Ile	Val
	195						200					205			
Ser	Ser	Leu	Asn	Arg	Asn	Val	Ser	Leu	Arg	Ser	Glu	Asp	Gly	Gln	Ala
	210				215						220				
Ile	Ser	Thr	Lys	Ala	Ile	Gln	Thr	Asp	Thr	Ala	Ile	Asn	Pro	Gly	Asn
225					230					235					240
Ser	Gly	Gly	Pro	Leu	Ile	Asn	Ile	Gln	Gly	Gln	Val	Ile	Gly	Ile	Thr
			245					250						255	
Ser	Ser	Lys	Ile	Ala	Thr	Asn	Gly	Gly	Thr	Ser	Val	Glu	Gly	Leu	Gly
		260					265						270		
Phe	Ala	Ile	Pro	Ala	Asn	Asp	Ala	Ile	Asn	Ile	Ile	Glu	Gln	Leu	Glu
	275					280						285			
Lys	Asn	Gly	Lys	Val	Thr	Arg	Pro	Ala	Leu	Gly	Ile	Gln	Met	Val	Asn
	290					295					300				
Leu	Ser	Asn	Val	Ser	Thr	Ser	Asp	Ile	Arg	Arg	Leu	Asn	Ile	Pro	Ser
305					310					315					320
Asn	Val	Thr	Ser	Gly	Val	Val	Val	Arg	Ser	Val	Gln	Ser	Asn	Met	Pro
			325					330						335	
Ala	Asn	Gly	His	Leu	Glu	Lys	Tyr	Asp	Val	Ile	Thr	Lys	Val	Asp	Asp
		340						345					350		

Lys	Glu	Ile	Ala	Ser	Ser	Thr	Asp	Leu	Gln	Ser	Ala	Leu	Tyr	Asn	His
		355					360					365			
Ser	Ile	Gly	Asp	Thr	Ile	Lys	Ile	Thr	Tyr	Tyr	Arg	Asn	Gly	Lys	Glu
	370					375					380				
Glu	Thr	Thr	Ser	Ile	Lys	Leu	Asn	Lys	Ser	Ser	Gly	Asp	Leu	Glu	Ser
385					390					395					400

(2) INFORMATION FOR SEQ ID NO:4601:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 310 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...310

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4601:

Pro	Met	Ile	Leu	Thr	Val	Thr	Met	Asn	Pro	Ser	Ile	Asp	Ile	Ser	Tyr
1				5				10				15			
Pro	Leu	Asp	Glu	Leu	Lys	Ile	Asp	Thr	Val	Asn	Arg	Val	Val	Asp	Val
		20					25					30			
Thr	Lys	Thr	Ala	Gly	Gly	Lys	Gly	Leu	Asn	Val	Thr	Arg	Val	Leu	Ser
	35					40						45			
Glu	Phe	Gly	Asp	Ser	Val	Leu	Ala	Thr	Gly	Leu	Val	Gly	Gly	Lys	Leu
	50					55					60				
Gly	Glu	Phe	Leu	Val	Glu	His	Ile	Asp	Asp	Gln	Val	Lys	Lys	Asp	Phe
65					70				75					80	
Phe	Ser	Ile	Gln	Gly	Glu	Thr	Arg	Asn	Cys	Ile	Ala	Ile	Leu	His	Gly
			85					90					95		
Asp	Asn	Gln	Thr	Glu	Val	Leu	Glu	Lys	Gly	Pro	Glu	Val	Leu	Glu	Gln
		100						105					110		
Glu	Gly	Gln	Asp	Phe	Leu	Glu	His	Phe	Lys	Lys	Leu	Leu	Glu	Ser	Val
	115						120					125			
Glu	Val	Val	Ala	Ile	Ser	Gly	Ser	Leu	Pro	Ala	Gly	Leu	Pro	Val	Asp
	130					135					140				
Tyr	Tyr	Ala	Ser	Leu	Val	Glu	Leu	Ala	Asn	Gln	Ala	Gly	Lys	Leu	Val
145					150					155					160
Val	Leu	Asp	Cys	Ser	Gly	Ala	Ala	Leu	Gln	Ala	Val	Leu	Glu	Ser	Pro
			165						170					175	
His	Lys	Pro	Thr	Val	Ile	Lys	Pro	Asn	Asn	Glu	Glu	Leu	Ser	Gln	Leu
		180						185					190		
Leu	Gly	Arg	Glu	Val	Ser	Glu	Asp	Leu	Glu	Glu	Leu	Lys	Glu	Val	Leu
	195						200					205			
Gln	Glu	Ser	Leu	Phe	Thr	Gly	Ile	Glu	Trp	Ile	Ile	Val	Ser	Leu	Gly
	210					215					220				
Ala	Asn	Gly	Thr	Phe	Ala	Lys	His	Gly	Asp	Thr	Phe	Tyr	Lys	Val	Asp
225					230					235					240

Ile	Pro	Arg	Ile	Gln	Val	Val	Asn	Pro	Val	Gly	Ser	Gly	Asp	Ser	Thr
				245					250					255	
Val	Ala	Gly	Ile	Ser	Ser	Gly	Leu	Leu	His	Lys	Glu	Ser	Asp	Ala	Gly
			260				265						270		
Leu	Leu	Ile	Lys	Ala	Asn	Val	Leu	Gly	Met	Leu	Asn	Ala	Gln	Glu	Lys
		275					280					285			
Met	Thr	Gly	His	Val	Asn	Met	Ala	Asn	Tyr	Gln	Ala	Leu	Tyr	Asp	Gln
	290					295					300				
Leu	Ile	Val	Lys	Glu	Val										
305					310										

(2) INFORMATION FOR SEQ ID NO:4602:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4602:

Glu	Thr	Asn	Met	Phe	Ile	Ser	Ile	Ser	Ala	Gly	Ile	Val	Thr	Phe	Leu
1				5					10					15	
Leu	Thr	Leu	Val	Gly	Ile	Pro	Ala	Phe	Ile	Gln	Phe	Tyr	Arg	Lys	Ala
			20				25						30		
Gln	Ile	Thr	Gly	Gln	Gln	Met	His	Glu	Asp	Val	Lys	Gln	His	Gln	Ala
		35				40						45			
Lys	Ala	Gly	Thr	Pro	Thr	Met	Gly	Gly	Leu	Val	Phe	Leu	Ile	Thr	Ser
	50				55						60				
Val	Leu	Val	Ala	Phe	Phe	Phe	Ala	Leu	Phe	Ser	Ser	Gln	Phe	Ser	Asn
65				70					75						80
Asn	Val	Gly	Met	Ile	Leu	Phe	Ile	Leu	Val	Leu	Tyr	Gly	Leu	Val	Gly
			85					90					95		
Phe	Leu	Asp	Asp	Phe	Leu	Lys	Val	Phe	Arg	Lys	Ile	Asn	Glu	Gly	Leu
		100					105					110			
Asn	Pro	Lys	Gln	Lys	Leu	Ala	Leu	Gln	Leu	Leu	Gly	Gly	Val	Ile	Phe
	115					120						125			
Tyr	Leu	Phe	Tyr	Glu	Arg	Gly	Gly	Asp	Met	Leu	Ser	Val	Phe	Gly	Tyr
	130					135					140				
Gln	Val	His	Leu	Gly	Ile	Phe	Tyr	Ile	Val	Phe	Ala	Leu	Phe	Trp	Leu
145				150						155					160
Val	Gly	Phe	Ser	Asn	Ala	Val	Asn	Leu	Thr	Asp	Gly	Val	Asp	Gly	Leu
			165					170					175		
Ala	Ser	Ile	Ser	Val	Val	Ile	Ser	Leu	Ser	Ala	Tyr	Gly	Val	Ile	Ala
		180					185						190		
Tyr	Val	Gln	Gly	Gln	Met	Asp	Ile	Leu	Leu	Val	Ile	Leu	Ala	Met	Ile
	195						200						205		

Gly	Gly	Leu	Leu	Ser	Phe	Phe	Ile	Phe	Asn	His	Lys	Pro	Ala	Lys	Ile
210						215					220				
Phe	Met	Gly	Asp	Val	Gly	Ser	Leu	Ala	Leu	Gly	Gly	Met	Leu	Ala	Ala
225					230					235					240
Ile	Ser	Met	Ala	Leu	His	Gln	Glu	Trp	Thr	Leu	Leu	Ile	Ile	Gly	Ile
				245					250					255	
Val	Tyr	Val	Phe	Glu	Thr	Thr	Ser	Val	Met	Met	Gln	Val	Ser	Tyr	Phe
			260					265					270		
Lys	Leu	Thr	Gly	Gly	Lys	Arg	Ile	Phe	Arg	Met	Thr	Pro	Val	His	His
		275					280					285			
His	Phe	Glu	Leu	Gly	Gly	Leu	Ser	Gly	Lys	Gly	Asn	Pro	Trp	Ser	Glu
	290					295					300				
Trp	Lys	Val	Asp	Phe	Phe	Phe	Trp	Gly	Val	Gly	Leu	Leu	Ala	Ser	Leu
305					310					315					320
Leu	Thr	Leu	Ala	Ile	Leu	Tyr	Leu	Met							
				325											

(2) INFORMATION FOR SEQ ID NO:4603:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4603:

Arg	Asn	Asn	Met	Met	Lys	Ser	Leu	Glu	Gly	Val	Ile	Asp	Met	Ser	Ser
1			5						10					15	
Lys	Ala	Asn	His	Ala	Lys	Thr	Ala	Ile	Cys	Gly	Ile	Ile	Asn	Val	Thr
		20					25					30			
Pro	Asp	Ser	Phe	Ser	Asp	Gly	Gly	Gln	Phe	Phe	Ala	Leu	Glu	Gln	Ala
		35				40						45			
Leu	Gln	Gln	Ala	Arg	Lys	Leu	Ile	Ala	Glu	Gly	Ala	Ser	Met	Leu	Asp
	50				55						60				
Ile	Gly	Gly	Glu	Ser	Thr	Arg	Pro	Gly	Ser	Ser	Tyr	Val	Glu	Val	Glu
65				70					75					80	
Ile	Glu	Glu	Glu	Ile	Gln	Arg	Val	Val	Pro	Val	Ile	Lys	Ala	Ile	Arg
			85					90					95		
Lys	Glu	Ser	Asp	Val	Leu	Ile	Ser	Ile	Asp	Thr	Trp	Lys	Ser	Gln	Val
		100					105						110		
Ala	Glu	Ala	Ala	Leu	Ala	Ala	Gly	Ala	Asn	Leu	Val	Asn	Asp	Ile	Thr
		115				120						125			
Gly	Leu	Met	Gly	Asp	Glu	Lys	Met	Ala	His	Val	Ile	Ala	Lys	Asp	Gly
	130					135					140				
Ala	Lys	Val	Val	Ile	Met	Phe	Asn	Leu	Val	Met	Ala	Arg	Pro	Gln	His
145					150				155						160

Pro	Ser	Ser	Leu	Ile	Phe	Pro	His	Phe	Gly	Phe	Asn	Gln	Ala	Phe	Thr
				165					170					175	
Glu	Glu	Glu	Leu	Ala	Asp	Phe	Glu	Thr	Leu	Pro	Ile	Glu	Glu	Leu	Met
			180					185					190		
Glu	Thr	Phe	Phe	Glu	Arg	Ala	Leu	Ala	Arg	Ala	Asn	Gln	Ala	Gly	Ile
		195					200					205			
Ala	Gln	Glu	Asn	Ile	Leu	Leu	Asp	Pro	Gly	Ile	Gly	Phe	Gly	Leu	Thr
	210					215					220				
Lys	Lys	Glu	Asn	Leu	Leu	Leu	Arg	Asp	Leu	Asp	Lys	Leu	His	Gln	
225				230					235					240	
Lys	Gly	Tyr	Pro	Ile	Phe	Leu	Gly	Val	Ser	Arg	Lys	Arg	Phe	Val	Ile
				245					250					255	
Asn	Ile	Leu	Glu	Glu	Asn	Gly	Phe	Glu	Val	Asn	Pro	Glu	Thr	Glu	Leu
			260					265					270		
Gly	Phe	His	Asn	Trp	Asp	Thr	Ala	Ser	Ala	His	Val	Thr	Ser	Ile	Ala
		275					280					285			
Ala	Arg	Gln	Gly	Val	Glu	Val	Val	Arg	Val	His	Asp	Val	Ala	Ser	His
	290					295					300				
Lys	Met	Ala	Val	Glu	Ile	Ala	Ser	Ala	Ile	Arg	Leu	Ala	Asp	Glu	Ala
305					310					315					320
Glu	Asn	Leu	Asp	Leu	Lys	Gln	Tyr	Lys							
				325											

(2) INFORMATION FOR SEQ ID NO:4604:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 690 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...690

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4604:

Val	Asn	Asn	Met	Ser	Phe	Lys	Val	Leu	His	Lys	Gly	Tyr	Gln	His	Ile
1			5					10					15		
Arg	Leu	Ser	Ser	Ser	Phe	Ser	Leu	Thr	Leu	Asp	Ile	Gln	Asn	Tyr	Leu
			20					25				30			
Arg	Ser	Leu	Ala	Arg	Asp	Glu	Lys	Gly	Ile	Glu	Ser	Ile	Gln	Phe	Tyr
		35				40					45				
Met	Asp	Gln	Gln	His	Phe	Thr	Leu	Arg	Ile	Lys	Glu	Gly	Phe	Ser	Val
	50					55				60					
Leu	Asp	Asn	Ala	Glu	Ala	Phe	Leu	Lys	Arg	Ile	Asp	Lys	Gly	Lys	Val
65				70						75				80	
Ser	Glu	Leu	Met	Thr	Leu	Pro	Ile	Arg	Arg	Glu	Glu	Ser	Ala	Tyr	Ser
			85					90					95		
Ile	Val	Ser	Gly	Ala	Ala	Val	Lys	Arg	Val	Leu	Phe	Arg	Ser	Phe	Val
			100					105					110		

Pro	Tyr	Pro	Ile	Arg	Tyr	Ile	Trp	Thr	Ser	Tyr	Gln	Ala	Leu	Gly	Tyr
		115					120					125			
Ile	Arg	Glu	Ala	Tyr	Gln	Thr	Ile	Ala	Arg	Lys	Glu	Leu	Thr	Met	Glu
	130					135					140				
Val	Leu	Asp	Cys	Ser	Ala	Ile	Leu	Leu	Ser	Leu	Phe	Met	Asn	Gln	Ser
145					150					155					160
Lys	Thr	Ala	Ser	Asn	Ile	Met	Phe	Met	Leu	Asp	Leu	Gly	Asn	His	Leu
				165					170					175	
Asp	Gln	Trp	Ser	Leu	Lys	Lys	Thr	Ala	Thr	Asp	Leu	Glu	Gln	Ser	Leu
			180					185						190	
Leu	Ala	Lys	Glu	Ser	Asp	Val	Phe	Leu	Val	Gln	Gly	Asp	Thr	Val	Val
		195					200					205			
Ser	Ile	Lys	Ser	Ser	Asp	Val	Gln	Ile	Gly	Asp	Val	Leu	Ile	Leu	Ser
	210					215					220				
Gln	Gly	Asn	Glu	Ile	Leu	Phe	Asp	Gly	Gln	Val	Val	Ser	Gly	Leu	Gly
225					230					235					240
Met	Val	Asn	Glu	Ser	Ser	Leu	Thr	Gly	Glu	Ser	Phe	Pro	Val	Glu	Lys
				245					250					255	
Arg	Glu	Ser	Asp	Leu	Val	Cys	Ala	Asn	Thr	Val	Leu	Glu	Thr	Gly	Glu
			260					265						270	
Leu	Arg	Ile	Arg	Val	Thr	Asp	Asn	Gln	Met	Asn	Ser	Arg	Ile	Leu	Gln
	275						280					285			
Leu	Ile	Glu	Leu	Met	Lys	Lys	Ser	Glu	Glu	Asn	Lys	Lys	Thr	Lys	Gln
	290					295					300				
Arg	Tyr	Phe	Ile	Lys	Met	Ala	Asp	Lys	Val	Val	Lys	Tyr	Asn	Phe	Leu
305					310					315					320
Gly	Ala	Gly	Leu	Thr	Tyr	Leu	Leu	Thr	Gly	Ser	Phe	Ser	Lys	Ala	Ile
				325					330					335	
Ser	Phe	Leu	Leu	Val	Asp	Phe	Ser	Cys	Ala	Leu	Lys	Ile	Ser	Thr	Pro
			340					345					350		
Val	Ala	Tyr	Leu	Thr	Val	Ile	Lys	Glu	Gly	Leu	Asn	Arg	Glu	Met	Val
	355						360					365			
Ile	Lys	Asp	Gly	Asp	Val	Leu	Glu	Lys	Tyr	Leu	Glu	Val	Asp	Thr	Phe
	370					375					380				
Leu	Phe	Asp	Lys	Thr	Gly	Thr	Ile	Thr	Thr	Ser	Tyr	Pro	Ile	Val	Glu
385					390					395					400
Lys	Val	Leu	Pro	Phe	Gly	Asp	Tyr	Ser	Glu	Glu	Asp	Ile	Leu	Arg	Ile
				405					410					415	
Ser	Ala	Cys	Leu	Glu	Glu	His	Ile	Tyr	His	Pro	Ile	Ala	Asn	Ala	Ile
			420					425					430		
Val	Lys	Gln	Ala	Glu	Ile	Glu	Gly	Ile	Glu	His	Glu	Glu	Met	His	Gly
	435						440					445			
Lys	Leu	Gln	Tyr	Ile	Ala	Ser	Lys	Gly	Ile	Lys	Ser	His	Ile	Asp	Gly
	450					455					460				
Gln	Pro	Val	Leu	Ile	Gly	Asn	Tyr	Val	Leu	Met	Gln	Asp	Glu	Gln	Ile
465					470					475					480
His	Ile	Ser	Ser	Glu	Gln	Asn	Ala	Leu	Ile	Glu	Glu	Tyr	Lys	Ser	His
				485					490					495	
Tyr	Asn	Leu	Leu	Phe	Leu	Ala	Tyr	Gln	Asn	Glu	Leu	Ile	Gly	Met	Phe
			500					505					510		
Cys	Ile	His	Thr	Pro	Leu	Arg	Lys	Glu	Ala	Lys	Thr	Ala	Leu	Asp	Lys
	515						520					525			
Leu	Lys	Ala	Gln	Gly	Lys	Lys	Leu	Ile	Leu	Ala	Thr	Gly	Asp	Thr	Leu
	530					535					540				
Ile	Arg	Thr	Glu	Glu	Leu	Val	Lys	Asp	Leu	Pro	Phe	Asp	Gln	Val	Tyr
545					550					555					560
Thr	Asp	Leu	Lys	Pro	Asp	Gly	Lys	Phe	Glu	Leu	Val	Glu	Lys	Leu	Gln

				565					570					575			
Lys	Ala	Gly	His	Thr	Ile	Leu	Met	Val	Gly	Asp	Gly	Leu	Asn	Asp	Ser		
			580					585					590				
Ala	Ala	Leu	Thr	Leu	Ser	Asp	Ile	Gly	Val	Val	Met	Asn	Glu	Ser	Ala		
		595				600						605					
Asp	Ile	Ser	Lys	Gln	Met	Ser	Asp	Ile	Leu	Leu	Leu	Asp	Asn	Arg	Leu		
	610					615					620						
Asp	Phe	Phe	Gln	Glu	Leu	Asp	Ser	Leu	Ser	Ser	Ser	Leu	Gln	Thr	Leu		
	625				630					635					640		
Ile	Lys	Lys	Asn	Ile	Gln	Asp	Thr	Val	Val	Val	Asn	Ser	Ser	Leu	Ile		
			645					650						655			
Gly	Phe	Gly	Leu	Phe	Asn	Trp	Phe	Ser	Pro	Ser	Asn	Leu	Ser	Ile	Leu		
		660				665					670						
His	Asn	Leu	Thr	Thr	Leu	Arg	Ile	Val	Leu	Arg	Ser	Leu	Ser	Ile	Lys		
		675				680						685					
Asn	Arg																
	690																

(2) INFORMATION FOR SEQ ID NO:4605:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...355

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4605:

Lys	Asn	Asn	Met	Lys	Lys	Ile	Val	Phe	Thr	Gly	Gly	Gly	Thr	Val	Gly		
1			5					10						15			
His	Val	Thr	Leu	Asn	Leu	Leu	Leu	Met	Pro	Lys	Phe	Ile	Glu	Asp	Gly		
		20					25					30					
Trp	Glu	Val	His	Tyr	Ile	Gly	Asp	Lys	Arg	Gly	Ile	Glu	His	Gln	Glu		
	35					40					45						
Ile	Leu	Lys	Ser	Gly	Leu	Asp	Val	Thr	Phe	His	Ser	Ile	Ala	Thr	Gly		
	50				55						60						
Lys	Leu	Arg	Arg	Tyr	Phe	Ser	Trp	Gln	Asn	Met	Leu	Asp	Val	Phe	Lys		
65				70				75						80			
Val	Gly	Trp	Gly	Ile	Val	Gln	Ser	Leu	Phe	Ile	Met	Leu	Arg	Leu	Arg		
		85				90							95				
Pro	Gln	Thr	Leu	Phe	Ser	Lys	Gly	Gly	Phe	Val	Ser	Val	Pro	Pro	Val		
		100				105							110				
Ile	Ala	Ala	Arg	Val	Ser	Gly	Val	Pro	Val	Phe	Ile	His	Glu	Ser	Asp		
	115					120						125					
Leu	Ser	Met	Gly	Leu	Ala	Asn	Lys	Ile	Ala	Tyr	Lys	Phe	Ala	Thr	Lys		
	130					135					140						
Met	Tyr	Ser	Thr	Phe	Glu	Gln	Ala	Ser	Ser	Leu	Ser	Lys	Val	Glu	His		

145		150		155		160
Val	Gly	Ala	Val	Thr	Lys	Val
		165		170		175
Glu	Leu	Val	Asp	Ile	Gln	Ser
		180		185		190
Leu	Phe	Val	Gly	Gly	Ser	Ala
		195		200		205
Thr	Asp	His	Lys	Lys	Glu	Leu
		210		215		220
Thr	Gly	Asp	Ser	Ser	Leu	Asn
		225		230		235
Asp	Tyr	Val	Thr	Asp	Leu	Tyr
		245		250		255
Val	Val	Thr	Arg	Gly	Gly	Ala
		260		265		270
Ala	Lys	Leu	His	Val	Ile	Val
		275		280		285
Asp	Gln	Ile	Glu	Asn	Ala	Ala
		290		295		300
Asp	Leu	Gln	Glu	Ser	Asp	Leu
		305		310		315
Ser	His	Leu	Leu	Ser	His	Lys
		325		330		335
Ser	Lys	Glu	Leu	Lys	Ser	Leu
		340		345		350
Asp	Leu	Ser				
		355				

(2) INFORMATION FOR SEQ ID NO:4606:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 79 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...79
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4606:

Gly	Asp	Asn	Met	Leu	Gly	Ser	Met	Phe	Val	Gly	Leu	Leu	Val	Gly	Phe
1				5				10						15	
Leu	Ala	Gly	Ala	Met	Thr	Asn	Arg	Gly	Glu	Arg	Met	Gly	Cys	Phe	Gly
			20					25					30		
Lys	Met	Phe	Leu	Gly	Trp	Ile	Gly	Ala	Phe	Leu	Gly	His	Leu	Leu	Phe
			35				40					45			
Gly	Thr	Trp	Gly	Pro	Val	Leu	Ser	Gly	Thr	Ala	Ile	Ile	Pro	Ala	Val
		50				55				60					
Leu	Gly	Ala	Met	Ile	Val	Leu	Ala	Ile	Phe	Trp	Arg	Arg	Gly	Ser	

(2) INFORMATION FOR SEQ ID NO:4607:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 286 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...286

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4607:

```

Gly Met Ile Leu Ser Lys Asn Arg Glu Asp Gly Leu Arg Lys Phe Ala
1      5      10      15
Thr Asn Ile Arg Leu Asn Thr Leu Arg Thr Leu Asn His Leu Gly Phe
20      25      30
Gly His Tyr Gly Gly Ser Leu Ser Ile Val Glu Val Leu Ala Val Leu
35      40      45
Tyr Gly Glu Ile Met Pro Met Thr Pro Glu Ile Phe Ala Ala Arg Asp
50      55      60
Arg Asp Tyr Phe Ile Leu Ser Lys Gly His Gly Gly Pro Ala Leu Tyr
65      70      75      80
Ser Thr Leu Tyr Leu Asn Gly Phe Phe Asp Lys Glu Phe Leu Tyr Ser
85      90      95
Leu Asn Thr Asn Gly Thr Lys Leu Pro Ser His Pro Asp Arg Asn Leu
100     105     110
Thr Pro Gly Ile Asp Met Thr Thr Gly Ser Leu Gly Gln Gly Ile Ser
115     120     125
Val Ala Thr Gly Leu Ala Tyr Gly Gln Arg Ile Arg Lys Ser Pro Phe
130     135     140
Tyr Thr Tyr Ala Ile Val Gly Asp Gly Glu Leu Asn Glu Gly Gln Cys
145     150     155     160
Trp Glu Ala Ile Gln Phe Ala Ser His Gln Gln Leu Ser Asn Leu Ile
165     170     175
Val Phe Val Asp Asp Asn Lys Lys Gln Leu Asp Gly Phe Thr Lys Asp
180     185     190
Ile Cys Asn Pro Gly Asp Phe Val Glu Lys Phe Ser Ala Phe Gly Phe
195     200     205
Glu Ser Ile Arg Val Lys Gly Ser Asp Ile Arg Glu Ile Tyr Glu Gly
210     215     220
Ile Val Gln Leu Lys Gln Ser His Asn Ser Ser Pro Lys Cys Ile Val
225     230     235     240
Leu Asp Thr Ile Lys Gly Gln Gly Val Gln Glu Leu Glu Glu Met Lys
245     250     255
Ser Asn His His Leu Arg Pro Thr Val Glu Glu Arg Gln Met Leu Thr
260     265     270
Ser Val Val Glu Arg Leu Ser Gln Glu Leu Glu Glu Thr Glu

```

(2) INFORMATION FOR SEQ ID NO:4608:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4608:

Leu	Val	Asn	Met	Glu	Val	Arg	Thr	Leu	Ala	Asn	Ile	Lys	Ser	Ala	Ile
1				5				10						15	
Lys	Arg	Ala	Glu	Leu	Asn	Val	Lys	Gln	Asn	Glu	Lys	Asn	Ser	Ala	Gln
			20					25					30		
Lys	Ser	Ala	Met	Arg	Thr	Ala	Ile	Lys	Ala	Phe	Glu	Ala	Asn	Pro	Ser
			35				40					45			
Glu	Glu	Leu	Phe	Arg	Ala	Ala	Ser	Ser	Ala	Ile	Asp	Lys	Ala	Glu	Thr
			50			55				60					
Lys	Gly	Leu	Ile	His	Lys	Asn	Lys	Ala	Ser	Arg	Asp	Lys	Ala	Arg	Leu
65					70				75					80	
Ser	Ala	Lys	Leu	Ala	Lys										
					85										

(2) INFORMATION FOR SEQ ID NO:4609:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 472 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...472

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4609:

Val	Val	Asn	Met	Lys	Leu	Asn	Lys	Lys	Ile	Tyr	Phe	Phe	Asp	Lys	Gly
-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----	-----

1				5				10					15			
Ile	Phe	Asn	Pro	Tyr	Arg	Met	Ser	Asn	Val	Lys	Leu	Lys	Val	Asn	Gln	
			20					25					30			
Ala	Val	Lys	Asp	Lys	Glu	Ile	Phe	Phe	Thr	Glu	Glu	Lys	Pro	Trp	Glu	
		35					40					45				
Ile	Arg	Phe	Asp	Asn	Ser	Tyr	Pro	Asn	Val	Phe	Phe	Asp	Asp	Leu	Ala	
	50					55					60					
Gly	Val	Tyr	Arg	Cys	Tyr	Tyr	Ser	Thr	Phe	Thr	Asp	Asp	Glu	Glu	Ser	
65					70					75					80	
Glu	Lys	Tyr	Ser	Leu	Glu	Glu	Arg	Lys	Glu	Arg	Gln	Tyr	Leu	Pro	Arg	
				85					90					95		
Ala	Lys	Arg	Ile	Val	Ser	Leu	Cys	Tyr	Ala	Glu	Ser	Lys	Asp	Gly	Val	
			100					105					110			
Asn	Trp	Val	Lys	Pro	Asn	Leu	Gly	Ile	Thr	Glu	Phe	Arg	Gly	Ser	Thr	
	115						120					125				
Glu	Asn	Asn	Ile	Ile	Gly	His	Phe	Leu	His	Gly	Thr	Ser	Val	Phe	Leu	
	130				135						140					
Asp	Lys	His	Asp	Ala	Asp	Glu	Asn	Arg	Arg	Tyr	Lys	Met	Phe	Thr	Lys	
145					150					155					160	
Ile	Asp	Tyr	Gly	Asn	Gly	Val	His	Phe	Ile	Ala	Val	Ala	Phe	Ser	Lys	
				165				170						175		
Asp	Gly	Leu	His	Phe	Asp	Glu	Tyr	Ile	Lys	Val	Pro	Asn	Phe	Asn	Pro	
		180					185						190			
Arg	Ala	Asp	Thr	His	Asn	His	Ile	Ile	Tyr	Asp	Glu	Ala	Leu	Asn	Arg	
	195						200					205				
Tyr	Val	Leu	Ile	Thr	Arg	Thr	Trp	Arg	Asp	Ser	Leu	Arg	Leu	Pro	Cys	
	210					215					220					
Val	Ser	Thr	Ser	Ala	Asp	Phe	Ile	Asn	Trp	Thr	Pro	Ile	Gln	Glu	Ile	
225					230					235					240	
Leu	Asn	Val	Cys	Asp	Tyr	Glu	Asn	Gln	Ile	Tyr	Ser	Met	Pro	Ile	Phe	
			245						250					255		
Lys	Arg	Gly	Asp	Tyr	Ile	Leu	Gly	Leu	Ala	Ser	Val	Phe	His	Glu	Gly	
			260				265						270			
Asp	Gln	Leu	Asn	Lys	Asn	Tyr	Asp	Thr	Val	Asp	Leu	Gln	Leu	Thr	Tyr	
	275						280					285				
Ser	Tyr	Arg	His	Val	Gly	Trp	His	Tyr	Leu	Asn	Thr	Asp	Thr	Pro	Leu	
	290					295					300					
Ile	Pro	Arg	Gly	Lys	Gly	Gln	Tyr	Gly	Asp	Gly	Glu	Phe	Asp	Cys	Gly	
305					310					315					320	
Cys	Ile	Tyr	Ser	Ser	Ala	Pro	Val	Thr	Ile	Gly	Asp	Arg	Thr	Tyr	Phe	
			325						330					335		
Tyr	Tyr	Met	Gly	Gly	Asn	Gly	Gln	His	Thr	Asn	Phe	Arg	Glu	Thr	Ser	
			340					345					350			
Leu	Ser	Arg	Ala	Tyr	Ile	Glu	Lys	Asp	His	Phe	Ala	Tyr	Trp	Asp	Thr	
		355					360					365				
Lys	Arg	Pro	Glu	Tyr	Pro	Gly	Val	Leu	Tyr	Thr	Asn	Gly	Phe	Ile	Phe	
	370					375					380					
Leu	Asn	Asp	Gln	Val	Tyr	Leu	Asp	Ala	Asp	Ile	Ala	Ala	Gly	Gly	Phe	
385					390					395					400	
Val	Thr	Ile	Glu	Leu	Phe	Glu	Asn	Asn	His	Thr	Pro	Met	Glu	Ile	Thr	
			405						410					415		
Ala	Ser	Leu	Glu	Lys	Ile	Glu	Asp	Gly	Arg	Tyr	Gln	Val	Leu	Phe	Ser	
			420					425					430			
Glu	Pro	Leu	Pro	Arg	Thr	Gln	Thr	Arg	Leu	Lys	Ile	Ser	Phe	Lys	Asn	
		435					440					445				
Ala	Lys	Ile	Tyr	Ala	Ile	Glu	Gly	Asn	Leu	Asp	Ile	Phe	Arg	Ile	Glu	
	450					455					460					

Ser Asp Asn Ala Leu Leu Arg Gly
465 470

(2) INFORMATION FOR SEQ ID NO:4610:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4610:

Lys	Ala	Asn	Met	Ile	Gln	Phe	Tyr	Leu	Lys	Lys	Asn	Lys	Lys	Gly	Asp
1				5				10						15	
Phe	Ile	Met	Thr	Leu	Lys	Thr	Leu	Ala	Leu	Ile	Ser	Gly	Ile	Val	Gly
			20				25						30		
Leu	Val	Gly	Gly	Ile	Leu	Leu	Leu	Ile	Gly	Pro	Phe	Val	Leu	Leu	Gly
		35				40					45				
Thr	Thr	Val	Asn	Thr	Ala	Ala	Thr	Thr	Leu	Asn	Gly	Gly	Ala	Thr	Ala
	50				55					60					
Gly	Ala	Phe	Ser	Gly	Val	Ala	Cys	Thr	Leu	Glu	Cys	Leu	Glu	Asp	
65				70					75						

(2) INFORMATION FOR SEQ ID NO:4611:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 194 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...194

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4611:

Arg	Lys	Asn	Met	Asp	Leu	Lys	Phe	Glu	Gly	Val	Asp	Leu	Glu	Tyr	Lys
1			5					10						15	
Lys	Ala	Lys	Asn	Asn	Leu	Pro	Glu	Ser	Phe	Trp	Glu	Thr	Tyr	Ser	Ala

		20					25				30				
Phe	Ala	Asn	Thr	Asn	Gly	Gly	Lys	Ile	Ile	Leu	Gly	Ile	Asp	Glu	Lys
	35						40					45			
Asn	Ile	Asp	Thr	Tyr	Gln	Arg	Val	Asn	Arg	Leu	Pro	Ala	Lys	Gln	Asn
	50					55					60				
Tyr	Glu	Ala	Ser	Lys	Gln	Leu	Thr	Asp	Ala	Arg	Phe	Lys	Arg	Leu	Val
65					70					75					80
Gly	Val	Gln	Arg	Thr	Thr	Phe	Glu	Glu	Met	Leu	Ala	Val	Leu	Lys	Thr
			85						90					95	
Ala	Tyr	Gln	Leu	Lys	His	Ala	Lys	Gly	Gly	Arg	Lys	Pro	Lys	Leu	Ser
			100					105					110		
Leu	Glu	Asp	Leu	Leu	Met	Ala	Thr	Leu	Gln	Tyr	Val	Arg	Glu	Tyr	Arg
	115						120					125			
Thr	Tyr	Glu	Glu	Ile	Ala	Ala	Asp	Phe	Gly	Ile	His	Glu	Ser	Asn	Leu
	130					135					140				
Ile	Arg	Arg	Ser	Gln	Trp	Val	Glu	Val	Thr	Leu	Val	Gln	Ser	Gly	Val
145					150					155					160
Thr	Ile	Ser	Arg	Thr	Leu	Leu	Ser	Ser	Glu	Asp	Thr	Val	Met	Ile	Asp
			165						170				175		
Ala	Thr	Glu	Val	Lys	Ile	Asn	Arg	Pro	Lys	Lys	Thr	Ile	Ser	Glu	Ser
			180					185					190		
Phe	Trp														

(2) INFORMATION FOR SEQ ID NO:4612:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 787 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...787

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4612:

Lys	Glu	Asn	Met	Lys	Asp	Arg	Ile	Lys	Glu	Tyr	Leu	Gln	Asp	Lys	Gly
1			5					10					15		
Lys	Val	Thr	Val	Asn	Asp	Leu	Ala	Gln	Ala	Leu	Gly	Lys	Asp	Ser	Ser
			20					25				30			
Lys	Asp	Phe	Arg	Glu	Leu	Ile	Lys	Thr	Leu	Ser	Leu	Met	Glu	Arg	Lys
	35					40					45				
His	Gln	Ile	Arg	Phe	Glu	Glu	Asp	Gly	Ser	Leu	Thr	Leu	Glu	Ile	Lys
	50					55				60					
Lys	Lys	His	Glu	Ile	Thr	Leu	Lys	Gly	Ile	Phe	His	Ala	His	Lys	Asn
65					70					75				80	
Gly	Phe	Gly	Phe	Val	Ser	Leu	Glu	Gly	Glu	Glu	Asp	Asp	Leu	Phe	Val
			85					90				95			
Gly	Lys	Asn	Asp	Val	Asn	Tyr	Ala	Ile	Asp	Gly	Asp	Thr	Val	Glu	Val

Glu	Gly	Lys	Trp	Ile	Gly	Val	Gly	Gly	Lys	Leu	Glu	Arg	Gly	Glu	Thr
		35					40					45			
Pro	Gln	Glu	Cys	Ala	Ala	Arg	Glu	Ile	Leu	Glu	Glu	Thr	Gly	Leu	Lys
		50				55					60				
Ala	Lys	Pro	Val	Leu	Lys	Gly	Val	Ile	Thr	Phe	Pro	Glu	Phe	Thr	Pro
65					70					75					80
Asp	Leu	Asp	Trp	Tyr	Thr	Tyr	Val	Phe	Lys	Val	Thr	Glu	Phe	Glu	Gly
			85						90					95	
Asp	Leu	Ile	Asp	Cys	Asn	Glu	Gly	Met	Leu	Glu	Trp	Val	Pro	Tyr	Asp
			100					105					110		
Glu	Val	Leu	Ser	Lys	Pro	Thr	Trp	Glu	Gly	Asp	His	Thr	Phe	Val	Glu
		115					120					125			
Trp	Leu	Leu	Glu	Asp	Lys	Pro	Phe	Phe	Ser	Ala	Lys	Phe	Val	Tyr	Asp
	130					135					140				
Gly	Asp	Lys	Leu	Leu	Asp	Thr	Gln	Val	Asp	Phe	Tyr	Glu			
145					150					155					

(2) INFORMATION FOR SEQ ID NO:4614:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 281 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...281

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4614:

Gly	Gly	Asn	Ile	Val	Gly	Ile	Arg	Val	Tyr	Lys	Pro	Thr	Thr	Asn	Gly
1			5					10						15	
Arg	Arg	Asn	Met	Thr	Ser	Leu	Asp	Phe	Ala	Glu	Ile	Thr	Thr	Ser	Thr
		20					25						30		
Pro	Glu	Lys	Ser	Leu	Leu	Val	Ala	Leu	Lys	Ser	Lys	Ala	Gly	Arg	Asn
		35				40						45			
Asn	Asn	Gly	Arg	Ile	Thr	Val	Arg	His	Gln	Gly	Gly	Gly	His	Lys	Arg
		50				55				60					
Phe	Tyr	Arg	Leu	Val	Asp	Phe	Lys	Arg	Asn	Lys	Asp	Asn	Val	Glu	Ala
65				70					75						80
Val	Val	Lys	Thr	Ile	Glu	Tyr	Asp	Pro	Asn	Arg	Ser	Ala	Asn	Ile	Ala
			85				90							95	
Leu	Val	His	Tyr	Thr	Asp	Gly	Val	Lys	Ala	Tyr	Ile	Ile	Ala	Pro	Lys
		100				105						110			
Gly	Leu	Glu	Val	Gly	Gln	Arg	Ile	Val	Ser	Gly	Pro	Glu	Ala	Asp	Ile
	115					120						125			
Lys	Val	Gly	Asn	Ala	Leu	Pro	Leu	Ala	Asn	Ile	Pro	Val	Gly	Thr	Leu
	130					135					140				
Ile	His	Asn	Ile	Glu	Leu	Lys	Pro	Gly	Arg	Gly	Gly	Glu	Leu	Val	Arg
145					150					155					160

Ala	Ala	Gly	Ala	Ser	Ala	Gln	Val	Leu	Gly	Ser	Glu	Gly	Lys	Tyr	Val
				165					170					175	
Leu	Val	Arg	Leu	Gln	Ser	Gly	Glu	Val	Arg	Met	Ile	Leu	Gly	Thr	Cys
			180					185					190		
Arg	Ala	Thr	Val	Gly	Val	Val	Gly	Asn	Glu	Gln	His	Gly	Leu	Val	Asn
		195					200					205			
Leu	Gly	Lys	Ala	Gly	Arg	Ser	Arg	Trp	Lys	Gly	Ile	Arg	Pro	Thr	Val
	210					215					220				
Arg	Gly	Ser	Val	Met	Asn	Pro	Asn	Asp	His	Pro	His	Gly	Gly	Gly	Glu
225					230					235					240
Gly	Lys	Ala	Pro	Val	Gly	Arg	Lys	Ala	Pro	Ser	Thr	Pro	Trp	Gly	Lys
				245				250						255	
Pro	Ala	Leu	Gly	Leu	Lys	Thr	Arg	Asn	Lys	Lys	Ala	Lys	Ser	Asp	Lys
			260					265					270		
Leu	Ile	Val	Arg	Arg	Arg	Asn	Glu	Lys							
		275					280								

(2) INFORMATION FOR SEQ ID NO:4615:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 621 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4615:

Ile	Leu	Asn	Ile	Ile	Glu	Glu	Ile	Met	Thr	Lys	Leu	Arg	Glu	Asp	Ile
1			5						10					15	
Arg	Asn	Ile	Ala	Ile	Ile	Ala	His	Val	Asp	His	Gly	Lys	Thr	Thr	Leu
			20					25					30		
Val	Asp	Glu	Leu	Leu	Lys	Gln	Ser	Glu	Thr	Leu	Asp	Ala	Arg	Thr	Glu
		35				40					45				
Leu	Ala	Glu	Arg	Ala	Met	Asp	Ser	Asn	Asp	Ile	Glu	Lys	Glu	Arg	Gly
	50					55				60					
Ile	Thr	Ile	Leu	Ala	Lys	Asn	Thr	Ala	Val	Ala	Tyr	Asn	Gly	Thr	Arg
65					70				75					80	
Ile	Asn	Ile	Met	Asp	Thr	Pro	Gly	His	Ala	Asp	Phe	Gly	Gly	Glu	Val
			85					90					95		
Glu	Arg	Ile	Met	Lys	Met	Val	Asp	Gly	Val	Val	Leu	Val	Val	Asp	Ala
			100					105					110		
Tyr	Glu	Gly	Thr	Met	Pro	Gln	Thr	Arg	Phe	Val	Leu	Lys	Lys	Ala	Leu
		115				120						125			
Glu	Gln	Asp	Leu	Val	Pro	Ile	Val	Val	Val	Asn	Lys	Ile	Asp	Lys	Pro
	130					135				140					
Ser	Ala	Arg	Pro	Ala	Glu	Val	Val	Asp	Glu	Val	Leu	Glu	Leu	Phe	Ile

145					150					155				160
Glu	Leu	Gly	Ala	Asp	Asp	Asp	Gln	Leu	Asp	Phe	Pro	Val	Val	Tyr
				165					170					175
Ser	Ala	Ile	Asn	Gly	Thr	Ser	Ser	Leu	Ser	Asp	Asp	Pro	Ala	Asp
			180					185					190	Gln
Glu	Ala	Thr	Met	Ala	Pro	Ile	Phe	Asp	Thr	Ile	Ile	Asp	His	Ile
		195					200					205		Pro
Ala	Pro	Val	Asp	Asn	Ser	Asp	Glu	Pro	Leu	Gln	Phe	Gln	Val	Ser
	210					215					220			Leu
Leu	Asp	Tyr	Asn	Asp	Phe	Val	Gly	Arg	Ile	Gly	Ile	Gly	Arg	Val
225				230						235				240
Arg	Gly	Thr	Val	Lys	Val	Gly	Asp	Gln	Val	Thr	Leu	Ser	Lys	Leu
				245					250					255
Gly	Thr	Thr	Lys	Asn	Phe	Arg	Val	Thr	Lys	Leu	Phe	Gly	Phe	Phe
			260					265					270	Gly
Leu	Glu	Arg	Arg	Glu	Ile	Gln	Glu	Ala	Lys	Ala	Gly	Asp	Leu	Ile
	275						280					285		Ala
Val	Ser	Gly	Met	Glu	Asp	Ile	Phe	Val	Gly	Glu	Thr	Ile	Thr	Pro
	290					295					300			Thr
Asp	Ala	Val	Glu	Ala	Leu	Pro	Ile	Leu	His	Ile	Asp	Glu	Pro	Thr
305				310						315				Leu
Gln	Met	Thr	Phe	Leu	Val	Asn	Asn	Ser	Pro	Phe	Ala	Gly	Lys	Glu
			325						330					Gly
Lys	Trp	Val	Thr	Ser	Arg	Lys	Val	Glu	Glu	Arg	Leu	Gln	Ala	Glu
	340							345					350	Leu
Gln	Thr	Asp	Val	Ser	Leu	Arg	Val	Asp	Pro	Thr	Asp	Ser	Pro	Asp
	355						360					365		Lys
Trp	Thr	Val	Ser	Gly	Arg	Gly	Glu	Leu	His	Leu	Ser	Ile	Leu	Ile
370						375					380			Glu
Thr	Met	Arg	Arg	Glu	Gly	Tyr	Glu	Leu	Gln	Val	Ser	Arg	Pro	Glu
385				390						395				Val
Ile	Val	Lys	Glu	Ile	Asp	Gly	Val	Lys	Cys	Glu	Pro	Phe	Glu	Arg
			405						410					Val
Gln	Ile	Asp	Thr	Pro	Glu	Glu	Tyr	Gln	Gly	Ser	Val	Ile	Gln	Ser
	420							425				430		Leu
Ser	Glu	Arg	Lys	Gly	Glu	Met	Leu	Asp	Met	Ile	Ser	Thr	Gly	Asn
	435					440						445		Gly
Gln	Thr	Arg	Leu	Val	Phe	Leu	Val	Pro	Ala	Arg	Gly	Leu	Ile	Gly
450						455					460			Tyr
Ser	Thr	Glu	Phe	Leu	Ser	Met	Thr	Arg	Gly	Tyr	Gly	Ile	Met	Asn
465				470						475				His
Thr	Phe	Asp	Gln	Tyr	Leu	Pro	Leu	Ile	Pro	Gly	Glu	Ile	Gly	Gly
			485						490					Arg
His	Arg	Gly	Ala	Leu	Val	Ser	Ile	Asp	Ala	Gly	Lys	Ala	Thr	Tyr
	500							505					510	
Ser	Ile	Met	Ser	Ile	Glu	Glu	Arg	Gly	Thr	Ile	Phe	Val	Asn	Pro
	515						520					525		Gly
Thr	Glu	Val	Tyr	Glu	Gly	Met	Ile	Ile	Gly	Glu	Asn	Ser	Arg	Glu
530						535					540			Asn
Asp	Leu	Thr	Val	Asn	Ile	Thr	Lys	Ala	Lys	Gln	Met	Thr	Asn	Val
545				550						555				Arg
Ser	Ala	Thr	Lys	Asp	Gln	Thr	Ala	Val	Ile	Lys	Thr	Pro	Arg	Ile
			565						570					Leu
Thr	Leu	Glu	Glu	Ser	Leu	Glu	Phe	Leu	Asn	Asp	Asp	Glu	Tyr	Met
	580						585					590		Glu
Val	Thr	Pro	Glu	Ser	Ile	Arg	Leu	Arg	Lys	Gln	Ile	Leu	Asn	Lys
	595						600					605		Ala

Glu Arg Glu Lys Ala Asn Lys Lys Lys Lys Ser Ala Glu
 610 615 620

(2) INFORMATION FOR SEQ ID NO:4616:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4616:

Arg	Val	Asn	Ile	Lys	Ser	Ala	Ser	Asp	Leu	Leu	Gly	Ile	Ser	Ala	Asp
1				5					10					15	
Thr	Ile	Arg	Tyr	Tyr	Glu	Arg	Val	Gly	Leu	Val	Pro	Pro	Ile	Thr	Arg
			20					25					30		
Thr	Ala	Thr	Gly	Ile	Arg	Asp	Phe	Gln	Asp	Gln	Asp	Ile	Glu	Ala	Leu
			35				40					45			
Glu	Phe	Ile	Lys	Cys	Phe	Arg	Ser	Ala	Gly	Val	Ser	Val	Asp	Ser	Leu
			50			55					60				
Val	Asp	Tyr	Met	Ser	Leu	Tyr	Gln	Lys	Gly	Asp	Glu	Thr	Arg	Glu	Glu
65					70				75					80	
Arg	Leu	Gly	Ile	Leu	Glu	Glu	Glu	Lys	Gln	Lys	Leu	Glu	Glu	Arg	Leu
			85					90						95	
Ser	Gln	Leu	Gln	Thr	Ala	Leu	Asn	Arg	Leu	Asn	Leu	Lys	Ile	Lys	Leu
			100					105						110	
Tyr	Lys	Glu	Gly	Lys	Phe										
															115

(2) INFORMATION FOR SEQ ID NO:4617:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 352 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4617:

Gly	Lys	Asn	Met	Thr	Glu	Tyr	Lys	Asn	Ile	Ile	Val	Thr	Gly	Gly	Ala
1				5					10					15	
Gly	Phe	Ile	Gly	Ser	Asn	Phe	Val	His	Tyr	Val	Tyr	Glu	Asn	Phe	Pro
			20					25					30		
Asp	Val	His	Val	Thr	Val	Leu	Asp	Lys	Leu	Thr	Tyr	Ala	Gly	Asn	Arg
		35					40					45			
Ala	Asn	Ile	Glu	Glu	Ile	Leu	Gly	Asn	Arg	Val	Glu	Leu	Val	Val	Gly
	50					55					60				
Asp	Ile	Ala	Asp	Ala	Glu	Leu	Val	Asp	Lys	Leu	Ala	Ala	Gln	Ala	Asp
65					70					75				80	
Ala	Ile	Val	His	Tyr	Ala	Ala	Glu	Ser	His	Asn	Asp	Asn	Ser	Leu	Asn
			85						90					95	
Asp	Pro	Ser	Pro	Phe	Ile	His	Thr	Asn	Phe	Ile	Gly	Thr	Tyr	Thr	Leu
			100					105					110		
Leu	Glu	Ala	Ala	Arg	Lys	Tyr	Asp	Ile	Arg	Phe	His	His	Val	Ser	Thr
		115					120					125			
Asp	Glu	Val	Tyr	Gly	Asp	Leu	Pro	Leu	Arg	Glu	Asp	Leu	Pro	Gly	His
	130					135					140				
Gly	Glu	Gly	Pro	Gly	Glu	Lys	Phe	Thr	Ala	Glu	Thr	Lys	Tyr	Asn	Pro
145					150					155				160	
Ser	Ser	Pro	Tyr	Ser	Ser	Thr	Lys	Ala	Ala	Ser	Asp	Leu	Ile	Val	Lys
				165					170					175	
Ala	Trp	Val	Arg	Ser	Phe	Gly	Val	Lys	Ala	Thr	Ile	Ser	Asn	Cys	Ser
			180					185					190		
Asn	Asn	Tyr	Gly	Pro	Tyr	Gln	His	Ile	Glu	Lys	Phe	Ile	Pro	Arg	Gln
		195					200					205			
Ile	Thr	Asn	Ile	Leu	Ser	Gly	Ile	Lys	Pro	Lys	Leu	Tyr	Gly	Glu	Gly
	210					215					220				
Lys	Asn	Val	Arg	Asp	Trp	Ile	His	Thr	Asn	Asp	His	Ser	Ser	Gly	Val
225					230					235				240	
Trp	Thr	Ile	Leu	Thr	Lys	Gly	Gln	Ile	Gly	Glu	Thr	Tyr	Leu	Ile	Gly
			245						250					255	
Ala	Asp	Gly	Glu	Lys	Asn	Asn	Lys	Glu	Val	Leu	Glu	Leu	Ile	Leu	Lys
			260					265					270		
Glu	Met	Gly	Gln	Ala	Ala	Asp	Ala	Tyr	Asp	His	Val	Thr	Asp	Arg	Ala
		275					280					285			
Gly	His	Asp	Leu	Arg	Tyr	Ala	Ile	Asp	Ala	Ser	Lys	Leu	Arg	Asp	Glu
	290					295					300				
Leu	Gly	Trp	Lys	Pro	Glu	Phe	Thr	Asn	Phe	Glu	Ala	Gly	Leu	Lys	Ala
				310						315				320	
Thr	Ile	Lys	Trp	Tyr	Thr	Asp	Asn	Gln	Glu	Trp	Trp	Lys	Ala	Glu	Lys
				325					330					335	
Glu	Ala	Val	Glu	Ala	Asn	Tyr	Ala	Lys	Thr	Gln	Glu	Ile	Ile	Thr	Val
			340					345					350		

(2) INFORMATION FOR SEQ ID NO:4618:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 320 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...320

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4618:

Asp	Arg	Asn	Met	Asp	Phe	Glu	Lys	Ile	Glu	Gln	Ala	Tyr	Thr	Tyr	Leu
1				5					10					15	
Leu	Glu	Asn	Val	Gln	Val	Ile	Gln	Ser	Asp	Leu	Ala	Thr	Asn	Phe	Tyr
			20					25					30		
Asp	Ala	Leu	Val	Glu	Gln	Asn	Ser	Ile	Tyr	Leu	Asp	Gly	Glu	Thr	Glu
			35				40					45			
Leu	Glu	Gln	Val	Lys	Asp	Asn	Asn	Gln	Thr	Leu	Lys	Arg	Leu	Ala	Leu
			50			55					60				
Arg	Lys	Glu	Glu	Trp	Leu	Lys	Thr	Tyr	Gln	Phe	Leu	Leu	Met	Lys	Ala
65					70					75					80
Gly	Gln	Thr	Glu	Pro	Leu	Gln	Ala	Asn	His	Gln	Phe	Thr	Pro	Asp	Ala
				85					90					95	
Ile	Ala	Leu	Leu	Val	Phe	Ile	Val	Glu	Glu	Leu	Phe	Thr	Glu	Glu	
			100				105						110		
Glu	Ile	Thr	Ile	Leu	Glu	Met	Gly	Ser	Gly	Met	Gly	Ile	Leu	Gly	Ala
			115				120						125		
Thr	Phe	Leu	Thr	Ser	Leu	Asp	Lys	Lys	Val	Asp	Tyr	Leu	Gly	Met	Glu
			130			135					140				
Val	Asp	Asp	Leu	Leu	Ile	Asp	Leu	Ala	Ala	Ser	Met	Ala	Asp	Val	Ile
145					150					155					160
Gly	Leu	Gln	Ala	Gly	Phe	Val	Gln	Gly	Asp	Ala	Val	Arg	Pro	Gln	Met
				165					170					175	
Leu	Lys	Glu	Ser	Asp	Val	Val	Ile	Ser	Asp	Leu	Pro	Val	Gly	Tyr	Tyr
			180					185					190		
Pro	Asp	Asp	Ala	Val	Ala	Ser	Arg	His	Gln	Val	Ala	Ser	Ser	Gln	Glu
		195				200					205				
His	Thr	Tyr	Ala	His	His	Leu	Leu	Met	Glu	Gln	Gly	Phe	Lys	Tyr	Leu
	210					215					220				
Lys	Ser	Asp	Gly	Tyr	Ala	Ile	Phe	Leu	Ala	Pro	Ser	Asp	Leu	Leu	Thr
225					230					235					240
Ser	Pro	Gln	Ser	Asp	Leu	Leu	Lys	Val	Trp	Leu	Lys	Glu	Glu	Ala	Ser
				245					250					255	
Leu	Val	Ala	Met	Ile	Ser	Leu	Pro	Glu	Asn	Leu	Phe	Ala	Asn	Ala	Lys
			260					265					270		
Gln	Ser	Lys	Thr	Ile	Phe	Ile	Leu	Gln	Lys	Lys	Asn	Glu	Ile	Ala	Val
		275					280					285			
Glu	Pro	Phe	Val	Tyr	Pro	Leu	Ala	Ser	Leu	Gln	Asp	Ala	Ser	Val	Leu
	290					295					300				
Met	Lys	Phe	Lys	Glu	Asn	Phe	Gln	Lys	Trp	Thr	Gln	Gly	Thr	Glu	Ile
305					310					315					320

(2) INFORMATION FOR SEQ ID NO:4619:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 621 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...621

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4619:

Ser	Arg	Asn	Ile	Met	Lys	Gln	Ser	Lys	Met	Pro	Ile	Pro	Thr	Leu	Arg	1	5	10	15
Glu	Met	Pro	Ser	Asp	Ala	Gln	Val	Ile	Ser	His	Ala	Leu	Met	Leu	Arg	20	25	30	
Ala	Gly	Tyr	Val	Arg	Gln	Val	Ser	Ala	Gly	Val	Tyr	Ser	Tyr	Leu	Pro	35	40	45	
Leu	Ala	Asn	Arg	Val	Ile	Glu	Lys	Ala	Lys	Asn	Ile	Met	Arg	Gln	Glu	50	55	60	
Phe	Glu	Lys	Ile	Gly	Ala	Val	Glu	Met	Leu	Ala	Pro	Ala	Leu	Leu	Ser	65	70	75	80
Ala	Glu	Leu	Trp	Arg	Glu	Ser	Gly	Arg	Tyr	Glu	Thr	Tyr	Gly	Glu	Asp	85	90	95	
Leu	Tyr	Lys	Leu	Lys	Asn	Arg	Glu	Lys	Ser	Asp	Phe	Ile	Leu	Gly	Pro	100	105	110	
Thr	His	Glu	Glu	Thr	Phe	Thr	Ala	Ile	Val	Arg	Asp	Ser	Val	Lys	Ser	115	120	125	
Tyr	Lys	Gln	Leu	Pro	Leu	Asn	Leu	Tyr	Gln	Ile	Gln	Pro	Lys	Tyr	Arg	130	135	140	
Asp	Glu	Lys	Arg	Pro	Arg	Asn	Gly	Leu	Leu	Arg	Thr	Arg	Glu	Phe	Ile	145	150	155	160
Met	Lys	Asp	Ala	Tyr	Ser	Phe	His	Ala	Asn	Tyr	Asp	Ser	Leu	Asp	Ser	165	170	175	
Val	Tyr	Asp	Glu	Tyr	Lys	Ala	Ala	Tyr	Glu	Arg	Ile	Phe	Thr	Arg	Ser	180	185	190	
Gly	Leu	Asp	Phe	Lys	Ala	Ile	Ile	Gly	Asp	Gly	Gly	Ala	Met	Gly	Gly	195	200	205	
Lys	Asp	Ser	Gln	Glu	Phe	Met	Ala	Ile	Thr	Ser	Ala	Arg	Thr	Asp	Leu	210	215	220	
Asp	Arg	Trp	Val	Val	Leu	Asp	Lys	Ser	Val	Ala	Ser	Phe	Asp	Glu	Ile	225	230	235	240
Pro	Ala	Glu	Val	Gln	Glu	Glu	Ile	Lys	Ala	Glu	Leu	Leu	Lys	Trp	Ile	245	250	255	
Val	Ser	Gly	Glu	Asp	Thr	Ile	Ala	Tyr	Ser	Ser	Glu	Ser	Ser	Tyr	Ala	260	265	270	
Ala	Asn	Leu	Glu	Met	Ala	Thr	Asn	Glu	Tyr	Lys	Pro	Ser	Asn	Arg	Val	275	280	285	
Val	Ala	Glu	Glu	Glu	Val	Thr	Arg	Val	Ala	Thr	Pro	Asp	Val	Lys	Ser	290	295	300	
Ile	Asp	Glu	Val	Ala	Ala	Phe	Leu	Asn	Val	Pro	Glu	Glu	Gln	Thr	Ile	305	310	315	320

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Lys Thr Leu Phe Tyr Ile Ala Asp Gly Glu Leu Val Ala Ala Leu Leu
      325      330      335
Val Gly Asn Asp Gln Leu Asn Glu Val Lys Leu Lys Asn His Leu Gly
      340      345      350
Ala Asp Phe Phe Asp Val Ala Ser Glu Glu Glu Val Ala Asn Val Val
      355      360      365
Gln Ala Gly Phe Gly Ser Leu Gly Pro Val Gly Leu Pro Glu Asn Ile
      370      375      380
Lys Ile Ile Ala Asp Arg Lys Val Gln Asp Val Arg Asn Ala Val Val
      385      390      395
Gly Ala Asn Glu Asp Gly Tyr His Leu Xaa Gly Val Asn Pro Gly Arg
      405      410      415
Asp Phe Thr Ala Glu Tyr Val Asp Ile Arg Glu Val Arg Glu Gly Glu
      420      425      430
Ile Ser Pro Asp Gly Gln Gly Val Leu Asn Phe Ala Arg Gly Ile Glu
      435      440      445
Ile Gly His Ile Phe Lys Leu Gly Thr Arg Tyr Ser Ala Ser Met Gly
      450      455      460
Ala Asp Val Leu Asp Glu Asn Gly Arg Ala Val Pro Ile Ile Met Gly
      465      470      475
Cys Tyr Gly Ile Gly Val Ser Arg Leu Leu Ser Ala Val Met Glu Gln
      485      490      495
His Ala Arg Leu Phe Val Asn Lys Thr Pro Lys Gly Glu Tyr Arg Tyr
      500      505      510
Ala Trp Gly Ile Asn Phe Pro Lys Glu Leu Ala Pro Phe Asp Val His
      515      520      525
Leu Ile Thr Val Asn Val Lys Asp Glu Glu Ala Gln Ala Leu Thr Glu
      530      535      540
Lys Leu Glu Ala Ser Leu Met Gly Ala Gly Tyr Glu Val Leu Thr Asp
      545      550      555
Asp Arg Asn Glu Arg Val Gly Val Lys Phe Ser Asp Ser Asp Leu Ile
      565      570      575
Gly Leu Pro Ile Arg Ile Thr Val Gly Lys Lys Ala Ala Asp Gly Ile
      580      585      590
Val Glu Val Lys Ile Lys Ala Thr Gly Asp Thr Ile Glu Val His Ala
      595      600      605
Asp Asn Val Leu Glu Thr Leu Glu Ile Leu Ser Lys Lys
      610      615      620

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(2) INFORMATION FOR SEQ ID NO:4620:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 394 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...394

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4620:

Lys	Phe	Asp	Ile	Met	Val	Val	Met	Asn	Arg	Ile	Arg	Val	Ser	Lys	Arg
1				5				10						15	
Val	Glu	Lys	Lys	Leu	Ala	Lys	Gly	Leu	Val	Leu	Leu	Glu	Ala	Ser	Asp
		20					25						30		
Leu	Glu	Asn	Val	Asn	Leu	Lys	Asp	Gln	Glu	Val	Glu	Val	Gln	Gly	Gln
		35					40					45			
Glu	Gly	Asn	Phe	Leu	Gly	Thr	Ala	Tyr	Leu	Ser	Gln	Gln	Asn	Lys	Gly
	50					55					60				
Leu	Gly	Trp	Phe	Val	Ser	Lys	Asp	Lys	Val	Ala	Phe	Asn	Gln	Ala	Phe
65					70					75					80
Phe	Glu	Thr	Leu	Phe	Arg	Lys	Ala	Lys	Glu	Lys	Arg	Asn	Ala	Tyr	Tyr
				85				90						95	
Gln	Asp	Asp	Leu	Thr	Thr	Ala	Phe	Arg	Leu	Phe	Asn	Gln	Glu	Gly	Asp
			100					105					110		
Gly	Phe	Gly	Gly	Leu	Thr	Val	Asp	Leu	Tyr	Gly	Asp	Tyr	Ala	Val	Phe
		115					120					125			
Ser	Trp	Tyr	Asn	Ser	Tyr	Val	Tyr	Gln	Ile	Arg	Gln	Thr	Ile	Ser	Glu
	130					135					140				
Ala	Phe	Arg	Gln	Val	Phe	Pro	Glu	Val	Leu	Gly	Ala	Tyr	Glu	Lys	Ile
145					150					155					160
Arg	Phe	Lys	Gly	Leu	Asp	Tyr	Glu	Ser	Ala	His	Val	Tyr	Gly	Gln	Glu
				165					170					175	
Ala	Pro	Asp	Phe	Thr	Val	Leu	Glu	Asn	Gly	Val	Leu	Tyr	Gln	Val	
		180					185					190			
Phe	Met	Asn	Asp	Gly	Leu	Met	Thr	Gly	Ile	Phe	Leu	Asp	Gln	His	Glu
	195					200						205			
Val	Arg	Gly	Ser	Leu	Val	Asp	Gly	Leu	Ala	Met	Gly	Lys	Ser	Leu	Leu
	210					215					220				
Asn	Met	Phe	Ser	Tyr	Thr	Ala	Ala	Phe	Ser	Val	Ala	Ala	Ala	Met	Gly
225					230					235					240
Gly	Ala	Ser	Gln	Thr	Thr	Ser	Val	Asp	Leu	Ala	Lys	Arg	Ser	Arg	Glu
				245					250					255	
Leu	Ser	Gln	Ala	His	Phe	Gln	Ala	Asn	Gly	Leu	Ser	Thr	Asp	Glu	His
		260					265						270		
His	Phe	Ile	Val	Met	Asp	Val	Phe	Glu	Tyr	Phe	Lys	Tyr	Ala	Lys	Arg
	275						280					285			
Lys	Asp	Leu	Thr	Tyr	Asp	Val	Ile	Val	Leu	Asp	Pro	Pro	Ser	Phe	Ala
	290					295					300				
Arg	Asn	Lys	Lys	Gln	Thr	Phe	Ser	Val	Ala	Lys	Asp	Tyr	His	Lys	Leu
305					310					315					320
Ile	Ser	Gln	Ser	Leu	Glu	Ile	Leu	Asn	Pro	Gly	Gly	Ile	Ile	Ile	Ala
				325					330					335	
Ser	Thr	Asn	Ala	Ala	Asn	Val	Ser	Arg	Gln	Lys	Phe	Thr	Glu	Gln	Ile
		340						345					350		
Asp	Lys	Gly	Phe	Ala	Gly	Arg	Ser	Tyr	Gln	Ile	Leu	Asn	Lys	Tyr	Gly
	355					360					365				
Leu	Pro	Ala	Asp	Phe	Ala	Tyr	Asn	Lys	Lys	Asp	Glu	Ser	Ser	Asn	Tyr
	370					375					380				
Leu	Lys	Val	Ile	Ser	Met	Lys	Val	Ser	Lys						
385					390										

(2) INFORMATION FOR SEQ ID NO:4621:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 275 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...275

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4621:

Thr	Phe	Asp	Ile	Asp	Ile	Ala	Asp	Leu	Arg	Ala	Pro	Leu	Asp	Ala	Glu	1	5	10	15
Glu	Met	Ser	Arg	Ile	Thr	Ile	Glu	Asp	Glu	Tyr	Thr	Leu	Ile	Ile	Val	20	25	30	
Asp	Val	Pro	Val	Thr	Glu	Glu	Arg	Asn	Asn	Arg	Thr	Tyr	Tyr	Val	Thr	35	40	45	
Ile	Pro	Leu	Gly	Ile	Ile	Ile	Thr	Glu	Glu	Thr	Ile	Ile	Thr	Thr	Cys	50	55	60	
Leu	Glu	Pro	Leu	Pro	Val	Leu	Asp	Val	Phe	Ile	Asn	Arg	Arg	Leu	Arg	65	70	75	80
Asn	Phe	Tyr	Thr	Phe	Met	Arg	Ser	Arg	Phe	Ile	Phe	Gln	Ile	Leu	Tyr	85	90	95	
Arg	Asn	Ala	Glu	Leu	Tyr	Leu	Thr	Ala	Leu	Arg	Ser	Ile	Asp	Arg	Lys	100	105	110	
Ser	Glu	Gln	Ile	Glu	Ser	Gln	Leu	His	Gln	Ser	Thr	Arg	Asn	Glu	Glu	115	120	125	
Leu	Ile	Glu	Leu	Met	Glu	Leu	Glu	Lys	Thr	Ile	Val	Tyr	Phe	Lys	Ala	130	135	140	
Ser	Leu	Lys	Thr	Asn	Glu	Arg	Val	Ile	Lys	Lys	Leu	Thr	Ser	Ser	Thr	145	150	155	160
Ser	Asn	Ile	Lys	Lys	Tyr	Leu	Glu	Asp	Glu	Asp	Leu	Leu	Glu	Asp	Thr	165	170	175	
Leu	Ile	Glu	Thr	Gln	Gln	Ala	Ile	Glu	Met	Ala	Asp	Ile	Tyr	Gly	Asn	180	185	190	
Val	Leu	His	Ser	Met	Thr	Glu	Thr	Phe	Ala	Ser	Ile	Ile	Ser	Asn	Asn	195	200	205	
Gln	Asn	Asn	Ile	Met	Lys	Thr	Leu	Ala	Leu	Val	Thr	Ile	Val	Met	Ser	210	215	220	
Ile	Pro	Thr	Met	Val	Phe	Ser	Ala	Tyr	Gly	Met	Asn	Phe	Lys	Asp	Asn	225	230	235	240
Glu	Ile	Pro	Leu	Asn	Gly	Glu	Pro	Asn	Ala	Phe	Trp	Leu	Ile	Val	Phe	245	250	255	
Ile	Ala	Phe	Ala	Met	Ser	Val	Ser	Leu	Thr	Leu	Tyr	Leu	Ile	His	Lys	260	265	270	
Lys	Trp	Phe														275			

(2) INFORMATION FOR SEQ ID NO:4622:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 198 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...198

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4622:

Thr	Lys	Asp	Met	Lys	His	Asp	Phe	Asn	His	Lys	Ala	Glu	Thr	Phe	Asp
1				5				10						15	
Ser	Pro	Lys	Asn	Ile	Phe	Leu	Ala	Asn	Leu	Val	Cys	Gln	Ala	Val	Glu
			20					25					30		
Lys	Gln	Ile	Asp	Ile	Leu	Ser	Asp	Lys	Val	Ile	Leu	Asp	Phe	Gly	Gly
		35					40					45			
Gly	Thr	Gly	Leu	Leu	Ala	Leu	Pro	Leu	Ala	Lys	Gln	Ala	Lys	Ser	Val
	50					55					60				
Thr	Leu	Val	Asp	Ile	Ser	Glu	Lys	Met	Leu	Glu	Gln	Ala	Arg	Leu	Lys
65				70						75				80	
Val	Glu	Gln	Gln	Ala	Ile	Lys	Asn	Ile	Gln	Phe	Leu	Glu	Gln	Asp	Leu
				85					90					95	
Pro	Lys	Asn	Pro	Leu	Glu	Lys	Glu	Phe	Asp	Cys	Leu	Ala	Val	Ser	Arg
			100					105					110		
Val	Leu	His	His	Met	Pro	Asp	Leu	Asp	Ala	Ala	Leu	Ser	Leu	Phe	His
		115					120					125			
Gln	His	Leu	Lys	Glu	Asp	Gly	Lys	Leu	Ile	Ile	Ala	Asp	Phe	Thr	Lys
		130					135					140			
Thr	Glu	Ala	Asn	His	His	Gly	Phe	Asp	Leu	Ala	Glu	Leu	Glu	Asn	Lys
145					150					155				160	
Leu	Ile	Glu	His	Gly	Phe	Ser	Ser	Val	His	Ser	Gln	Ile	Leu	Tyr	Ser
				165						170				175	
Ala	Glu	Asp	Leu	Phe	Gln	Gly	Asn	His	Ser	Glu	Phe	Phe	Leu	Ile	Val
			180					185						190	
Ala	Gln	Lys	Ser	Leu	Ala										
															195

(2) INFORMATION FOR SEQ ID NO:4623:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 80 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4623:

Asn	Met	Asp	Ile	Lys	Ser	Glu	Val	Ile	Glu	Ile	Ile	Asp	Glu	Leu	Phe
1				5					10					15	
Met	Glu	Asp	Val	Ser	Asp	Met	Met	Asp	Glu	Asp	Leu	Phe	Asp	Ala	Gly
			20					25					30		
Val	Leu	Asp	Ser	Met	Gly	Thr	Val	Glu	Leu	Ile	Val	Glu	Ile	Glu	Asn
			35				40					45			
Arg	Phe	Asp	Ile	Arg	Val	Pro	Val	Thr	Glu	Phe	Gly	Arg	Asp	Asp	Trp
	50				55					60					
Asn	Thr	Ala	Asn	Lys	Ile	Ile	Ala	Gly	Ile	Val	Glu	Leu	Gln	Asn	Ala
65					70				75					80	

(2) INFORMATION FOR SEQ ID NO:4624:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...243

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4624:

Ile	Met	Asp	Ile	Lys	Leu	Lys	Asp	Phe	Glu	Gly	Pro	Leu	Asp	Leu	Leu
1				5					10					15	
Leu	His	Leu	Val	Ser	Lys	Tyr	Gln	Met	Asp	Ile	Tyr	Asp	Val	Pro	Ile
			20					25					30		
Thr	Glu	Val	Ile	Glu	Gln	Tyr	Leu	Ala	Tyr	Val	Ser	Thr	Leu	Gln	Ala
			35				40					45			
Met	Arg	Leu	Glu	Val	Thr	Gly	Glu	Tyr	Met	Val	Met	Ala	Ser	Gln	Leu
	50				55					60					
Met	Leu	Ile	Lys	Ser	Arg	Lys	Leu	Leu	Pro	Lys	Val	Ala	Glu	Val	Thr
65					70				75					80	
Asp	Leu	Gly	Asp	Asp	Leu	Glu	Gln	Asp	Leu	Leu	Ser	Gln	Ile	Glu	Glu
			85					90				95			
Tyr	Arg	Lys	Phe	Lys	Leu	Leu	Gly	Glu	His	Leu	Glu	Ala	Lys	His	Gln
			100				105					110			
Glu	Arg	Ala	Gln	Tyr	Tyr	Ser	Lys	Ala	Pro	Thr	Glu	Leu	Ile	Tyr	Glu
		115				120					125				
Asp	Ala	Glu	Leu	Val	His	Asp	Lys	Thr	Thr	Ile	Asp	Leu	Phe	Leu	Ala
130						135					140				

Phe	Ser	Asn	Ile	Leu	Ala	Lys	Lys	Lys	Glu	Glu	Phe	Ala	Gln	Asn	His
145					150				155						160
Thr	Thr	Ile	Leu	Arg	Asp	Glu	Tyr	Lys	Ile	Glu	Asp	Met	Met	Ile	Ile
			165						170						175
Val	Lys	Glu	Ser	Leu	Ile	Gly	Arg	Asp	Gln	Leu	Arg	Leu	Gln	Asp	Leu
			180						185						190
Phe	Lys	Glu	Ala	Gln	Asn	Val	Gln	Glu	Val	Ile	Thr	Leu	Phe	Leu	Ala
			195					200					205		
Thr	Leu	Glu	Leu	Ile	Lys	Thr	Gln	Glu	Leu	Ile	Leu	Val	Gln	Glu	Glu
			210				215					220			
Ser	Phe	Gly	Asp	Ile	Tyr	Leu	Met	Glu	Lys	Lys	Glu	Glu	Ser	Gln	Val
225					230					235					240
Pro	Gln	Ser													

(2) INFORMATION FOR SEQ ID NO:4625:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4625:

Lys	Met	Asp	Ile	Val	Tyr	Ala	Thr	Asp	Asn	Asn	Phe	Val	Asp	Val	Leu
1				5					10					15	
Ser	Ala	Ser	Ile	Lys	Ser	Leu	Tyr	Thr	Thr	Asn	Ser	Asp	Leu	Asp	Leu
			20					25					30		
Asn	Leu	Trp	Ile	Ile	Ala	Asp	Lys	Val	Ser	Asp	Arg	Asn	Lys	Glu	Lys
		35					40				45				
Ile	Asn	Arg	Leu	Ser	Lys	Gln	Phe	Ala	Gln	Arg	Glu	Ile	Asn	Trp	Ile
	50					55					60				
Glu	Asn	Val	Glu	Ile	Pro	Phe	Lys	Leu	His	Leu	Asp	Arg	Gly	Ser	Ile
65					70					75					80
Ser	Ser	Phe	Ser	Arg	Leu	Phe	Leu	Gly	Ser	Val	Leu	Pro	Ser	Ser	Met
				85					90					95	
Ser	Lys	Val	Leu	Tyr	Leu	Asp	Ser	Asp	Ile	Ile	Val	Met	Asp	Ser	Leu
			100					105					110		
Arg	Ser	Ile	Leu	Asp	Ile	Asp	Phe	Lys	Asp	Lys	Ile	Leu	Tyr	Gly	Val
		115					120					125			
Asn	Asp	Thr	Phe	Asn	Lys	Glu	Tyr	Lys	Gln	Val	Leu	Gly	Ile	Pro	Ile
		130				135					140				
Asp	Lys	Pro	Met	Phe	Asn	Ala	Gly	Val	Met	Leu	Ile	Asn	Leu	Glu	Leu
145					150				155						160
Trp	Arg	Asn	Asn	Asn	Val	Glu	Glu	Lys	Phe	Leu	Gln	Val	Ile	Gln	Lys
				165					170					175	

Phe	Asn	Gly	Thr	Ile	Leu	Gln	Gly	Asp	Leu	Gly	Val	Leu	Asn	Ala	Val
			180					185					190		
Leu	Tyr	Asn	Ser	Phe	Gly	Val	Leu	Pro	Pro	Glu	Tyr	Asn	Tyr	Met	Thr
		195					200					205			
Ile	Phe	Glu	Asp	Leu	Thr	Tyr	Glu	Glu	Met	Ile	Val	Phe	Lys	Lys	Pro
	210					215					220				
Ile	Asn	Tyr	Tyr	Ser	Lys	Glu	Glu	Ile	Lys	Asn	Ala	Arg	Glu	Arg	Ile
225					230					235					240
Val	Leu	Arg	His	Phe	Thr	Thr	Cys	Phe	Leu	Ser	Leu	Arg	Pro	Trp	Gln
			245					250						255	
Glu	Asn	Ser	Glu	Val	Ala	His	Val	Glu	Ile	Phe	Lys	Lys	Tyr	Tyr	Arg
			260					265					270		
Gly	Thr	Tyr	Lys	Gln	Val	Ser	Pro	Ser	Lys	Leu	Ser	Arg	Ile	Tyr	Lys
			275					280					285		
Ile	Leu	Pro	Lys	Lys	Met	Ser	Leu	Tyr	Leu	Leu	Gly	Phe	Ile	Gln	Ser
	290					295					300				
Lys	Val	Arg	Pro	Lys	Leu	Tyr	Arg	Ile	Leu	Lys					
305					310					315					

(2) INFORMATION FOR SEQ ID NO:4626:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4626:

Thr	Leu	Cys	Ile	Phe	Arg	Lys	Cys	Val	Asn	Leu	Lys	Glu	Gln	Ile	Phe
1				5					10					15	
Leu	Met	Gly	Gly	Asn	Pro	Pro	Met	Lys	Lys	Tyr	Ser	Ile	Val	Asp	Lys
			20					25					30		
Ile	Val	Leu	Ser	Thr	Lys	Ile	Lys	Arg	Ile	Ile	Ile	Phe	Thr	Val	Phe
			35				40					45			
Arg	Glu	Asn	Trp	Glu	Pro	Tyr	Met	Lys	Lys	Tyr	Thr	Glu	Val	Phe	Gln
			50			55				60					
Ser	Gln	Phe	Pro	Asn	Leu	Asn	Ile	Asp	Tyr	Leu	Leu	Leu	Asp	Thr	Glu
65				70					75					80	
Gln	Ile	Asp	Leu	Asp	Ser	Tyr	Leu	Asp	Ala	Asp	Ile	Ile	Ile	Ile	Gly
			85					90					95		
Gly	Gly	Asn	Thr	Glu	Lys	Tyr	Ile	Ala	Thr	Tyr	Val	Asn	Gln	Glu	Phe
			100					105					110		
Lys	Ser	Tyr	Ile	Asp	His	Met	Leu	Asn	Lys	Glu	Ala	Lys	Ile	Ile	Gly
		115				120						125			
Phe	Ser	Ala	Gly	Ala	Leu	Leu	Leu	Gly	Glu	Lys	Val	Tyr	Val	Ser	Pro

130		135		140	
Asn	Asp	Asn	Ser	Asp	His
145		150		155	
Phe	Ser	Gln	Phe	Leu	Ile
		165		170	
Ala	Asn	Lys	Asp	Arg	Ala
		180		185	
Leu	Asn	Asp	His	Ser	Cys
		195		200	
Glu	Lys	Ile	Asp		
210					

(2) INFORMATION FOR SEQ ID NO:4627:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 570 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...570

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4627:

Leu	Leu	Cys	Ile	His	Ser	Ser	Lys	Asn	Thr	Leu	Ile	Lys	Glu	Leu	Trp
1				5					10					15	
Leu	Val	His	Leu	Lys	Asp	Lys	Lys	Arg	Lys	Asn	Lys	Arg	Ser	Phe	Leu
		20						25					30		
Met	Lys	Phe	Lys	Thr	Phe	Ser	Lys	Ser	Ala	Val	Leu	Leu	Thr	Ala	Ser
		35					40					45			
Leu	Ala	Val	Leu	Ala	Ala	Cys	Gly	Ser	Lys	Asn	Thr	Ala	Ser	Ser	Pro
	50					55					60				
Asp	Tyr	Lys	Leu	Glu	Gly	Val	Thr	Phe	Pro	Leu	Gln	Glu	Lys	Lys	Thr
65				70					75					80	
Leu	Lys	Phe	Met	Thr	Ala	Ser	Ser	Pro	Leu	Ser	Pro	Lys	Asp	Pro	Asn
			85					90					95		
Glu	Lys	Leu	Ile	Leu	Gln	Arg	Leu	Glu	Lys	Glu	Thr	Gly	Val	His	Ile
		100					105					110			
Asp	Trp	Thr	Asn	Tyr	Gln	Ser	Asp	Phe	Ala	Glu	Lys	Arg	Asn	Leu	Asp
	115					120						125			
Ile	Ser	Ser	Gly	Asp	Leu	Pro	Asp	Ala	Ile	His	Asn	Asp	Gly	Ala	Ser
	130				135						140				
Asp	Val	Asp	Leu	Met	Asn	Trp	Ala	Lys	Lys	Gly	Val	Ile	Ile	Pro	Val
145				150					155					160	
Glu	Asp	Leu	Ile	Asp	Lys	Tyr	Met	Pro	Asn	Leu	Lys	Lys	Ile	Leu	Asp
		165					170					175			
Glu	Lys	Pro	Glu	Tyr	Lys	Ala	Leu	Met	Thr	Ala	Pro	Asp	Gly	His	Ile
	180					185					190				
Tyr	Ser	Phe	Pro	Trp	Ile	Glu	Glu	Leu	Gly	Asp	Gly	Lys	Glu	Ser	Ile

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...755

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4628:

Gly	Arg	Cys	Met	Leu	Cys	Gln	Asn	Cys	Lys	Ile	Asn	Asp	Ser	Thr	Ile
1				5					10					15	
His	Leu	Tyr	Thr	Asn	Leu	Asn	Gly	Lys	Gln	Lys	Gln	Ile	Asp	Leu	Cys
			20					25					30		
Gln	Asn	Cys	Tyr	Lys	Ile	Ile	Lys	Thr	Asp	Pro	Asn	Asn	Ser	Leu	Phe
		35					40					45			
Lys	Gly	Met	Thr	Asp	Leu	Asn	Asn	Arg	Asp	Phe	Asp	Pro	Phe	Gly	Asp
	50					55					60				
Phe	Phe	Asn	Asp	Leu	Asn	Asn	Phe	Arg	Pro	Ser	Ser	Asn	Thr	Pro	Pro
65					70					75					80
Ile	Pro	Pro	Thr	Gln	Ser	Gly	Gly	Gly	Tyr	Gly	Gly	Asn	Gly	Gly	Tyr
				85					90					95	
Gly	Ser	Gln	Asn	Arg	Gly	Ser	Ala	Gln	Thr	Pro	Pro	Pro	Ser	Gln	Glu
			100					105					110		
Lys	Gly	Leu	Leu	Lys	Glu	Phe	Gly	Ile	Asn	Val	Thr	Glu	Ile	Ala	Arg
		115					120					125			
Arg	Gly	Asp	Ile	Asp	Pro	Val	Ile	Gly	Arg	Asp	Asp	Glu	Ile	Ile	Arg
	130					135					140				
Val	Ile	Glu	Ile	Leu	Asn	Arg	Arg	Thr	Lys	Asn	Asn	Pro	Val	Leu	Ile
145					150					155					160
Gly	Glu	Pro	Gly	Val	Gly	Lys	Thr	Ala	Val	Val	Glu	Gly	Leu	Ala	Gln
				165					170					175	
Lys	Ile	Val	Asp	Gly	Asp	Val	Pro	His	Lys	Leu	Gln	Gly	Lys	Gln	Val
			180					185					190		
Ile	Arg	Leu	Asp	Val	Val	Ser	Leu	Val	Gln	Gly	Thr	Gly	Ile	Arg	Gly
	195						200					205			
Gln	Phe	Glu	Glu	Arg	Met	Gln	Lys	Leu	Met	Glu	Glu	Ile	Arg	Lys	Arg
	210					215					220				
Glu	Asp	Ile	Ile	Leu	Phe	Ile	Asp	Glu	Ile	His	Glu	Ile	Val	Gly	Ala
225					230					235					240
Gly	Ser	Ala	Ser	Asp	Gly	Asn	Met	Asp	Ala	Gly	Asn	Ile	Leu	Lys	Pro
				245					250					255	
Ala	Leu	Ala	Arg	Gly	Glu	Leu	Gln	Leu	Val	Gly	Ala	Thr	Thr	Leu	Asn
			260					265					270		
Glu	Tyr	Arg	Ile	Ile	Glu	Lys	Asp	Ala	Ala	Leu	Glu	Arg	Arg	Met	Gln
	275						280					285			
Pro	Val	Lys	Val	Asp	Glu	Pro	Thr	Val	Asp	Glu	Thr	Ile	Thr	Ile	Leu
	290					295					300				
Lys	Gly	Ile	Gln	Lys	Lys	Tyr	Glu	Asp	Tyr	His	His	Val	Gln	Tyr	Thr
305					310					315					320
Asp	Ala	Ala	Ile	Glu	Ala	Ala	Ala	Thr	Leu	Ser	Asn	Arg	Tyr	Ile	Gln
				325					330					335	
Asp	Arg	Phe	Leu	Pro	Asp	Lys	Ala	Ile	Asp	Leu	Leu	Asp	Glu	Ala	Gly
			340					345					350		
Ser	Lys	Met	Asn	Leu	Thr	Leu	Asn	Phe	Val	Asp	Pro	Lys	Val	Ile	Asp
		355					360						365		

Gln	Arg	Leu	Ile	Glu	Ala	Glu	Asn	Leu	Lys	Ser	Gln	Ala	Thr	Arg	Glu
370						375					380				
Glu	Asp	Phe	Glu	Lys	Ala	Ala	Tyr	Phe	Arg	Asp	Gln	Ile	Ala	Lys	Tyr
385					390					395					400
Lys	Glu	Met	Gln	Lys	Lys	Lys	Ile	Thr	Asp	Gln	Asp	Thr	Pro	Ile	Ile
			405						410					415	
Ser	Glu	Lys	Thr	Ile	Glu	His	Ile	Ile	Glu	Gln	Lys	Thr	Asn	Ile	Pro
			420					425					430		
Val	Gly	Asp	Leu	Lys	Glu	Lys	Glu	Gln	Ser	Gln	Leu	Ile	His	Leu	Ala
		435					440					445			
Glu	Asp	Leu	Lys	Ser	His	Val	Ile	Gly	Gln	Asp	Asp	Ala	Val	Asp	Lys
	450					455					460				
Ile	Ala	Lys	Ala	Ile	Arg	Arg	Asn	Arg	Val	Gly	Leu	Gly	Thr	Pro	Asn
465					470					475					480
Arg	Pro	Ile	Gly	Ser	Phe	Leu	Phe	Val	Gly	Pro	Thr	Gly	Val	Gly	Lys
			485						490					495	
Thr	Glu	Leu	Ser	Lys	Gln	Leu	Ala	Ile	Glu	Leu	Phe	Gly	Ser	Ala	Asp
			500					505					510		
Ser	Met	Ile	Arg	Phe	Asp	Met	Ser	Glu	Tyr	Met	Glu	Lys	His	Ser	Val
	515					520						525			
Ala	Lys	Leu	Val	Gly	Ala	Pro	Pro	Gly	Tyr	Val	Gly	Tyr	Asp	Glu	Ala
	530				535						540				
Gly	Gln	Leu	Thr	Glu	Lys	Val	Arg	His	Asn	Pro	Tyr	Ser	Leu	Ile	Leu
545					550					555					560
Leu	Asp	Glu	Val	Glu	Lys	Ala	His	Pro	Asp	Val	Met	His	Met	Phe	Leu
			565						570					575	
Gln	Val	Leu	Asp	Asp	Gly	Arg	Leu	Thr	Asp	Gly	Gln	Gly	Arg	Thr	Val
		580						585					590		
Ser	Phe	Lys	Asp	Ala	Ile	Ile	Ile	Met	Thr	Ser	Asn	Ala	Gly	Thr	Gly
	595					600						605			
Lys	Thr	Glu	Ala	Ser	Val	Gly	Phe	Gly	Ala	Thr	Arg	Glu	Gly	Arg	Thr
	610					615					620				
Asn	Ser	Val	Leu	Gly	Glu	Leu	Gly	Asn	Phe	Phe	Ser	Pro	Glu	Phe	Met
625				630					635						640
Asn	Arg	Phe	Asp	Gly	Ile	Ile	Glu	Phe	Lys	Ala	Leu	Ser	Lys	Asp	Asn
			645						650					655	
Leu	Leu	Gln	Ile	Val	Glu	Leu	Met	Leu	Ala	Asp	Val	Asn	Lys	Arg	Leu
		660					665						670		
Ser	Ser	Asn	Asn	Ile	Arg	Leu	Asp	Val	Thr	Asp	Lys	Val	Lys	Glu	Lys
	675						680					685			
Leu	Val	Asp	Leu	Gly	Tyr	Asp	Pro	Lys	Met	Gly	Ala	Arg	Pro	Leu	Arg
	690					695					700				
Arg	Thr	Ile	Gln	Asp	Tyr	Ile	Glu	Asp	Thr	Ile	Thr	Asp	Tyr	Tyr	Leu
705					710					715					720
Glu	Asn	Pro	Ser	Glu	Lys	Asp	Leu	Lys	Ala	Val	Met	Thr	Ser	Lys	Gly
			725						730					735	
Asn	Ile	Gln	Ile	Lys	Ser	Ala	Lys	Lys	Ala	Glu	Val	Lys	Ser	Ser	Glu
			740					745					750		
Lys	Glu	Lys													
		755													

(2) INFORMATION FOR SEQ ID NO:4629:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 194 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...194
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4629:

```

His Lys Cys Ile Ile Leu Tyr Ile Asp Lys Asn Ile Asp Lys Arg Lys
1      5      10      15
Asp Thr Asn Met Val Leu Ala Ile Ile Leu Val Thr Phe Leu Ile Arg
      20      25      30
Leu Ile Phe Leu Lys Arg Ser Ile Glu Asn Glu Lys Arg Ile Leu Ser
      35      40      45
Asn Gly Gly Lys Glu Phe Gly Val Glu Asn Thr Lys Arg Leu Thr Leu
      50      55      60
Ala His Ile Val Phe Tyr Leu Ser Cys Leu Val Glu Ala Met Val His
      65      70      75      80
Lys Thr Met Phe Asp Gly Met Ser Met Val Gly Leu Val Leu Leu Ile
      85      90      95
Phe Ser Met Leu Met Leu Met Leu Val Ile His Leu Leu Gly Asp Ile
      100     105     110
Trp Thr Val Lys Leu Met Leu Val Asn Asn His Lys Tyr Val Asp His
      115     120     125
Ile Leu Phe Arg Thr Val Lys His Pro Asn Tyr Phe Leu Asn Ile Leu
      130     135     140
Pro Glu Leu Ile Gly Leu Thr Leu Leu Ser His Ala Tyr Met Thr Phe
      145     150     155     160
Val Leu Val Phe Pro Val Tyr Ala Val Ile Leu Tyr Arg Arg Ile Ala
      165     170     175
Glu Glu Glu Lys Leu Leu His Glu Val Ile Ile Pro Asn Gly Ser Ile
      180     185     190
Lys Arg

```

(2) INFORMATION FOR SEQ ID NO:4630:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 391 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:

```
(A) NAME/KEY: misc_feature
(B) LOCATION 1...391
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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4630:

Gly 1	Glu	Cys	Met	Arg 5	Tyr	Leu	Thr	Ala	Gly 10	Glu	Ser	His	Gly	Pro 15	Arg
Leu	Thr	Ala	Ile 20	Ile	Glu	Gly	Ile	Pro 25	Ala	Gly	Leu	Pro	Leu 30	Thr	Ala
Glu	Asp	Ile 35	Asn	Glu	Asp	Leu	Arg 40	Arg	Arg	Gln	Gly	Gly 45	Tyr	Gly	Arg
Gly 50	Gly	Arg	Met	Lys	Ile	Glu	Ser 55	Asp	Gln	Val	Val	Phe	Thr	Ser	Gly
Val 65	Arg	His	Gly	Lys 70	Thr	Thr	Gly	Ala	Pro	Ile	Thr	Met	Asp	Val	Ile 80
Asn	Lys	Asp	His	Gln 85	Lys	Trp	Leu	Asp	Ile 90	Met	Ser	Ala	Glu	Asp	Ile 95
Glu	Asp	Arg	Leu 100	Lys	Ser	Lys	Arg	Lys 105	Ile	Thr	His	Pro	Arg	Pro	Gly
His	Ala	Asp 115	Leu	Val	Gly	Gly	Ile 120	Lys	Tyr	Arg	Phe	Asp	Asp	Leu	Arg
Asn	Ser	Leu	Glu	Arg	Ser	Ser	Ala 135	Arg	Glu	Thr	Thr	Met	Arg	Val	Ala
Val 145	Gly	Ala	Val	Ala 150	Lys	Arg	Leu	Leu	Ala	Glu	Leu	Asp	Met	Glu	Ile 160
Ala	Asn	His	Val	Val 165	Val	Phe	Gly	Gly	Lys	Glu	Ile	Asp	Val	Pro	Glu
Asn	Leu	Thr	Val	Ala 180	Glu	Ile	Lys	Gln	Arg	Ala	Ala	Gln	Ser	Glu	Val
Ser	Ile	Val	Asn	Gln	Glu	Arg	Glu	Gln	Glu	Ile	Lys	Asp	Tyr	Ile	Asp
Gln	Ile	Lys	Arg	Asp	Gly	Asp	Thr	Ile	Gly	Gly	Val	Val	Glu	Thr	Val
Val 225	Gly	Gly	Val	Pro	Val	Gly	Leu	Gly	Ser	Tyr	Val	Gln	Trp	Asp	Arg
Lys	Leu	Asp	Ala	Arg	Leu	Ala	Gln	Ala	Val	Val	Ser	Ile	Asn	Ala	Phe
Lys	Gly	Val	Glu	Phe	Gly	Leu	Gly	Phe	Glu	Ala	Gly	Tyr	Arg	Lys	Gly
Ser	Gln	Val	Met	Asp	Glu	Ile	Leu	Trp	Ser	Lys	Glu	Asp	Gly	Tyr	Thr
Arg	Arg	Thr	Asn	Asn	Leu	Gly	Gly	Phe	Glu	Gly	Gly	Met	Thr	Asn	Gly
Gln 305	Pro	Ile	Val	Val	Arg	Gly	Val	Met	Lys	Pro	Ile	Pro	Thr	Leu	Tyr
Lys	Pro	Leu	Met	Ser	Val	Asp	Ile	Glu	Thr	His	Glu	Pro	Tyr	Lys	Ala
Thr	Val	Glu	Arg	Ser	Asp	Pro	Thr	Ala	Leu	Pro	Ala	Ala	Gly	Met	Val
Met	Glu	Ala	Val	Val	Ala	Thr	Val	Leu	Ala	Gln	Glu	Ile	Leu	Glu	Lys
Phe	Ser	Ser	Asp	Asn	Leu	Glu	Glu	Leu	Lys	Glu	Ala	Val	Ala	Lys	His
Arg 385	Asp	Tyr	Thr	Lys	Asn	Tyr									

(2) INFORMATION FOR SEQ ID NO:4631:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 491 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...491
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4631:

Arg	Arg	Cys	Ile	Val	Ser	Arg	Lys	Gln	Glu	Gln	Met	Glu	Thr	Leu	Leu
1			5					10						15	
Leu	Leu	Leu	Arg	Asp	Ser	Lys	Asp	Tyr	Ile	Ser	Ala	Lys	Val	Leu	Gly
		20					25					30			
Glu	Lys	Leu	Asn	Cys	Ser	Asp	Lys	Thr	Val	Tyr	Arg	Leu	Val	Lys	Gly
	35					40					45				
Ile	Asn	Lys	Asp	Cys	Pro	Val	Glu	Ala	Phe	Ile	Leu	Ser	Glu	Lys	Gly
	50				55					60					
Arg	Gly	Phe	Lys	Leu	Asn	Pro	Arg	Ser	Ser	Leu	Val	Asp	Val	Asp	Gly
65				70					75					80	
Asn	Phe	Thr	Glu	Ala	Phe	Asp	Pro	Glu	Val	Arg	Arg	Glu	Lys	Leu	Leu
		85					90						95		
Glu	Arg	Leu	Leu	Leu	Thr	Ala	Pro	Lys	Pro	His	Ser	Ile	Tyr	Asp	Leu
	100						105					110			
Gly	Glu	Glu	Phe	Tyr	Val	Ser	Glu	Ser	Val	Val	Leu	Lys	Asp	Arg	Gln
	115					120					125				
Ile	Leu	Gln	Glu	Ser	Leu	Ala	Ile	Tyr	Gly	Leu	Asp	Leu	Lys	Met	Arg
	130				135					140					
Gln	Arg	Lys	Leu	Phe	Ile	Asp	Gly	Asp	Glu	Ala	Gln	Ile	Arg	Ser	Ala
145				150					155					160	
Ile	Leu	Asn	Leu	Leu	Pro	Met	Phe	Asn	Gln	Leu	Asp	Leu	Glu	Gln	Ile
		165					170						175		
Thr	Gln	Asn	Lys	Val	Gln	Pro	Leu	Asp	Gly	Glu	Leu	Ala	His	Phe	Cys
	180					185						190			
Leu	Gly	Leu	Leu	Ile	Thr	Leu	Glu	Arg	Glu	Leu	Gly	Val	Asn	Ile	Pro
	195					200					205				
Tyr	Pro	Tyr	Asn	Ile	Asn	Ile	Phe	Ser	His	Leu	Tyr	Ile	Phe	Ile	Ser
	210				215					220					
Arg	Asn	Arg	Arg	Ser	Thr	Ser	Ile	His	Val	Val	Ala	Pro	Ser	Lys	Pro
225				230					235					240	
Thr	Ile	Val	Asp	Glu	Lys	Ile	Tyr	Ser	Val	Cys	Gln	Lys	Ile	Ile	Gln
		245					250						255		
Glu	Ile	Glu	Gln	Tyr	Phe	Arg	Met	Lys	Val	Asp	Ala	Val	Glu	Ile	Asp
	260						265					270			
Tyr	Leu	Tyr	Gln	Tyr	Val	Val	Ser	Ser	Arg	Leu	Gln	Lys	Pro	Phe	Ser
	275					280					285				
Ser	Gly	Lys	Leu	Pro	Phe	Ser	Gln	Arg	Val	Leu	Asp	Val	Thr	His	Tyr
	290					295				300					

Tyr	Phe	Ser	Arg	Met	Cys	Met	Asp	Asn	Arg	Glu	Ile	Glu	Thr	Thr	Asp
305					310					315					320
Pro	Asp	Phe	Val	Asp	Leu	Ala	Ser	His	Ile	Ser	Pro	Leu	Leu	Arg	Arg
				325					330						335
Leu	Asp	Asn	Arg	Val	Gln	Ile	Lys	Asn	Ser	Leu	Leu	Ser	Gln	Ile	Leu
				340				345						350	
Leu	Thr	Tyr	Pro	Asn	Leu	Val	Lys	Glu	Leu	Thr	Thr	Ile	Ser	Lys	Glu
				355			360					365			
Val	Ser	Leu	Val	Phe	Gly	Phe	Ala	Ser	Leu	Ser	Leu	Asp	Glu	Ile	Gly
				370			375				380				
Phe	Leu	Val	Leu	Tyr	Phe	Ala	Arg	Phe	Gln	Glu	Lys	Arg	Ala	Arg	Pro
385					390					395					400
Leu	Lys	Thr	Val	Val	Met	Cys	Thr	Ser	Gly	Val	Gly	Thr	Ser	Glu	Leu
				405					410					415	
Leu	Arg	Ala	Arg	Leu	Glu	Lys	Gln	Phe	Ser	Glu	Leu	Asp	Ile	Ile	Asp
				420				425					430		
Val	Val	Ala	Tyr	His	Gln	Leu	Asp	Glu	Leu	Ile	Asn	Leu	Tyr	Pro	Asp
				435			440					445			
Leu	Asp	Phe	Ile	Val	Thr	Thr	Val	Ala	Leu	Gln	Glu	Pro	Ala	Ser	Val
				450			455				460				
Pro	Phe	Val	Leu	Val	Ser	Val	Phe	Leu	Thr	Glu	Gly	Asp	Lys	Gln	Arg
465					470					475					480
Leu	Gln	Ala	Lys	Ile	Gln	Glu	Ile	Asn	Tyr	Glu					
				485				490							

(2) INFORMATION FOR SEQ ID NO:4632:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 217 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4632:

Gly	Gln	Leu	Leu	Cys	Arg	Gln	Lys	Met	Trp	Pro	Arg	Glu	Ser	Arg	Ser
1				5				10						15	
Cys	Arg	Leu	Thr	Lys	Val	Lys	Ile	Cys	Gly	Leu	Ser	Thr	Lys	Glu	Ala
				20				25					30		
Val	Glu	Thr	Ala	Val	Ser	Ala	Gly	Ala	Asp	Tyr	Ile	Gly	Phe	Val	Phe
				35			40					45			
Ala	Pro	Ser	Lys	Arg	Gln	Val	Thr	Leu	Glu	Glu	Ala	Ala	Glu	Leu	Ala
				50		55					60				
Lys	Leu	Ile	Pro	Ala	Asp	Val	Lys	Lys	Val	Gly	Val	Phe	Val	Ser	Pro
65					70					75					80
Ser	Arg	Val	Glu	Leu	Glu	Ala	Ile	Asp	Lys	Val	Asp	Leu	Asp	Leu	
				85				90						95	

Val	Gln	Val	His	Gly	Gln	Val	Ala	Asp	Asp	Leu	Phe	Glu	Asn	Leu	Pro
			100					105					110		
Cys	Ala	Ser	Ile	Gln	Ala	Val	Gln	Val	Asp	Gly	Asn	Gly	His	Val	Pro
		115					120					125			
Asn	Ser	Gln	Ala	Asp	Tyr	Leu	Leu	Phe	Asp	Ala	Pro	Val	Ala	Gly	Ser
		130				135					140				
Gly	Gln	Ser	Phe	Asp	Trp	Gly	Gln	Leu	Asp	Thr	Thr	Gly	Leu	Ala	Gln
145				150					155						160
Pro	Phe	Phe	Ile	Ala	Gly	Gly	Leu	Asn	Glu	Asp	Asn	Val	Val	Lys	Ala
				165					170						175
Ile	Gln	His	Phe	Thr	Pro	Tyr	Ala	Val	Asp	Val	Ser	Ser	Gly	Val	Glu
			180				185						190		
Thr	Asp	Gly	Gln	Lys	Asp	His	Glu	Lys	Ile	Arg	Arg	Phe	Ile	Glu	Arg
		195				200						205			
Val	Lys	His	Gly	Ile	Ser	Gly	Thr	Lys							
	210					215									

(2) INFORMATION FOR SEQ ID NO:4633:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 185 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...185

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4633:

Glu	Asn	Ser	Met	Glu	Ile	Lys	Phe	Thr	Ile	Lys	Gln	Val	Val	Ala	Val
1			5					10						15	
Gly	Ile	Gly	Ala	Ala	Leu	Phe	Val	Val	Ile	Gly	Met	Ile	Asn	Ile	Pro
		20					25					30			
Thr	Pro	Val	Pro	Asn	Thr	Ser	Ile	Gln	Leu	Gln	Tyr	Ala	Val	Gln	Ala
		35				40					45				
Leu	Leu	Ser	Ile	Ile	Phe	Gly	Pro	Ile	Ile	Gly	Leu	Leu	Val	Gly	Leu
	50					55				60					
Ile	Gly	His	Ala	Ile	Lys	Asp	Ser	Leu	Val	Gly	Tyr	Gly	Leu	Trp	Trp
65				70				75						80	
Thr	Trp	Ile	Ile	Ser	Ser	Gly	Leu	Phe	Gly	Leu	Val	Val	Gly	Leu	Phe
			85			90							95		
Arg	Lys	Tyr	Val	Arg	Val	Ile	Asn	Ser	Val	Phe	Asp	Trp	Lys	Asp	Ile
		100				105						110			
Leu	Ile	Phe	Asn	Leu	Ile	Gln	Leu	Leu	Ala	Asn	Ala	Leu	Val	Trp	Gly
		115				120					125				
Val	Leu	Ala	Pro	Leu	Gly	Asp	Val	Val	Ile	Tyr	Gln	Glu	Ala	Ala	Glu
	130				135					140					
Lys	Val	Phe	Ala	Gln	Gly	Ile	Val	Ala	Gly	Ile	Ala	Asn	Gly	Val	Ser
145				150				155							160

Val	Ala	Ile	Ala	Gly	Thr	Leu	Leu	Leu	Leu	Ala	Tyr	Ala	Gly	Thr	Gln
				165					170					175	
Thr	Arg	Ala	Gly	Ser	Leu	Lys	Lys	Asp							
			180					185							

(2) INFORMATION FOR SEQ ID NO:4634:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 190 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4634:

Gly	Asn	Ser	Met	Ile	Tyr	Leu	Arg	Lys	Leu	Lys	Arg	Glu	Asp	Leu	Met
1				5					10					15	
Ser	Leu	Trp	Glu	Met	Ala	Tyr	Ser	Gln	Leu	Asn	Pro	Val	Trp	Lys	Gln
			20					25					30		
Tyr	Asp	Ala	Pro	Tyr	Tyr	Asp	Asp	Tyr	Gln	Tyr	Phe	Ser	Asn	Phe	Lys
		35					40					45			
Glu	Phe	Glu	Leu	Gln	Lys	Ser	Glu	Ser	Ile	Leu	Ser	Asn	Ser	Asn	Arg
	50					55					60				
Leu	Gly	Ile	Phe	Val	Asp	Asp	Lys	Leu	Val	Gly	Thr	Val	Ser	Arg	Tyr
65					70					75				80	
Trp	Val	Cys	Lys	Gln	Thr	Arg	Trp	Met	Glu	Leu	Gly	Ile	Gly	Ile	Tyr
			85					90					95		
Asp	Lys	Lys	Phe	Trp	Asn	Thr	Gly	Ile	Gly	Lys	Val	Ala	Met	Leu	Gln
			100				105						110		
Trp	Ile	Asp	Arg	Thr	Phe	Gln	Asp	Tyr	Leu	Glu	Leu	Glu	His	Leu	Gly
		115					120					125			
Leu	Thr	Thr	Trp	Ser	Gly	Asn	Leu	Gly	Met	Met	Lys	Leu	Ala	Glu	Lys
	130					135					140				
Leu	Arg	Met	Lys	Lys	Glu	Ala	His	Ile	Pro	Lys	Val	Arg	Tyr	Tyr	Gln
145					150					155					160
Gly	Lys	Tyr	Phe	Asp	Ser	Ile	Lys	Tyr	Gly	Ile	Leu	Arg	Glu	Asp	Trp
				165					170					175	
Glu	Lys	Met	Asn	Asp	Gly	Tyr	Tyr	Gln	Ile	Asn	Gly	Asn	Ser		
			180					185					190		

(2) INFORMATION FOR SEQ ID NO:4635:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...264
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4635:

```

Met Asp Ser Met Ile Leu Gly Arg Tyr Ile Pro Gly Asp Ser Ile Val
1      5      10      15
His Arg Leu Asp Pro Arg Ser Lys Leu Leu Ala Met Met Leu Leu Ile
      20      25      30
Leu Ile Val Phe Trp Ala Asn Asn Pro Leu Thr Asn Leu Ile Leu Phe
      35      40      45
Ile Ala Thr Gly Ile Phe Ile Ala Leu Ser Gly Val Ser Leu Ser Phe
      50      55      60
Phe Ile Gln Gly Leu Lys Ser Met Phe Phe Leu Ile Ala Phe Thr Thr
      65      70      75      80
Ile Phe Gln Leu Phe Phe Ile Ser Asn Gly Asn Val Leu Phe Glu Phe
      85      90      95
Ser Phe Val Arg Ile Thr Asp Tyr Ala Leu Gln Gln Ala Gly Ile Ile
      100     105     110
Phe Cys Arg Phe Val Leu Ile Ile Phe Phe Ser Thr Leu Leu Thr Leu
      115     120     125
Thr Thr Met Pro Leu Ser Leu Ala Ser Ala Val Glu Ala Leu Leu Ala
      130     135     140
Pro Leu Lys Arg Val Lys Val Pro Val His Glu Ile Gly Leu Met Leu
      145     150     155     160
Ser Met Ser Leu Arg Phe Val Pro Thr Leu Met Asp Asp Thr Thr Arg
      165     170     175
Ile Met Asn Ala Gln Lys Ala Arg Gly Val Asp Phe Gly Glu Gly Ser
      180     185     190
Ile Val Gln Lys Val Lys Ala Met Ile Pro Ile Leu Ile Pro Leu Phe
      195     200     205
Ala Thr Ser Leu Lys Arg Ala Asp Ser Leu Ala Ile Ala Met Glu Ala
      210     215     220
Arg Gly Tyr Gln Gly Gly Lys Gly Arg Ser Gln Tyr Arg Gln Leu Lys
      225     230     235     240
Trp Thr Leu Lys Asp Thr Leu Thr Ile Leu Val Ile Leu Val Leu Gly
      245     250     255
Cys Cys Leu Phe Phe Leu Lys Ser
      260

```

(2) INFORMATION FOR SEQ ID NO:4636:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 88 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4636:

Tyr	Tyr	Ser	Ile	Trp	Glu	Lys	Met	Met	Pro	Ala	Asn	Thr	Lys	Val	Ile
1				5					10					15	
Phe	Gln	Glu	Met	Phe	Ala	Asp	Phe	Gln	Asn	Tyr	Tyr	Val	Leu	Ile	Gly
			20					25					30		
Gly	Thr	Ala	Thr	Ser	Ile	Val	Leu	Asp	Ser	Gln	Gly	Phe	Lys	Ser	Arg
			35				40					45			
Thr	Thr	Lys	Asp	Tyr	Asp	Met	Val	Ile	Ile	Asp	Glu	Val	Lys	Asn	Lys
			50			55					60				
Glu	Phe	Tyr	Thr	Thr	Trp	Asn	His	Phe	Leu	Glu	Leu	Gly	Glu	Tyr	Gln
65					70				75					80	
Gly	Ser	Gln	Lys	Asp	Glu	Lys	Ala								
					85										

(2) INFORMATION FOR SEQ ID NO:4637:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4637:

Xaa	Val	Ser	Ile	Ile	Ala	Thr	Ile	Leu	Val	Leu	Phe	Phe	Asn	Lys	Arg
1				5				10						15	
Leu	Glu	Ile	Ile	Glu	Leu	Gly	Glu	Glu	Ile	Ala	Ile	Gly	Leu	Gly	Ala
			20					25					30		
Asn	Pro	Glu	Leu	Ser	Arg	Leu	Val	Leu	Ile	Phe	Cys	Ala	Val	Ser	Leu
			35				40					45			
Thr	Ala	Phe	Ser	Thr	Ser	Ile	Thr	Gly	Pro	Ile	Ala	Cys	Ile	Ser	Phe
			50			55					60				
Leu	Ala	Gly	Pro	Ile	Ala	Leu	Asn	Ile	Gly	Lys	Lys	Arg	Ser	Pro	Ile
65					70				75					80	
Leu	Ala	Gly	Leu	Val	Gly	Ile	Leu	Leu	Val	Leu	Leu	Ser	Asp	Ile	Phe
			85						90					95	
Ser	Gln	Asn	Ile	Leu	Pro	Ala	Arg	Tyr	Pro	Val	Gly	Val	Val	Thr	Ala

		100					105					110					
Leu	Leu	Val	Ser	Gln	Tyr	Leu	Ile	Tyr	Leu	Leu	Ile	Lys	Met	Asn	Arg		
		115					120					125					
Arg	Asn	Ile															
		130															

(2) INFORMATION FOR SEQ ID NO:4638:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 62 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...62
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4638:

Asp	Lys	Ser	Ile	Ile	Leu	Asn	Ile	Lys	Ser	Glu	Gln	Asn	Gln	Leu	Ser		
1				5				10						15			
Asp	Thr	Gln	Asn	Ser	Val	Leu	Phe	Ala	Phe	Leu	Ser	Asn	Leu	Ser	Ile		
		20					25					30					
Leu	Lys	Ile	Tyr	Asn	Lys	Glu	Phe	Leu	Lys	Ser	Lys	Ser	Phe	Tyr	Pro		
		35				40					45						
Arg	Leu	Phe	Ser	Phe	Lys	Pro	Asn	Thr	Phe	Tyr	Lys	His	Phe				
	50				55					60							

(2) INFORMATION FOR SEQ ID NO:4639:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 495 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...495
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4639:

Met Lys Ser Ile Lys Leu Asn Ala Leu Ser Tyr Met Gly Ile Arg Val

1				5				10				15			
Leu	Asn	Ile	Ile	Phe	Pro	Ile	Leu	Thr	Gly	Thr	Tyr	Val	Ala	Arg	Val
			20					25					30		
Leu	Asp	Arg	Thr	Asp	Tyr	Gly	Tyr	Phe	Asn	Ser	Val	Asp	Thr	Ile	Leu
		35					40					45			
Ser	Phe	Phe	Leu	Pro	Phe	Ala	Thr	Tyr	Gly	Val	Tyr	Ser	Tyr	Gly	Leu
	50					55					60				
Arg	Ala	Ile	Ser	Asn	Val	Lys	Asp	Asn	Lys	Lys	Asp	Leu	Asn	Arg	Thr
65					70					75					80
Phe	Ser	Ser	Leu	Phe	Tyr	Leu	Cys	Ile	Ala	Cys	Thr	Ile	Leu	Thr	Thr
				85					90					95	
Ala	Val	Tyr	Ile	Leu	Ala	Tyr	Pro	Leu	Phe	Phe	Thr	Asp	Asn	Pro	Ile
			100					105					110		
Val	Lys	Lys	Val	Tyr	Leu	Val	Met	Gly	Ile	Gln	Leu	Ile	Ala	Gln	Ile
		115					120					125			
Phe	Ser	Ile	Glu	Trp	Val	Asn	Glu	Ala	Leu	Glu	Asn	Tyr	Ser	Phe	Leu
	130					135					140				
Phe	Tyr	Lys	Thr	Ala	Phe	Ile	Arg	Ile	Leu	Met	Leu	Val	Ser	Ile	Phe
145					150					155					160
Leu	Phe	Val	Lys	Asn	Glu	His	Asp	Ile	Val	Val	Tyr	Thr	Leu	Val	Met
			165						170					175	
Ser	Leu	Ser	Thr	Leu	Ile	Asn	Tyr	Leu	Ile	Ser	Tyr	Phe	Trp	Ile	Lys
			180					185					190		
Arg	Asp	Ile	Lys	Leu	Val	Lys	Ile	His	Leu	Ser	Asp	Phe	Lys	Pro	Leu
		195				200						205			
Phe	Leu	Pro	Leu	Thr	Ala	Met	Leu	Val	Phe	Ala	Asn	Ala	Asn	Met	Leu
	210					215					220				
Phe	Thr	Phe	Leu	Asp	Arg	Leu	Phe	Leu	Val	Lys	Thr	Gly	Ile	Asp	Val
225				230						235					240
Asn	Val	Ser	Tyr	Tyr	Thr	Ile	Ala	Gln	Arg	Ile	Val	Thr	Val	Ile	Ala
			245					250						255	
Gly	Val	Val	Thr	Gly	Ala	Ile	Gly	Val	Ser	Val	Pro	Arg	Leu	Ser	Tyr
			260					265					270		
Tyr	Leu	Gly	Lys	Gly	Asp	Lys	Glu	Ala	Tyr	Val	Ser	Leu	Val	Asn	Arg
		275				280						285			
Gly	Ser	Arg	Ile	Phe	Asn	Phe	Phe	Ile	Ile	Pro	Leu	Ser	Phe	Gly	Leu
	290				295						300				
Met	Val	Leu	Gly	Pro	Asn	Ala	Ile	Leu	Leu	Tyr	Gly	Ser	Glu	Lys	Tyr
305					310					315					320
Ile	Gly	Gly	Gly	Ile	Leu	Thr	Ser	Leu	Phe	Ala	Phe	Arg	Thr	Ile	Ile
			325					330						335	
Leu	Ala	Leu	Asp	Thr	Ile	Leu	Gly	Ser	Gln	Ile	Leu	Phe	Thr	Asn	Gly
			340				345						350		
Tyr	Glu	Lys	Arg	Ile	Thr	Val	Tyr	Thr	Val	Phe	Ala	Gly	Leu	Leu	Asn
		355					360					365			
Leu	Gly	Leu	Asn	Ser	Leu	Leu	Phe	Phe	Asn	His	Ile	Val	Ala	Pro	Glu
	370					375					380				
Tyr	Tyr	Leu	Leu	Thr	Thr	Met	Leu	Ser	Glu	Thr	Ser	Leu	Leu	Val	Phe
385					390					395					400
Tyr	Ile	Ile	Phe	Ile	His	Arg	Lys	Gln	Leu	Ile	His	Leu	Gly	His	Ile
			405					410						415	
Phe	Ser	Tyr	Thr	Val	Arg	Tyr	Ser	Leu	Phe	Ser	Leu	Ser	Phe	Val	Ala
			420				425						430		
Ile	Tyr	Phe	Leu	Ile	Asn	Phe	Val	Tyr	Pro	Val	Asp	Met	Val	Ile	Asn
		435				440					445				
Leu	Pro	Phe	Leu	Ile	Asn	Thr	Gly	Leu	Ile	Val	Leu	Leu	Ser	Ala	Ile

450		455		460
Ser Tyr Ile Ser Leu Leu Val Phe Thr Lys Asp Ser Ile Phe Tyr Glu				
465		470		480
Phe Leu Asn His Val Leu Ala Leu Lys Asn Lys Phe Lys Lys Ser				
	485		490	495

(2) INFORMATION FOR SEQ ID NO:4640:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 490 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...490

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4640:

Lys	Glu	Ser	Met	Ser	Ile	Thr	Ser	Phe	Val	Lys	Arg	Ile	Gln	Asp	Ile
1				5					10					15	
Thr	Arg	Asn	Asp	Ala	Gly	Val	Asn	Gly	Asp	Ala	Gln	Arg	Ile	Glu	Gln
			20					25					30		
Met	Ser	Trp	Leu	Leu	Phe	Leu	Lys	Ile	Tyr	Asp	Ser	Arg	Glu	Met	Val
		35					40					45			
Trp	Glu	Leu	Glu	Glu	Asp	Glu	Tyr	Glu	Ser	Ile	Ile	Pro	Glu	Glu	Leu
	50					55					60				
Lys	Trp	Arg	Asn	Trp	Ala	His	Ala	Gln	Asn	Gly	Glu	Arg	Val	Leu	Thr
65				70					75					80	
Gly	Asp	Glu	Leu	Leu	Asp	Phe	Val	Asn	Asn	Lys	Leu	Phe	Lys	Glu	Leu
				85					90					95	
Lys	Glu	Leu	Glu	Ile	Thr	Ser	Asn	Met	Pro	Ile	Arg	Lys	Thr	Ile	Val
		100						105					110		
Lys	Ser	Ala	Phe	Glu	Asp	Ala	Asn	Asn	Tyr	Met	Lys	Asn	Gly	Val	Leu
		115					120					125			
Leu	Arg	Gln	Val	Ile	Asn	Val	Ile	Asp	Glu	Val	Asp	Phe	Asn	Ser	Pro
	130					135					140				
Glu	Asp	Arg	His	Ser	Phe	Asn	Asp	Ile	Tyr	Glu	Lys	Ile	Leu	Lys	Asp
145				150					155					160	
Ile	Gln	Asn	Ala	Gly	Asn	Ser	Gly	Glu	Phe	Tyr	Thr	Pro	Arg	Ala	Ala
			165						170					175	
Thr	Asp	Phe	Ile	Ala	Glu	Val	Leu	Asp	Pro	Lys	Leu	Gly	Glu	Ser	Met
		180					185						190		
Ala	Asp	Leu	Ala	Cys	Gly	Thr	Gly	Gly	Phe	Leu	Thr	Ser	Thr	Leu	Asn
	195					200						205			
Arg	Leu	Ser	Ser	Gln	Arg	Lys	Thr	Ser	Glu	Asp	Thr	Lys	Lys	Tyr	Asn
	210					215					220				
Thr	Ala	Val	Phe	Gly	Ile	Glu	Lys	Lys	Ala	Phe	Pro	His	Leu	Leu	Ala
225				230					235					240	
Val	Thr	Asn	Leu	Phe	Leu	His	Glu	Ile	Asp	Asp	Pro	Lys	Ile	Val	His

				245				250					255				
Gly	Asn	Thr	Leu	Glu	Lys	Asn	Val	Arg	Glu	Tyr	Thr	Asp	Asp	Glu	Lys		
			260					265					270				
Phe	Asp	Ile	Met	Met	Asn	Pro	Pro	Phe	Gly	Gly	Ser	Glu	Leu	Glu			
		275				280						285					
Thr	Ile	Lys	Asn	Asn	Phe	Pro	Ala	Glu	Leu	Arg	Ser	Ser	Glu	Thr	Ala		
	290					295					300						
Asp	Leu	Phe	Met	Ala	Val	Ile	Met	Tyr	Arg	Leu	Lys	Glu	Asn	Gly	Arg		
305				310						315					320		
Val	Gly	Val	Ile	Leu	Pro	Asp	Gly	Phe	Leu	Phe	Gly	Glu	Gly	Val	Lys		
			325					330						335			
Thr	Arg	Leu	Lys	Gln	Lys	Leu	Val	Asp	Glu	Phe	Asn	Leu	His	Thr	Ile		
		340						345					350				
Ile	Arg	Leu	Pro	His	Ser	Val	Phe	Ala	Pro	Tyr	Thr	Gly	Ile	His	Thr		
	355					360						365					
Asn	Ile	Leu	Phe	Phe	Asp	Lys	Thr	Lys	Lys	Thr	Glu	Glu	Thr	Trp	Phe		
	370					375					380						
Tyr	Arg	Leu	Asp	Met	Pro	Asp	Gly	Tyr	Lys	Asn	Phe	Ser	Lys	Thr	Lys		
385				390						395					400		
Pro	Met	Lys	Ser	Glu	His	Phe	Asn	Pro	Val	Arg	Asp	Trp	Trp	Glu	Asn		
			405					410						415			
Arg	Glu	Glu	Ile	Leu	Glu	Gly	Lys	Phe	Tyr	Lys	Ser	Lys	Ser	Phe	Thr		
		420						425					430				
Pro	Ser	Glu	Leu	Ala	Glu	Leu	Asn	Tyr	Asn	Leu	Asp	Gln	Cys	Gly	Phe		
		435					440				445						
Pro	Lys	Glu	Glu	Glu	Glu	Ile	Leu	Asn	Pro	Phe	Glu	Leu	Ile	Gln	Asn		
	450					455					460						
Tyr	Gln	Ala	Glu	Arg	Ala	Thr	Leu	Asn	His	Lys	Ile	Asp	Asn	Val	Leu		
465				470						475					480		
Ala	Asp	Ile	Leu	Gln	Leu	Leu	Glu	Asp	Lys								
			485					490									

(2) INFORMATION FOR SEQ ID NO:4641:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 331 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4641:

Glu	Glu	Ser	Ile	Met	Ile	Gln	His	Pro	Arg	Ile	Gly	Ile	Arg	Pro	Thr		
1				5				10						15			
Ile	Asp	Gly	Arg	Arg	Gln	Gly	Val	Arg	Glu	Ser	Leu	Glu	Val	Gln	Thr		
		20						25					30				
Met	Asn	Met	Ala	Lys	Ser	Val	Ala	Asp	Leu	Ile	Ser	Ser	Thr	Leu	Lys		

	35					40					45				
Tyr	Pro	Asp	Gly	Glu	Pro	Val	Glu	Cys	Val	Ile	Ser	Pro	Ser	Thr	Ile
	50					55					60				
Gly	Arg	Val	Pro	Glu	Ala	Ala	Ser	His	Glu	Leu	Phe	Lys	Lys	Ser	
65					70				75					80	
Asn	Val	Cys	Ala	Thr	Ile	Thr	Val	Thr	Pro	Cys	Trp	Cys	Tyr	Gly	Ser
				85					90					95	
Glu	Thr	Met	Asp	Met	Ser	Pro	Asp	Ile	Pro	His	Ala	Ile	Trp	Gly	Phe
			100					105					110		
Asn	Gly	Thr	Glu	Arg	Pro	Gly	Ala	Val	Tyr	Leu	Ala	Ala	Val	Leu	Ala
			115				120					125			
Ser	His	Thr	Gln	Lys	Gly	Ile	Pro	Ala	Phe	Gly	Ile	Tyr	Gly	Arg	Asp
	130					135					140				
Val	Gln	Glu	Ala	Asn	Asp	Thr	Ala	Ile	Pro	Glu	Asp	Val	Lys	Glu	Lys
145					150					155					160
Leu	Leu	Arg	Tyr	Ala	Arg	Ala	Ala	Leu	Ala	Thr	Gly	Leu	Met	Arg	Asp
				165					170					175	
Thr	Ala	Tyr	Leu	Ser	Met	Gly	Ser	Val	Ser	Met	Gly	Ile	Gly	Gly	Ser
			180					185					190		
Ile	Val	Asn	Pro	Asp	Phe	Phe	Gln	Glu	Tyr	Leu	Gly	Met	Arg	Asn	Glu
		195					200					205			
Ser	Val	Asp	Met	Thr	Glu	Phe	Thr	Arg	Arg	Met	Asp	Arg	Gly	Ile	Tyr
	210					215					220				
Asp	Pro	Glu	Glu	Phe	Glu	Arg	Ala	Leu	Lys	Trp	Val	Lys	Glu	Asn	Val
225					230					235					240
Lys	Glu	Gly	Phe	Asp	His	Asn	Arg	Glu	Asp	Leu	Val	Leu	Ser	Arg	Glu
				245					250					255	
Glu	Lys	Asp	Arg	Gln	Trp	Glu	Phe	Val	Ile	Lys	Met	Phe	Met	Ile	Gly
			260					265					270		
Arg	Asp	Leu	Met	Val	Gly	Asn	Pro	Arg	Leu	Ala	Glu	Leu	Gly	Phe	Glu
		275					280					285			
Glu	Glu	Ala	Val	Gly	His	His	Ala	Leu	Val	Ala	Gly	Phe	Gln	Gly	Gln
	290					295					300				
Arg	Gln	Trp	Thr	Asp	His	Phe	Pro	Asn	Gly	Asp	Phe	Met	Glu	Thr	Phe
305					310					315					320
Leu	Asn	Thr	Gln	Phe	Asp	Trp	Asn	Gly	Ile	Arg					
				325					330						

(2) INFORMATION FOR SEQ ID NO:4642:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 806 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...806

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4642:

Tyr	Gly	Ser	Met	Ile	Arg	Asn	Lys	Lys	Gln	Asp	Tyr	Val	Leu	Ala	Tyr
1				5					10					15	
Lys	Gln	Pro	Ala	Ser	Thr	Thr	Tyr	Met	Gly	Trp	Glu	Glu	Glu	Ala	Leu
			20					25					30		
Pro	Ile	Gly	Asn	Gly	Ser	Leu	Gly	Ala	Lys	Val	Phe	Gly	Leu	Ile	Gly
		35					40					45			
Ser	Glu	Arg	Ile	Gln	Phe	Asn	Glu	Lys	Ser	Leu	Trp	Ser	Gly	Gly	Pro
	50					55					60				
Leu	Pro	Asp	Ser	Ser	Asp	Tyr	Gln	Gly	Gly	Asn	Leu	Gln	Asp	Gln	Tyr
65					70					75					80
Val	Phe	Leu	Ala	Glu	Ile	Arg	Gln	Ala	Leu	Glu	Lys	Arg	Asp	Tyr	Asn
				85					90					95	
Leu	Ala	Lys	Glu	Leu	Ala	Glu	Gln	His	Leu	Ile	Gly	Pro	Lys	Thr	Ser
			100					105					110		
Gln	Tyr	Gly	Thr	Tyr	Leu	Ser	Phe	Gly	Asp	Ile	His	Ile	Glu	Phe	Ser
		115					120					125			
Gln	Gln	Gly	Thr	Thr	Leu	Ser	Gln	Val	Thr	Asp	Tyr	Gln	Arg	Gln	Leu
		130				135					140				
Asn	Ile	Ser	Lys	Ala	Leu	Ala	Thr	Thr	Ser	Tyr	Val	Tyr	Lys	Gly	Thr
145					150					155					160
Arg	Phe	Glu	Arg	Glu	Ala	Phe	Ala	Ser	Phe	Pro	Asp	Asp	Leu	Leu	Val
				165					170					175	
Gln	Cys	Phe	Thr	Lys	Glu	Gly	Leu	Glu	Thr	Leu	Asp	Phe	Thr	Ile	Glu
			180					185					190		
Leu	Ser	Leu	Thr	Cys	Asp	Leu	Ala	Ser	Asp	Gly	Lys	Tyr	Glu	Gln	Glu
		195					200					205			
Lys	Ser	Asp	Tyr	Lys	Glu	Cys	Lys	Leu	Asp	Ile	Thr	Asp	Ser	His	Ile
	210					215					220				
Leu	Met	Lys	Gly	Arg	Val	Lys	Asp	Asn	Asp	Leu	Arg	Phe	Ala	Ser	Tyr
225					230					235					240
Leu	Ala	Trp	Glu	Thr	Asp	Gly	Asp	Ile	Arg	Val	Trp	Ser	Asp	Arg	Val
				245					250					255	
Gln	Ile	Ser	Gly	Ala	Ser	Tyr	Ala	Asn	Leu	Phe	Leu	Ala	Ala	Lys	Thr
			260					265					270		
Asp	Phe	Ala	Gln	Asn	Pro	Ala	Ser	Asn	Tyr	Arg	Lys	Lys	Leu	Asp	Leu
		275					280					285			
Glu	Gln	Gln	Val	Ile	Asp	Leu	Val	Asp	Thr	Ala	Lys	Glu	Lys	Gly	Tyr
	290					295					300				
Thr	Gln	Leu	Lys	Ser	Arg	His	Ile	Glu	Asp	Tyr	Gln	Ala	Leu	Phe	Gln
305					310					315					320
Arg	Val	Gln	Leu	Asp	Leu	Glu	Ala	Asp	Val	Asp	Ala	Ser	Thr	Thr	Asp
				325					330					335	
Asp	Leu	Leu	Lys	Asn	Tyr	Lys	Pro	Gln	Glu	Gly	Gln	Ala	Leu	Glu	Glu
			340					345					350		
Leu	Phe	Phe	Gln	Tyr	Gly	Arg	Tyr	Leu	Leu	Ile	Ser	Ser	Ser	Arg	Asp
		355					360					365			
Cys	Pro	Asp	Ala	Leu	Pro	Ala	Asn	Leu	Gln	Gly	Val	Trp	Asn	Ala	Val
	370					375					380				
Asp	Asn	Pro	Pro	Trp	Asn	Ser	Asp	Tyr	His	Leu	Asn	Val	Asn	Leu	Gln
385					390					395					400
Met	Asn	Tyr	Trp	Pro	Ala	Tyr	Val	Thr	Asn	Leu	Leu	Glu	Thr	Val	Phe
				405					410					415	
Pro	Val	Ile	Asn	Tyr	Val	Asp	Asp	Leu	Arg	Val	Tyr	Gly	Arg	Leu	Ala
			420					425					430		
Ala	Val	Lys	Tyr	Ala	Gly	Ile	Val	Ser	Gln	Lys	Gly	Glu	Glu	Asn	Gly
		435					440					445			

Trp	Leu	Val	His	Thr	Gln	Ala	Thr	Pro	Phe	Gly	Trp	Thr	Ala	Pro	Gly
450						455					460				
Trp	Asp	Tyr	Tyr	Trp	Gly	Trp	Ser	Pro	Ala	Ala	Asn	Ala	Trp	Met	Met
465					470					475					480
Gln	Thr	Val	Tyr	Glu	Ala	Tyr	Ser	Phe	Tyr	Arg	Asp	Gln	Asp	Tyr	Leu
				485					490					495	
Arg	Glu	Lys	Ile	Tyr	Pro	Met	Leu	Arg	Glu	Thr	Val	Arg	Phe	Trp	Asn
			500					505					510		
Ala	Phe	Leu	His	Lys	Asp	Gln	Gln	Ala	Gln	Arg	Trp	Val	Ser	Ser	Pro
		515					520					525			
Ser	Tyr	Ser	Pro	Glu	His	Gly	Pro	Ile	Ser	Ile	Gly	Asn	Thr	Tyr	Asp
	530					535					540				
Gln	Ser	Leu	Ile	Trp	Gln	Leu	Phe	His	Asp	Phe	Ile	Gln	Ala	Ala	Gln
545					550					555					560
Glu	Leu	Gly	Leu	Asp	Glu	Asp	Leu	Leu	Thr	Glu	Val	Lys	Glu	Lys	Ser
				565					570					575	
Asp	Leu	Leu	Asn	Pro	Leu	Gln	Ile	Thr	Gln	Ser	Gly	Arg	Ile	Arg	Glu
			580					585					590		
Trp	Tyr	Glu	Glu	Glu	Glu	Gln	Tyr	Phe	Gln	Asn	Glu	Lys	Val	Glu	Ala
		595					600					605			
Gln	His	Arg	His	Ala	Ser	His	Leu	Val	Gly	Leu	Tyr	Pro	Gly	Asn	Leu
610						615					620				
Phe	Ser	Tyr	Lys	Gly	Gln	Glu	Tyr	Ile	Glu	Ala	Ala	Arg	Ala	Ser	Leu
625					630					635					640
Asn	Asp	Arg	Gly	Asp	Gly	Gly	Thr	Gly	Trp	Ser	Lys	Ala	Asn	Lys	Ile
			645						650					655	
Asn	Leu	Trp	Ala	Arg	Leu	Gly	Asp	Gly	Asn	Arg	Ala	His	Lys	Leu	Leu
		660						665					670		
Ala	Glu	Gln	Leu	Lys	Thr	Ser	Thr	Leu	Gln	Asn	Leu	Trp	Cys	Ser	His
		675					680					685			
Pro	Pro	Phe	Gln	Ile	Asp	Gly	Asn	Phe	Gly	Ala	Thr	Ser	Gly	Met	Ala
	690					695					700				
Glu	Met	Leu	Leu	Gln	Ser	His	Ala	Ala	Tyr	Leu	Val	Pro	Leu	Ala	Ala
705				710						715					720
Leu	Pro	Asp	Ala	Trp	Ser	Thr	Gly	Ser	Val	Ser	Gly	Leu	Met	Ala	Arg
			725						730					735	
Gly	His	Phe	Glu	Val	Ser	Met	Ser	Trp	Glu	Asp	Lys	Lys	Leu	Leu	Gln
		740						745					750		
Leu	Thr	Ile	Leu	Ser	Arg	Ser	Gly	Gly	Asp	Leu	Arg	Val	Ser	Tyr	Pro
	755						760					765			
Asp	Ile	Glu	Lys	Ser	Val	Ile	Lys	Met	Asn	Gln	Glu	Lys	Ile	Lys	Ala
	770					775					780				
Lys	Cys	Met	Gly	Lys	Asp	Cys	Ile	Ser	Val	Ala	Thr	Ala	Glu	Gly	Asp
785				790						795					800
Leu	Val	Gln	Phe	Tyr	Phe										
				805											

(2) INFORMATION FOR SEQ ID NO:4643:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 385 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...385

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4643:

Val	Gly	Ser	Ile	Val	Met	Lys	Leu	Lys	Phe	Leu	Ile	Thr	Asn	Leu	Phe
1				5					10					15	
His	Val	Leu	Leu	Ser	Asn	Leu	Ile	Thr	Ile	Leu	Thr	Ser	Val	Ile	Val
				20					25				30		
Val	Leu	Ile	Leu	Pro	Lys	Ile	Met	Gly	Val	Thr	Glu	Tyr	Ser	Tyr	Trp
				35					40				45		
Gln	Leu	Tyr	Ile	Phe	Tyr	Leu	Thr	Tyr	Ile	Gly	Phe	Phe	His	Leu	Gly
				50					55				60		
Trp	Ile	Asp	Gly	Ile	Tyr	Leu	Lys	Tyr	Gly	Gly	Leu	Glu	Tyr	Gln	Asn
65						70				75					80
Leu	Asp	Lys	Lys	Gln	Phe	Tyr	Ser	Gln	Ile	Leu	Gln	Phe	Ser	Ser	Phe
				85					90					95	
Leu	Ile	Leu	Ile	Ser	Phe	Leu	Leu	Phe	Gly	Phe	Asn	Leu	Leu	Thr	Val
				100					105					110	
Thr	Asp	Gln	Asn	Ala	Lys	Tyr	Ile	Tyr	Asn	Met	Thr	Ile	Ile	Ser	Met
				115					120					125	
Ile	Val	Thr	Asn	Leu	Arg	Met	Leu	Phe	Val	Tyr	Ile	Leu	Gln	Met	Thr
				130					135					140	
Asn	Arg	Leu	Lys	Asp	Ser	Ser	Ile	Ile	Leu	Ile	Ser	Asp	Arg	Val	Ile
145						150						155			160
Tyr	Val	Ile	Leu	Leu	Phe	Leu	Phe	Ile	Ile	Phe	Lys	Trp	His	Glu	Tyr
				165						170				175	
Lys	Val	Met	Ile	Trp	Ala	Asp	Val	Leu	Gly	Arg	Thr	Phe	Ser	Leu	Leu
				180					185				190		
Leu	Ser	Phe	Trp	Ile	Cys	Lys	Asp	Ile	Val	Phe	Gln	Ser	Leu	Ser	Glu
				195					200				205		
Phe	Ile	Leu	Asp	Leu	Arg	Glu	Ser	Phe	Asp	Asn	Ile	Arg	Val	Gly	Ile
				210						220					
Asn	Leu	Met	Leu	Ser	Asn	Ile	Ala	Ser	Ser	Met	Ile	Ile	Gly	Ile	Val
225						230				235					240
Arg	Met	Gly	Ile	Gln	Trp	Asn	Trp	Asn	Ile	Glu	Thr	Phe	Gly	Lys	Val
				245						250				255	
Ser	Leu	Thr	Leu	Ser	Ile	Ser	Asn	Leu	Leu	Met	Thr	Phe	Ile	Asn	Ala
				260					265					270	
Ile	Gly	Leu	Val	Val	Phe	Pro	Leu	Leu	Lys	Arg	Thr	Lys	Thr	Glu	Asn
				275					280					285	
Leu	Ser	Lys	Ile	Tyr	Ser	Asn	Leu	Lys	Asn	Val	Leu	Met	Leu	Ile	Met
				290					295				300		
Phe	Ala	Ile	Leu	Leu	Ile	Tyr	Tyr	Pro	Leu	Lys	Ile	Val	Leu	Tyr	Leu
305						310				315					320
Trp	Leu	Ser	Ala	Tyr	Gln	Asp	Ala	Leu	Ile	Phe	Met	Asn	Leu	Ile	Phe
				325						330				335	
Pro	Met	Ser	Val	Tyr	Glu	Arg	Lys	Met	Ala	Leu	Val	Ile	Asn	Thr	Tyr
				340					345					350	
Leu	Lys	Gly	Leu	Lys	Met	Glu	Arg	Asp	Ile	Leu	Lys	Ile	Asn	Thr	Leu
				355					360				365		
Ile	Met	Leu	Phe	Ser	Met	Leu	Val	Tyr	Leu	Asn	Asn	Tyr	Ser	Ile	Ile

	370	375	380
Lys			
385			

(2) INFORMATION FOR SEQ ID NO:4644:

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(B) LOCATION 1...327

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4644:

260	265	270
Phe Glu His Ile Leu Cys Gly Ala Ser Met Val Gln Val Gly Thr Thr		
275	280	285
Leu His Lys Glu Gly Val Ser Ala Phe Asp Arg Ile Thr Asn Glu Leu		
290	295	300
Lys Ala Ile Met Val Glu Lys Gly Tyr Glu Ser Leu Glu Asp Phe Arg		
305	310	315
Gly Lys Leu Arg Tyr Ile Asp		320
325		

(2) INFORMATION FOR SEQ ID NO:4645:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...87

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4645:

Ile Tyr Gly Ile His Val Ala Lys Ile Ala Gly Leu Pro Ala Asp Leu		
1	5	10
Leu Ala Arg Ala Asp Lys Ile Leu Thr Gln Leu Glu Asn Gln Gly Thr		
20	25	30
Glu Ser Pro Pro Pro Met Arg Gln Thr Ser Ala Val Thr Glu Gln Ile		
35	40	45
Ser Leu Phe Asp Arg Ala Glu His Pro Ile Leu Ala Glu Leu Ala		
50	55	60
Lys Leu Asp Val Tyr Asn Met Thr Pro Met Gln Val Met Asn Val Leu		
65	70	75
Val Glu Leu Lys Gln Lys Leu		80
85		

(2) INFORMATION FOR SEQ ID NO:4646:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4646:

Ile	Ile	Gly	Ile	Phe	Ile	Gly	Asn	Arg	Ile	His	Gly	Phe	Met	Asp	Phe
1				5					10					15	
His	Thr	Ser	Ser	Asn	Leu	Lys	Glu	Cys	Thr	Asn	Thr	Leu	Arg	Lys	Ser
			20					25					30		
Leu	Gln	Thr	Ala	Ser	Thr	Leu	Ser	Ala	Thr	Ser	Lys	Gln	Cys	Phe	Glu
		35					40					45			
Gln	Pro	Ala	Ala	Ser	Phe	Leu	Val	Cys	Ser	Leu	Ile	Phe	Ile	Glu	Tyr
	50					55				60					
Lys	Leu	Ser	Ile	Ala	Gln	Leu	Gly	Arg	Ile	Gly	Lys	Asp	Leu	Lys	
65					70					75					

(2) INFORMATION FOR SEQ ID NO:4647:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 92 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...92

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4647:

Asp	Arg	Gly	Met	Asn	Leu	Lys	Val	Lys	Gln	Lys	Ile	Pro	Leu	Lys	Ile
1				5					10					15	
Lys	Arg	Met	Gly	Ile	Asn	Gly	Glu	Gly	Ile	Gly	Phe	Tyr	Gln	Lys	Thr
			20					25					30		
Leu	Val	Phe	Val	Pro	Gly	Ala	Leu	Lys	Gly	Glu	Asp	Ile	Tyr	Cys	Gln
		35				40						45			
Ile	Thr	Ser	Ile	Arg	Arg	Asn	Phe	Val	Glu	Ala	Lys	Leu	Leu	Lys	Val
	50					55				60					
Asn	Lys	Lys	Ser	Lys	Phe	Arg	Ile	Val	Pro	Ser	Cys	Thr	Ile	Tyr	Asn
65					70					75					80
Glu	Cys	Gly	Gly	Cys	Ala	Asn	His	Ala	Pro	Ala	Leu				
			85						90						

(2) INFORMATION FOR SEQ ID NO:4648:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 627 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...627

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4648:

Gly	Thr	Ile	Phe	Pro	Tyr	Phe	Phe	Cys	Tyr	Asn	Gly	Thr	Met	Asn	Asn
1				5					10					15	
Leu	Ile	Lys	Ser	Lys	Leu	Glu	Leu	Leu	Pro	Thr	Ser	Pro	Gly	Cys	Tyr
		20						25					30		
Ile	His	Lys	Asp	Lys	Asn	Gly	Thr	Ile	Ile	Tyr	Val	Gly	Lys	Ala	Lys
		35				40						45			
Asn	Leu	Arg	Asn	Arg	Val	Arg	Ser	Tyr	Phe	Arg	Gly	Ser	His	Asn	Thr
	50					55					60				
Lys	Thr	Glu	Ala	Leu	Val	Ser	Glu	Ile	Val	Asp	Phe	Glu	Phe	Ile	Val
65					70					75					80
Thr	Glu	Ser	Asn	Ile	Glu	Ala	Leu	Leu	Leu	Glu	Ile	Asn	Leu	Ile	Lys
				85					90					95	
Glu	Asn	Lys	Pro	Lys	Tyr	Asn	Ile	Met	Leu	Lys	Asp	Asp	Lys	Ser	Tyr
			100					105					110		
Pro	Phe	Ile	Lys	Ile	Thr	Asn	Glu	Arg	Tyr	Pro	Arg	Leu	Ile	Ile	Thr
		115					120					125			
Arg	Gln	Val	Lys	Lys	Asp	Gly	Gly	Leu	Tyr	Phe	Gly	Pro	Tyr	Pro	Asp
	130					135					140				
Val	Gly	Ala	Ala	Asn	Glu	Ile	Lys	Arg	Leu	Leu	Asp	Arg	Ile	Phe	Pro
145					150					155					160
Phe	Arg	Lys	Cys	Thr	Asn	Pro	Pro	Ser	Lys	Val	Cys	Phe	Tyr	Tyr	His
			165					170					175		
Ile	Gly	Gln	Cys	Met	Ala	His	Thr	Ile	Cys	Lys	Lys	Asp	Glu	Ala	Tyr
		180					185					190			
Phe	Lys	Ser	Met	Ala	Gln	Glu	Val	Ser	Asp	Phe	Leu	Lys	Gly	Gln	Asp
	195						200					205			
Asp	Lys	Ile	Ile	Asp	Asp	Leu	Lys	Ser	Lys	Met	Ala	Val	Ala	Ala	Gln
	210					215					220				
Ser	Met	Glu	Phe	Glu	Arg	Ala	Ala	Glu	Tyr	Arg	Asp	Leu	Ile	Gln	Ala
225					230					235					240
Ile	Gly	Thr	Leu	Arg	Thr	Lys	Gln	Arg	Val	Met	Ala	Lys	Asp	Leu	Gln
			245						250					255	
Asn	Arg	Asp	Val	Phe	Gly	Tyr	Tyr	Val	Asp	Lys	Gly	Trp	Met	Cys	Val
		260					265					270			
Gln	Val	Phe	Phe	Val	Arg	Gln	Gly	Lys	Leu	Ile	Glu	Arg	Asp	Val	Asn
	275						280					285			
Leu	Phe	Pro	Tyr	Phe	Asn	Asp	Pro	Asp	Glu	Asp	Phe	Leu	Thr	Tyr	Val
	290					295					300				
Gly	Gln	Phe	Tyr	Gln	Glu	Lys	Ser	His	Leu	Val	Pro	Asn	Glu	Val	Leu
305					310					315					320
Ile	Pro	Gln	Asp	Ile	Asp	Glu	Glu	Ala	Val	Lys	Ala	Leu	Val	Asp	Ser
				325					330					335	

Lys	Ile	Leu	Lys	Pro	Gln	Arg	Gly	Glu	Lys	Lys	Gln	Leu	Val	Asn	Leu	340	345	350
Ala	Ile	Lys	Asn	Ala	Arg	Val	Ser	Leu	Glu	Gln	Lys	Phe	Asn	Leu	Leu	355	360	365
Glu	Lys	Ser	Val	Glu	Lys	Thr	Gln	Gly	Ala	Ile	Glu	Asn	Leu	Gly	Arg	370	375	380
Leu	Leu	Gln	Ile	Pro	Thr	Pro	Val	Arg	Ile	Glu	Ser	Phe	Asp	Asn	Ser	385	390	395
Asn	Ile	Met	Gly	Thr	Ser	Pro	Val	Ser	Ala	Met	Val	Val	Phe	Val	Asn	405	410	415
Gly	Lys	Pro	Ser	Lys	Lys	Asp	Tyr	Arg	Lys	Tyr	Lys	Ile	Lys	Thr	Val	420	425	430
Val	Gly	Pro	Asp	Asp	Tyr	Ala	Ser	Met	Arg	Glu	Val	Ile	Arg	Arg	Arg	435	440	445
Tyr	Gly	Arg	Val	Gln	Arg	Glu	Ala	Leu	Thr	Pro	Pro	Asp	Leu	Ile	Val	450	455	460
Ile	Asp	Gly	Gly	Gln	Gly	Gln	Val	Asn	Ile	Ala	Lys	Gln	Val	Ile	Gln	465	470	475
Glu	Glu	Leu	Gly	Leu	Asp	Ile	Pro	Ile	Ala	Gly	Leu	Gln	Lys	Asn	Asp	485	490	495
Lys	His	Gln	Thr	His	Glu	Leu	Leu	Phe	Gly	Asp	Pro	Leu	Glu	Val	Val	500	505	510
Asp	Leu	Ser	Arg	Asn	Ser	Gln	Glu	Phe	Phe	Leu	Leu	Gln	Arg	Ile	Gln	515	520	525
Asp	Glu	Val	His	Arg	Phe	Ala	Ile	Thr	Phe	His	Arg	Gln	Leu	Arg	Ser	530	535	540
Lys	Asn	Ser	Phe	Ser	Ser	Gln	Leu	Asp	Gly	Ile	Asp	Gly	Leu	Gly	Pro	545	550	555
Lys	Arg	Lys	Gln	Asn	Leu	Met	Lys	His	Phe	Lys	Ser	Leu	Thr	Lys	Ile	565	570	575
Lys	Glu	Ala	Ser	Val	Asp	Glu	Ile	Val	Glu	Val	Gly	Val	Pro	Arg	Val	580	585	590
Val	Ala	Glu	Ala	Val	Gln	Arg	Lys	Leu	Asn	Pro	Gln	Gly	Glu	Ala	Leu	595	600	605
Pro	Gln	Val	Ala	Glu	Glu	Arg	Val	Asp	Tyr	Gln	Thr	Glu	Gly	Asn	His	610	615	620
Asn	Glu	Pro														625		

(2) INFORMATION FOR SEQ ID NO:4649:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4649:

Leu	Gln	Ile	Phe	Gln	Gly	Phe	Ile	Ser	Gln	Phe	Ser	Ile	Val	Val	Gly
1				5					10					15	
Phe	Phe	Tyr	Thr	Glu	Ile	Asp	Ile	Pro	Leu	Thr	Leu	Ile	Gly	Lys	Ala
			20					25					30		
Phe	Leu	Asp	Gln	Val	Phe	His	Lys	Thr	Asp	Asp	Val	Cys	His	Lys	Leu
		35					40					45			
His	Tyr	Thr	Arg	Met	Ala	Ser	Arg	Arg	Phe	His	Ala	Gln	Cys	Arg	His
	50					55					60				
Ile	Leu	Thr	Lys	Gly	Ser	Asp	Val	Leu	Ile	Arg	Asn	Leu	Leu	Arg	Cys
65				70						75				80	
Asp	Ala	Phe	Phe	Pro	Gly	Thr	Val	Asp	Asn	Leu	Ile	Ile	His	Ile	Cys
				85				90						95	
Lys	Ile	Gly	Asn	Ile	Gly	Asn	Leu	Ile	Pro	Thr	Val	Leu	Lys	Ile	Ala
			100					105					110		
Thr	Asn	Arg	Ile	Lys	Ser	Tyr	Arg	Arg	Thr	Gly	Val	Ser	His	Val	Asn
		115					120					125			
Ile	Val	Val	His	Gly	Trp	Pro	Thr	Asn	Ile	His	Leu	Asp	Leu	Ala	Val
	130					135					140				
Leu	Asn	Arg	Asp	Lys	Phe	Ser	Gln	Ile	Thr	Arg	His	Gly	Val	Ile	Asp
145					150					155					160
Phe	Asn	His	Lys	Ser											
				165											

(2) INFORMATION FOR SEQ ID NO:4650:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 455 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...455

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4650:

Gly	Lys	Ile	Leu	Met	Tyr	Gln	Ala	Leu	Tyr	Arg	Lys	Tyr	Arg	Ser	Gln
1				5					10					15	
Asn	Phe	Ser	Gln	Leu	Val	Gly	Gln	Glu	Val	Val	Ala	Lys	Thr	Leu	Lys
			20					25					30		
Gln	Ala	Val	Glu	Gln	Glu	Lys	Ile	Ser	His	Ala	Tyr	Leu	Phe	Ser	Gly
		35					40					45			
Pro	Arg	Gly	Thr	Gly	Lys	Thr	Ser	Val	Ala	Lys	Ile	Phe	Ala	Lys	Ala
	50					55					60				
Met	Asn	Cys	Pro	Asn	Gln	Val	Gly	Gly	Glu	Pro	Cys	Asn	Asn	Cys	Tyr
65				70						75				80	
Ile	Cys	Gln	Ala	Val	Thr	Asp	Gly	Ser	Leu	Glu	Asp	Val	Ile	Glu	Met
				85					90					95	

Asp	Ala	Ala	Ser	Asn	Asn	Gly	Val	Asp	Glu	Ile	Arg	Glu	Ile	Arg	Asp
			100					105					110		
Lys	Ser	Thr	Tyr	Ala	Pro	Ser	Leu	Ala	Arg	Tyr	Lys	Val	Tyr	Ile	Ile
		115					120					125			
Asp	Glu	Val	His	Met	Leu	Ser	Thr	Gly	Ala	Phe	Asn	Ala	Leu	Leu	Lys
	130					135					140				
Thr	Leu	Glu	Glu	Pro	Thr	Gln	Asn	Val	Val	Phe	Ile	Leu	Ala	Thr	Thr
145					150					155					160
Glu	Leu	His	Lys	Ile	Pro	Ala	Thr	Ile	Leu	Ser	Arg	Val	Gln	Arg	Phe
			165						170					175	
Glu	Phe	Lys	Ser	Ile	Lys	Thr	Gln	Asp	Ile	Lys	Glu	His	Ile	His	Tyr
		180						185				190			
Ile	Leu	Glu	Lys	Glu	Asn	Ile	Ser	Ser	Glu	Pro	Glu	Ala	Val	Glu	Ile
	195						200				205				
Ile	Ala	Arg	Arg	Ala	Glu	Gly	Gly	Met	Arg	Asp	Ala	Leu	Ser	Ile	Leu
	210					215				220					
Asp	Gln	Ala	Leu	Ser	Leu	Thr	Gln	Gly	Asn	Glu	Leu	Thr	Thr	Ala	Ile
225					230					235					240
Ser	Glu	Glu	Ile	Thr	Gly	Thr	Ile	Ser	Leu	Ser	Ala	Leu	Asp	Asp	Tyr
			245					250					255		
Val	Ala	Ala	Leu	Ser	Gln	Gln	Asp	Val	Pro	Lys	Ala	Leu	Ser	Cys	Leu
		260						265				270			
Asn	Leu	Leu	Phe	Asp	Asn	Gly	Lys	Ser	Met	Thr	Arg	Phe	Val	Thr	Asp
	275					280						285			
Leu	Leu	His	Tyr	Leu	Arg	Asp	Leu	Leu	Ile	Val	Gln	Thr	Gly	Gly	Glu
	290					295				300					
Asn	Thr	His	His	Ser	Ser	Val	Phe	Val	Glu	Asn	Leu	Ala	Leu	Pro	Gln
305					310					315					320
Lys	Asn	Leu	Phe	Glu	Met	Ile	Arg	Leu	Ala	Thr	Val	Asn	Leu	Ala	Asp
			325					330						335	
Ile	Lys	Ser	Ser	Leu	Gln	Pro	Lys	Ile	Tyr	Ala	Glu	Met	Met	Thr	Val
		340					345					350			
Arg	Leu	Ala	Glu	Ile	Lys	Pro	Glu	Pro	Ala	Leu	Ser	Gly	Ala	Val	Glu
	355					360						365			
Asn	Glu	Ile	Ala	Thr	Leu	Arg	Gln	Glu	Val	Ala	Arg	Leu	Lys	Gln	Glu
	370					375				380					
Leu	Ser	Asn	Ala	Gly	Ala	Val	Pro	Lys	Gln	Val	Ala	Pro	Ala	Pro	Ser
385					390					395					400
Arg	Pro	Ala	Thr	Gly	Lys	Thr	Val	Tyr	Arg	Val	Asp	Arg	Asn	Lys	Val
			405					410					415		
Gln	Ser	Ile	Leu	Gln	Glu	Ala	Val	Glu	Asn	Pro	Asp	Leu	Thr	Arg	Gln
		420					425					430			
Asn	Leu	Ile	Arg	Leu	Gln	Asn	Ala	Trp	Gly	Glu	Val	Ile	Glu	Ser	Leu
	435					440						445			
Gly	Gly	Pro	Asp	Lys	Leu	Cys									
	450					455									

(2) INFORMATION FOR SEQ ID NO:4651:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4651:

```

Val Pro Phe Ile Ile Pro Gln Thr Ser His Pro Asp Gln Phe Val Leu
1          5          10          15
His Phe Gln Gly Trp Asn Arg Gln Gln Lys Glu Pro Cys Phe Ser Glu
          20          25          30
Lys Glu Val Ser Leu Leu Ser Leu Tyr Ser Met Lys Ile Lys Glu Gln
          35          40          45
Thr Arg Lys Leu Ala Thr Gly Cys Ser Lys His Arg Phe Glu Val Ala
          50          55          60
Asp Lys Thr Asp Thr Val
65          70
  
```

(2) INFORMATION FOR SEQ ID NO:4652:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 115 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...115

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4652:

```

Ser Ile Ile Ile Val Ile Asn Ile Glu Glu Glu Asn Ile Met Val Lys
1          5          10          15
Ile Gly Leu Phe Cys Ala Ala Gly Phe Ser Thr Gly Met Leu Val Asn
          20          25          30
Asn Met Lys Ile Ala Ala Gln Ala Ser Gly Val Glu Ala Glu Ile Glu
          35          40          45
Ala Phe Ser Gln Ser Lys Leu Ala Asp Tyr Ala Pro Asn Ile Asp Val
          50          55          60
Ala Leu Leu Gly Pro Gln Val Ala Tyr Thr Leu Asp Lys Ser Lys Glu
65          70          75          80
Ile Cys Asp Lys Cys Asp Val Pro Ile Ala Val Ile Pro Met Met Asp
          85          90          95
Tyr Gly Met Leu Asp Gly Lys Lys Val Leu Asp Leu Ala Leu Ser Leu
          100          105          110
Ile Ser Gly
  
```

(A) LENGTH: 237 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4653:

Ala	Val	Ile	Met	Pro	Asn	His	Glu	Gly	Leu	Asp	Leu	Gln	Leu	Pro	Lys
1				5					10					15	
Lys	Cys	Val	Tyr	Ala	Leu	Val	Gly	Glu	Glu	Ile	Asp	Arg	Tyr	Ala	Arg
			20					25					30		
Glu	Val	Gly	Ala	Asp	Cys	Val	Gly	Glu	Phe	Val	Ser	Ala	Thr	Lys	Thr
		35					40					45			
Tyr	Pro	Val	Tyr	Val	Ile	Asn	Tyr	Lys	Gly	Glu	Glu	Val	Cys	Leu	Ala
		50				55					60				
Gln	Ala	Pro	Val	Gly	Ser	Ala	Pro	Ala	Ala	Gln	Phe	Met	Asp	Trp	Leu
65					70					75				80	
Ile	Gly	Tyr	Gly	Val	Glu	Gln	Ile	Ile	Ser	Thr	Gly	Thr	Cys	Gly	Val
				85					90					95	
Leu	Ala	Asp	Ile	Glu	Glu	Asn	Ala	Phe	Leu	Val	Pro	Val	Arg	Ala	Leu
			100					105					110		
Arg	Asp	Glu	Gly	Ala	Ser	Tyr	His	Tyr	Val	Ala	Pro	Cys	Arg	Tyr	Met
			115				120					125			
Glu	Met	Gln	Pro	Glu	Ala	Ile	Ala	Ala	Ile	Glu	Glu	Val	Leu	Glu	Asp
		130				135					140				
Arg	Gly	Ile	Pro	Tyr	Glu	Glu	Val	Met	Thr	Trp	Thr	Thr	Asp	Gly	Phe
145					150					155				160	
Tyr	Arg	Glu	Thr	Ala	Glu	Lys	Val	Ala	Tyr	Arg	Lys	Glu	Glu	Gly	Cys
				165					170					175	
Ala	Val	Val	Glu	Met	Glu	Cys	Ser	Ala	Leu	Ala	Ala	Val	Ala	Gln	Leu
			180					185					190		
Arg	Gly	Val	Leu	Trp	Gly	Glu	Leu	Leu	Phe	Thr	Ala	Asp	Ser	Leu	Ala
		195				200						205			
Asp	Leu	Asp	Gln	Tyr	Asp	Ser	Arg	Asp	Trp	Gly	Ser	Glu	Ala	Phe	Asn
	210					215					220				
Lys	Ala	Leu	Glu	Leu	Ser	Leu	Ala	Ser	Val	His	His	Leu			
225					230					235					

(2) INFORMATION FOR SEQ ID NO:4654:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4654:

Glu	Pro	Ile	Met	Glu	Phe	Glu	Glu	Lys	Thr	Leu	Ser	Arg	Lys	Glu	Ile	1	5	10	15
Tyr	Gln	Gly	Pro	Ile	Phe	Lys	Leu	Val	Gln	Asp	Gln	Val	Glu	Leu	Pro	20	25	30	
Glu	Gly	Lys	Gly	Thr	Ala	Arg	Arg	Asp	Leu	Ile	Phe	His	Asn	Gly	Ala	35	40	45	
Val	Cys	Val	Leu	Ala	Val	Thr	Asp	Glu	Gln	Lys	Leu	Ile	Leu	Val	Lys	50	55	60	
Gln	Tyr	Arg	Lys	Ala	Ile	Glu	Ala	Val	Ser	Tyr	Glu	Ile	Pro	Ala	Gly	65	70	75	80
Lys	Leu	Glu	Val	Gly	Glu	Asn	Thr	Ala	Pro	Val	Ala	Ala	Ala	Leu	Arg	85	90	95	
Glu	Leu	Glu	Glu	Glu	Thr	Ala	Tyr	Thr	Gly	Lys	Leu	Glu	Leu	Leu	Tyr	100	105	110	
Asp	Phe	Tyr	Ser	Ala	Ile	Gly	Phe	Cys	Asn	Glu	Lys	Leu	Lys	Leu	Tyr	115	120	125	
Leu	Ala	Ser	Asp	Leu	Thr	Lys	Val	Glu	Asn	Pro	Arg	Pro	Gln	Asp	Glu	130	135	140	
Asp	Glu	Thr	Leu	Glu	Val	Leu	Glu	Val	Ser	Leu	Glu	Glu	Ala	Lys	Glu	145	150	155	160
Leu	Ile	Gln	Ser	Gly	His	Ile	Cys	Asp	Ala	Lys	Thr	Ile	Met	Ala	Val	165	170	175	
Gln	Tyr	Trp	Glu	Leu	Gln	Lys	Lys									180			

(2) INFORMATION FOR SEQ ID NO:4655:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...81

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4655:

Gly	Thr	Ile	Ile	Cys	Gly	Phe	Phe	Arg	Tyr	Phe	Ile	Pro	Lys	Tyr	Val
1				5					10					15	
Ser	Glu	Ser	Arg	Val	Leu	Tyr	Leu	Asp	Ser	Asp	Ile	Val	Val	Arg	Lys
			20					25					30		
Ser	Ile	Asp	Glu	Leu	Trp	Asp	Leu	Asp	Leu	Thr	Ala	Ile	Pro	Leu	Ala
		35				40						45			
Ala	Val	Arg	Asp	Asp	Phe	Tyr	Thr	His	Asn	Phe	Asn	Ser	Gly	Val	Leu
	50					55					60				
Leu	Ile	Asn	Asp	Gly	Met	Trp	Arg	Ala	Glu	Asn	Val	Thr	Gln	Asp	Leu
65					70					75					80
Ile															

(2) INFORMATION FOR SEQ ID NO:4656:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 332 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...332

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4656:

Arg	Asp	Ile	Met	Lys	Tyr	Ile	Ile	Asn	His	Ser	Asn	Asp	Thr	Ala	Phe
1				5					10					15	
Asn	Ile	Ala	Leu	Glu	Glu	Tyr	Ala	Phe	Lys	His	Leu	Leu	Asp	Glu	Asp
			20					25					30		
Gln	Ile	Phe	Leu	Leu	Trp	Ile	Asn	Lys	Pro	Ser	Ile	Ile	Val	Gly	Arg
		35				40						45			
His	Gln	Asn	Thr	Ile	Glu	Glu	Ile	Asn	Arg	Asp	Tyr	Val	Arg	Glu	Asn
	50					55					60				
Gly	Ile	Glu	Val	Val	Arg	Arg	Ile	Ser	Gly	Gly	Gly	Ala	Val	Tyr	His
65					70					75					80
Asp	Leu	Asn	Asn	Leu	Asn	Tyr	Thr	Ile	Ile	Ser	Lys	Glu	Asp	Glu	Asn
			85						90					95	
Lys	Ala	Phe	Asp	Phe	Lys	Ser	Phe	Ser	Thr	Pro	Val	Ile	Asn	Thr	Leu
		100						105					110		
Ala	Gln	Leu	Gly	Val	Lys	Ala	Glu	Phe	Thr	Gly	Arg	Asn	Asp	Leu	Glu
		115					120						125		
Ile	Asp	Gly	Lys	Lys	Phe	Cys	Gly	Asn	Ala	Gln	Ala	Tyr	Ile	Asn	Gly
	130					135					140				
Arg	Ile	Met	His	His	Gly	Cys	Leu	Leu	Phe	Asp	Val	Asp	Leu	Ser	Val

145		150		155		160									
Leu	Ala	Asn	Ala	Leu	Lys	Val	Ser	Lys	Asp	Lys	Phe	Glu	Ser	Lys	Gly
		165							170					175	
Val	Lys	Ser	Val	Arg	Ala	Arg	Val	Thr	Asn	Ile	Ile	Asn	Glu	Leu	Pro
		180							185					190	
Lys	Lys	Ile	Thr	Val	Glu	Lys	Phe	Arg	Asp	Leu	Leu	Leu	Glu	Tyr	Met
		195						200					205		
Lys	Lys	Glu	Tyr	Pro	Glu	Met	Thr	Glu	Tyr	Val	Phe	Ser	Glu	Glu	Glu
		210				215					220				
Leu	Ala	Glu	Ile	Asn	His	Ile	Lys	Asp	Thr	Lys	Phe	Gly	Thr	Trp	Asp
225				230						235				240	
Trp	Asn	Tyr	Gly	Lys	Ser	Pro	Glu	Phe	Asn	Val	Arg	Arg	Gly	Thr	Lys
			245						250					255	
Phe	Thr	Ser	Gly	Lys	Val	Glu	Val	Phe	Ala	Asn	Val	Thr	Glu	Ser	Lys
			260					265					270		
Ile	Gln	Asp	Ile	Lys	Ile	Tyr	Gly	Asp	Phe	Phe	Gly	Ile	Glu	Asp	Val
		275				280						285			
Ala	Ala	Val	Glu	Asp	Val	Leu	Arg	Gly	Val	Lys	Tyr	Glu	Arg	Glu	Asp
		290				295					300				
Val	Leu	Lys	Ala	Leu	Lys	Thr	Ile	Asp	Ile	Thr	Arg	Tyr	Phe	Ala	Gly
305				310					315					320	
Ile	Ser	Arg	Glu	Glu	Ile	Ala	Glu	Ala	Val	Val	Gly				
			325						330						

(2) INFORMATION FOR SEQ ID NO:4657:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4657:

Phe	Phe	Ile	Ile	Arg	Ile	Phe	Leu	Ile	Ser	Ser	Ile	Gly	Pro	Met	Thr
1			5					10					15		
Arg	Lys	Ala	Arg	Thr	Gly	Ala	Lys	Pro	Lys	Leu	Glu	Ser	Arg	Glu	Ala
		20				25						30			
Pro	Ile	Lys	Ala	Ser	Ala	Ser	Leu	Gln	Ser	Glu	Arg	Arg	Lys	Ala	Lys
		35			40						45				
Ile	Ile	Lys	Ser	Arg	Met	Ala	Lys	Arg	Gly	Val	Ala	Leu	Ile	Glu	Val
	50				55					60					
Arg	Ile	Arg	Val	Gly	Thr										
65					70										

(2) INFORMATION FOR SEQ ID NO:4658:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 348 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...348
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4658:

Glu	Val	Ile	Met	Asp	Ile	Arg	Gln	Val	Thr	Glu	Thr	Ile	Ala	Met	Ile
1				5				10					15		
Glu	Glu	Gln	Asn	Phe	Asp	Ile	Arg	Thr	Ile	Thr	Met	Gly	Ile	Ser	Leu
			20				25					30			
Leu	Asp	Cys	Ile	Asp	Pro	Asp	Ile	Asn	Arg	Ala	Ala	Glu	Lys	Ile	Tyr
		35					40					45			
Gln	Lys	Ile	Thr	Thr	Lys	Ala	Ala	Asn	Leu	Val	Ala	Val	Gly	Asp	Glu
		50				55				60					
Ile	Ala	Ala	Glu	Leu	Gly	Ile	Pro	Ile	Val	Asn	Lys	Arg	Val	Ser	Val
65					70				75					80	
Thr	Pro	Ile	Ser	Leu	Ile	Gly	Ala	Ala	Thr	Asp	Ala	Thr	Asp	Tyr	Val
				85					90					95	
Val	Leu	Ala	Lys	Ala	Leu	Asp	Lys	Ala	Ala	Lys	Glu	Ile	Gly	Val	Asp
			100					105					110		
Phe	Ile	Gly	Gly	Phe	Ser	Ala	Leu	Val	Gln	Lys	Gly	Tyr	Gln	Lys	Gly
		115					120					125			
Asp	Glu	Ile	Leu	Ile	Asn	Ser	Ile	Pro	Arg	Ala	Leu	Ala	Glu	Thr	Asp
		130				135					140				
Lys	Val	Cys	Ser	Ser	Val	Asn	Ile	Gly	Ser	Thr	Lys	Ser	Gly	Ile	Asn
145					150				155					160	
Met	Thr	Ala	Val	Ala	Asp	Met	Gly	Pro	Ile	Ile	Lys	Glu	Thr	Ala	Asn
				165				170						175	
Leu	Ser	Glu	Ile	Gly	Val	Ala	Lys	Leu	Val	Val	Phe	Ala	Asn	Ala	Val
			180					185					190		
Glu	Asp	Asn	Pro	Phe	Met	Ala	Gly	Ala	Phe	His	Gly	Val	Gly	Glu	Ala
		195					200				205				
Asp	Val	Ile	Ile	Asn	Val	Gly	Val	Ser	Gly	Pro	Gly	Val	Val	Lys	Arg
		210				215					220				
Ala	Leu	Glu	Lys	Val	Arg	Gly	Gln	Ser	Phe	Asp	Val	Val	Ala	Glu	Thr
225					230				235					240	
Val	Lys	Lys	Thr	Ala	Phe	Lys	Ile	Thr	Arg	Ile	Gly	Gln	Leu	Val	Gly
				245					250					255	
Gln	Met	Ala	Ser	Glu	Arg	Leu	Gly	Val	Glu	Phe	Gly	Ile	Val	Asp	Leu
			260					265					270		
Ser	Leu	Ala	Pro	Thr	Pro	Ala	Val	Gly	Asp	Ser	Val	Ala	Arg	Val	Leu
		275					280					285			
Glu	Glu	Met	Gly	Leu	Glu	Thr	Val	Gly	Thr	His	Gly	Thr	Thr	Ala	Ala
		290				295					300				
Leu	Ala	Leu	Leu	Asn	Asp	Gln	Val	Lys	Lys	Gly	Gly	Val	Met	Ala	Cys

305		310		315		320									
Asn	Gln	Val	Gly	Gly	Leu	Ser	Gly	Ala	Xaa	Ile	Pro	Val	Ser	Glu	Gly
		325		330		335									
Glu	Gly	Met	Ile	Ala	Ala	Val	Arg	Lys	Trp	Leu	Ser				
		340		345											

(2) INFORMATION FOR SEQ ID NO:4659:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 158 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...158

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4659:

Phe	Pro	Ile	Ile	Met	Gly	Ser	Lys	Ser	Asp	Trp	Ala	Thr	Met	Gln	Lys
1				5					10					15	
Thr	Ala	Glu	Val	Leu	Asp	Arg	Phe	Gly	Val	Ala	Tyr	Glu	Lys	Lys	Val
			20					25					30		
Val	Ser	Ala	His	Arg	Thr	Pro	Asp	Leu	Met	Phe	Lys	His	Ala	Glu	Glu
		35					40					45			
Ala	Arg	Ser	Arg	Gly	Ile	Lys	Ile	Ile	Ile	Ala	Gly	Ala	Gly	Gly	Ala
		50				55					60				
Ala	His	Leu	Pro	Gly	Met	Val	Ala	Ala	Xaa	Thr	Thr	Tyr	Pro	Val	Ile
65				70					75					80	
Gly	Val	Pro	Val	Lys	Ser	Arg	Ala	Leu	Ser	Gly	Val	Asp	Ser	Leu	Tyr
			85						90				95		
Ser	Ile	Val	Gln	Met	Pro	Gly	Gly	Val	Pro	Val	Ala	Thr	Met	Ala	Ile
		100					105						110		
Gly	Glu	Ala	Gly	Ala	Thr	Asn	Ala	Ala	Leu	Phe	Ala	Ile	Arg	Leu	Leu
		115				120						125			
Ser	Val	Glu	Asp	Lys	Ser	Ile	Ala	Asp	Ala	Leu	Ala	Asn	Phe	Ala	Glu
		130				135					140				
Glu	Gln	Gly	Lys	Ile	Ala	Glu	Glu	Ser	Ser	Asn	Glu	Leu	Ile		
145					150					155					

(2) INFORMATION FOR SEQ ID NO:4660:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 186 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...186

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4660:

Gly	Ser	Ile	Met	Lys	Ser	Ile	Gly	Thr	Gln	Ile	Leu	Gln	Thr	Glu	Arg
1				5					10					15	
Leu	Ile	Leu	Arg	Arg	Phe	Val	Glu	Ser	Asp	Ala	Glu	Ala	Met	Phe	Gln
			20					25					30		
Asn	Trp	Ala	Ser	Ser	Ala	Glu	Asn	Leu	Thr	Tyr	Val	Thr	Trp	Asn	Pro
			35				40					45			
His	Pro	Asp	Val	Glu	Ile	Thr	Arg	Asn	Ser	Ile	Arg	Asn	Trp	Val	Ala
	50					55					60				
Ser	Tyr	Thr	Asn	Leu	Asn	Tyr	Tyr	Lys	Trp	Ala	Ile	Cys	Leu	Lys	Glu
65				70					75					80	
Asn	Pro	Glu	Gln	Val	Ile	Gly	Asp	Ile	Ser	Ile	Val	Lys	Ile	Asp	Glu
			85					90					95		
Ala	Asp	Leu	Ser	Cys	Glu	Ile	Gly	Tyr	Val	Leu	Gly	Lys	Ala	Tyr	Trp
		100					105					110			
Gly	His	Gly	Met	Met	Thr	Glu	Ala	Leu	Lys	Ala	Val	Leu	Asp	Phe	Cys
	115					120						125			
Phe	Thr	Gln	Ala	Gly	Phe	Gln	Lys	Val	Arg	Ala	Arg	Tyr	Ala	Ser	Leu
	130					135					140				
Asn	Pro	Ala	Ser	Gly	Arg	Val	Met	Glu	Lys	Ala	Gly	Met	Ser	Tyr	Leu
145				150					155					160	
Gln	Thr	Ile	Val	Asn	Gly	Val	Glu	Arg	Lys	Gly	Tyr	Leu	Ala	Asp	Leu
			165					170						175	
Ile	Tyr	Tyr	Gly	Ile	Ser	Arg	Glu	Glu	Cys						
		180					185								

(2) INFORMATION FOR SEQ ID NO:4661:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 484 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...484

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4661:

Val	Leu	Ile	Met	Ser	Arg	Arg	Phe	Lys	Lys	Ser	Gly	Ser	Gln	Lys	Val
1				5				10					15		

Lys	Arg	Ser	Val	Asn	Ile	Val	Leu	Leu	Thr	Ile	Tyr	Leu	Leu	Leu	Val
			20					25					30		
Cys	Phe	Leu	Leu	Phe	Leu	Ile	Phe	Lys	Tyr	Asn	Ile	Leu	Ala	Phe	Arg
		35					40					45			
Tyr	Leu	Asn	Leu	Val	Ala	Thr	Ala	Phe	Val	Leu	Leu	Val	Ala	Leu	Ile
	50					55					60				
Gly	Leu	Leu	Ser	Ile	Ile	Tyr	Lys	Lys	Ala	Glu	Lys	Phe	Thr	Ile	Phe
65					70					75					80
Leu	Leu	Val	Leu	Ser	Ile	Leu	Val	Ser	Ser	Val	Ser	Leu	Phe	Ala	Val
				85					90					95	
Gln	Gln	Phe	Val	Gly	Leu	Thr	Asn	Arg	Leu	Asn	Ala	Thr	Ser	Asn	Tyr
			100					105						110	
Ser	Glu	Tyr	Ser	Leu	Ser	Val	Ala	Val	Leu	Ala	Asp	Ser	Glu	Ile	Glu
		115					120					125			
Asn	Val	Thr	Gln	Leu	Thr	Ser	Val	Thr	Ala	Pro	Thr	Gly	Thr	Asp	Asn
		130				135						140			
Glu	Asn	Ile	Gln	Lys	Leu	Leu	Ala	Asp	Ile	Lys	Ser	Ser	Gln	Asn	Ile
145					150					155					160
Asp	Leu	Thr	Val	Asn	Gln	Ser	Ser	Ser	Tyr	Leu	Ser	Ala	Tyr	Arg	Ser
			165						170					175	
Leu	Ile	Ala	Gly	Glu	Thr	Lys	Ala	Ile	Val	Leu	Asn	Ser	Val	Phe	Glu
			180					185					190		
Asn	Ile	Ile	Glu	Ser	Glu	Tyr	Pro	Asp	His	Ala	Ser	Lys	Ile	Lys	Lys
		195					200					205			
Ile	Tyr	Thr	Lys	Gly	Phe	Ile	Lys	Lys	Val	Glu	Ala	Pro	Lys	Thr	Ser
	210					215						220			
Lys	Asn	Gln	Ser	Phe	Asn	Ile	Tyr	Val	Ser	Gly	Ile	Asp	Thr	Tyr	Gly
225					230					235					240
Pro	Ile	Ser	Ser	Val	Ser	Arg	Ser	Asp	Val	Asn	Ile	Leu	Met	Thr	Val
				245					250					255	
Asn	Arg	Asp	Thr	Lys	Lys	Ile	Leu	Leu	Thr	Thr	Thr	Pro	Arg	Asp	Ala
			260					265					270		
Tyr	Val	Pro	Ile	Ala	Asp	Gly	Gly	Asn	Asn	Gln	Lys	Asp	Lys	Leu	Thr
		275				280						285			
His	Ala	Gly	Ile	Tyr	Gly	Val	Asp	Ser	Ser	Ile	His	Thr	Leu	Glu	Asn
	290					295					300				
Leu	Tyr	Gly	Val	Asp	Ile	Asn	Tyr	Tyr	Val	Arg	Leu	Asn	Phe	Thr	Ser
305					310					315					320
Phe	Leu	Lys	Leu	Ile	Asp	Leu	Leu	Gly	Gly	Val	Asp	Val	Tyr	Asn	Asp
				325					330					335	
Gln	Glu	Phe	Thr	Ala	Leu	Ala	Asn	Lys	Lys	His	Tyr	Ser	Ile	Gly	Asn
			340					345					350		
Val	His	Leu	Asp	Ser	Glu	Glu	Ala	Leu	Ala	Phe	Val	Arg	Glu	Arg	Tyr
		355					360					365			
Ser	Leu	Ala	Asp	Gly	Asp	Arg	Asp	Arg	Gly	Arg	Asn	Gln	Gln	Lys	Val
	370					375					380				
Ile	Val	Ala	Ile	Leu	Gln	Lys	Leu	Thr	Ser	Thr	Glu	Val	Leu	Lys	Asn
385					390					395					400
Tyr	Ser	Thr	Ile	Ile	Asp	Ser	Leu	Gln	Asp	Ser	Ile	Gln	Thr	Asn	Met
			405						410					415	
Pro	Leu	Glu	Thr	Met	Ile	Asn	Leu	Val	Asn	Ala	Gln	Leu	Glu	Ser	Gly
			420					425					430		
Gly	Thr	Tyr	Lys	Val	Asn	Ser	Gln	Asp	Leu	Lys	Gly	Arg	Gly	Arg	Thr
		435					440					445			
Asp	Leu	Pro	Ser	Tyr	Ala	Met	Pro	Asp	Ser	Asn	Leu	Tyr	Val	Met	Glu
	450					455					460				
Ile	Asn	Asp	Ser	Ser	Leu	Ala	Ser	Val	Lys	Thr	Ala	Ile	Gln	Asp	Val

465 470 475 480
 Leu Glu Gly Arg

(2) INFORMATION FOR SEQ ID NO:4662:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 255 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4662:

Cys	Arg	Ile	Met	Glu	Lys	Phe	Glu	Met	Ile	Ser	Ile	Thr	Asp	Ile	Gln	1	5	10	15
Lys	Asn	Pro	Tyr	Gln	Pro	Arg	Lys	Glu	Phe	Asp	Arg	Glu	Lys	Leu	Asp	20	25	30	
Glu	Leu	Ala	Gln	Ser	Ile	Lys	Glu	Asn	Gly	Val	Ile	Gln	Pro	Ile	Ile	35	40	45	
Val	Arg	Gln	Ser	Pro	Val	Ile	Gly	Tyr	Glu	Ile	Leu	Ala	Gly	Glu	Arg	50	55	60	
Arg	Tyr	Arg	Ala	Ser	Leu	Leu	Ala	Gly	Leu	Arg	Ser	Ile	Pro	Ala	Val	65	70	75	80
Val	Lys	Gln	Ile	Ser	Asp	Gln	Glu	Met	Met	Val	Gln	Ser	Ile	Ile	Glu	85	90	95	
Asn	Leu	Gln	Arg	Glu	Asn	Leu	Asn	Pro	Ile	Glu	Glu	Ala	Arg	Ala	Tyr	100	105	110	
Glu	Ser	Leu	Val	Glu	Lys	Gly	Phe	Thr	His	Ala	Glu	Ile	Ala	Asp	Lys	115	120	125	
Met	Gly	Lys	Ser	Arg	Pro	Tyr	Ile	Ser	Asn	Ser	Ile	Arg	Leu	Leu	Ser	130	135	140	
Leu	Pro	Glu	Gln	Ile	Leu	Ser	Glu	Val	Glu	Asn	Gly	Lys	Leu	Ser	Gln	145	150	155	160
Ala	His	Ala	Arg	Ser	Leu	Val	Gly	Leu	Asn	Lys	Glu	Gln	Gln	Asp	Tyr	165	170	175	
Phe	Phe	Gln	Arg	Ile	Ile	Glu	Glu	Asp	Ile	Ser	Val	Arg	Lys	Leu	Glu	180	185	190	
Ala	Leu	Leu	Thr	Glu	Lys	Lys	Gln	Lys	Lys	Gln	Gln	Lys	Thr	Asn	His	195	200	205	
Phe	Ile	Gln	Asn	Glu	Glu	Lys	Gln	Leu	Arg	Lys	Leu	Leu	Gly	Leu	Asp	210	215	220	
Val	Glu	Ile	Lys	Leu	Ser	Lys	Lys	Asp	Ser	Gly	Lys	Ile	Ile	Ile	Ser	225	230	235	240
Phe	Ser	Asn	Gln	Glu	Glu	Tyr	Ser	Arg	Ile	Ile	Asn	Ser	Leu	Lys		245	250	255	

(2) INFORMATION FOR SEQ ID NO:4663:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 274 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...274

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4663:

Lys	Gly	Ile	Ile	Met	Asp	Gln	Leu	Gln	Ile	Lys	Asp	Leu	Glu	Met	Phe
1				5				10					15		
Ala	Tyr	His	Gly	Leu	Phe	Pro	Ser	Glu	Lys	Glu	Leu	Gly	Gln	Lys	Phe
			20					25					30		
Val	Val	Ser	Ala	Ile	Leu	Ser	Tyr	Asp	Met	Thr	Lys	Ala	Ala	Thr	Asp
		35					40					45			
Leu	Asp	Leu	Thr	Ala	Ser	Val	His	Tyr	Gly	Glu	Leu	Cys	Gln	Gln	Trp
	50					55				60					
Thr	Thr	Trp	Phe	Gln	Glu	Thr	Ser	Glu	Asp	Leu	Ile	Glu	Thr	Val	Ala
65				70					75					80	
Tyr	Lys	Leu	Val	Glu	Arg	Thr	Phe	Glu	Ser	Tyr	Pro	Leu	Val	Gln	Glu
			85					90						95	
Met	Lys	Leu	Glu	Leu	Lys	Lys	Pro	Trp	Ala	Pro	Val	His	Leu	Ser	Leu
			100					105					110		
Asp	Thr	Cys	Ser	Val	Thr	Ile	His	Arg	Arg	Lys	Gln	Arg	Ala	Phe	Ile
	115					120					125				
Ala	Leu	Gly	Ser	Asn	Met	Gly	Asp	Lys	Gln	Ala	Asn	Leu	Lys	Gln	Ala
	130					135					140				
Ile	Asp	Lys	Leu	Arg	Ala	Arg	Gly	Ile	Tyr	Ile	Leu	Lys	Glu	Ser	Ser
145				150					155					160	
Val	Leu	Ala	Thr	Glu	Pro	Trp	Gly	Gly	Val	Glu	Gln	Asp	Ser	Phe	Ala
			165					170						175	
Asn	Gln	Val	Val	Glu	Val	Glu	Thr	Trp	Leu	Pro	Ala	Gln	Asp	Leu	Leu
		180					185					190			
Glu	Thr	Leu	Leu	Ala	Ile	Glu	Ser	Glu	Leu	Gly	Arg	Val	Arg	Glu	Val
	195					200					205				
His	Trp	Gly	Pro	Arg	Leu	Ile	Asp	Leu	Asp	Leu	Leu	Phe	Val	Glu	Asp
	210				215					220					
Gln	Ile	Leu	Tyr	Thr	Asp	Asp	Leu	Ile	Leu	Pro	His	Pro	Tyr	Ile	Ala
225				230					235					240	
Glu	Arg	Leu	Phe	Val	Leu	Glu	Ser	Leu	Gln	Glu	Ile	Ala	Pro	His	Phe
			245					250					255		
Ile	His	Pro	Ile	Leu	Lys	Gln	Pro	Ile	Arg	Asn	Leu	Tyr	Asp	Ala	Leu
			260					265					270		
Lys	Lys														

(2) INFORMATION FOR SEQ ID NO:4664:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...71

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4664:

Ser	Thr	Ile	Ile	Val	Phe	Phe	Ser	Leu	Leu	Ile	Ser	Trp	Phe	Phe	Cys
1				5					10					15	
Phe	Trp	Leu	Phe	Ser	Trp	Leu	Leu	Trp	Phe	Trp	Cys	Gly	Ser	Trp	Leu
		20					25					30			
Arg	Ser	Arg	Arg	Trp	Phe	Trp	Leu	Phe	Ser	Trp	Cys	Phe	Trp	Gly	Trp
		35				40					45				
Ser	Phe	Trp	Ser	Trp	Ser	Trp	Phe	Phe	Trp	Leu	Ile	Asn	Cys	Phe	Leu
	50					55				60					
Lys	Val	Ser	Phe	Ser	Phe	Phe									
65					70										

(2) INFORMATION FOR SEQ ID NO:4665:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...94

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4665:

Ser	Trp	Ile	Ile	Leu	Ile	Arg	Ile	Thr	Leu	Tyr	Cys	Tyr	Phe	Arg	Asn
1				5				10						15	
Trp	Gly	Gly	Leu	Met	Glu	Ser	Ile	Gly	Leu	Val	Ile	Val	Ser	His	Ser
		20					25					30			
Lys	His	Ile	Ala	Glu	Gly	Val	Val	Ala	Leu	Ile	Ser	Lys	Val	Ala	Lys
		35				40					45				

Asp	Val	Pro	Ile	Thr	Tyr	Val	Gly	Gly	Thr	Glu	Gly	Gly	Gly	Ile	Gly
50						55					60				
Thr	Ser	Phe	Asp	Gln	Val	Asp	Arg	Val	Val	Ser	Glu	Asn	Pro	Ala	Asp
65					70					75					80
Thr	Leu	Leu	Ala	Phe	Phe	Asp	Leu	Gly	Ser	Ala	Ile	Lys	Cys		
				85					90						

(2) INFORMATION FOR SEQ ID NO:4666:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 338 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...338

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4666:

Ala	Gly	Ile	Ile	Ala	Leu	Ser	Ser	Phe	Val	Leu	Met	Ala	Leu	Arg	Phe
1				5					10					15	
Ser	Ser	Met	Val	Tyr	Asp	Thr	Asn	Gly	Glu	Gln	Val	Lys	Gln	Leu	Phe
			20					25					30		
Gly	Gly	Ala	Ile	Pro	Phe	Phe	Ser	Leu	Asn	Ala	Ser	Ser	Leu	Phe	Met
		35					40					45			
Ala	Ile	Thr	Ile	Gly	Leu	Val	Thr	Ala	Glu	Ile	Tyr	Arg	Met	Phe	Ile
		50				55					60				
Gln	Arg	Gly	Ile	Thr	Ile	Lys	Met	Pro	Ser	Gly	Val	Pro	Asp	Val	Val
65					70					75					80
Ser	Lys	Ser	Phe	Ser	Ala	Leu	Leu	Pro	Gly	Phe	Thr	Thr	Phe	Val	Leu
			85						90					95	
Trp	Ala	Leu	Val	Leu	Lys	Gly	Leu	Glu	Ala	Ala	Gly	Val	Ala	Gly	Gly
		100						105					110		
Leu	Asn	Gly	Phe	Leu	Gly	Ala	Ile	Val	Gly	Thr	Pro	Leu	Lys	Leu	Ile
		115					120					125			
Ala	Gly	Thr	Leu	Pro	Gly	Met	Ile	Leu	Cys	Val	Ile	Val	Asn	Ser	Phe
		130				135						140			
Phe	Trp	Phe	Cys	Gly	Val	Asn	Gly	Gly	Gln	Val	Leu	Asn	Ala	Phe	Val
145					150					155					160
Asp	Pro	Val	Trp	Leu	Gln	Phe	Thr	Thr	Glu	Asn	Gln	Glu	Ala	Val	Ala
				165					170					175	
Ala	Gly	Gln	Thr	Leu	Gln	His	Ile	Ile	Thr	Leu	Pro	Phe	Lys	Asp	Leu
			180					185					190		
Phe	Val	Phe	Ile	Gly	Gly	Gly	Gly	Ala	Thr	Ile	Gly	Leu	Ala	Ile	Cys
		195					200					205			
Leu	Phe	Leu	Phe	Ser	Lys	Ser	Arg	Ala	Asn	Lys	Thr	Leu	Gly	Lys	Leu
		210				215					220				
Ala	Ile	Ile	Pro	Ser	Ile	Phe	Asn	Ile	Asn	Thr	Ala	Ile	Leu	Phe	Thr
225					230					235					240

Phe	Pro	Thr	Val	Leu	Asn	Pro	Ile	Met	Leu	Ile	Pro	Phe	Ile	Ala	Thr
				245					250					255	
Pro	Thr	Ile	Asn	Ala	Leu	Ile	Thr	Tyr	Val	Ser	Met	Ala	Val	Gly	Leu
			260					265					270		
Val	Pro	Tyr	Thr	Thr	Gly	Val	Ile	Leu	Pro	Trp	Thr	Met	Pro	Pro	Ile
		275					280					285			
Ile	Gly	Gly	Phe	Leu	Ala	Thr	Gly	Ala	Ser	Trp	Arg	Gly	Ala	Leu	Leu
	290					295					300				
Gln	Val	Val	Leu	Ile	Leu	Val	Ser	Val	Ala	Ile	Tyr	Tyr	Pro	Phe	Phe
305					310					315					320
Lys	Ile	Ala	Asp	Lys	Arg	Asn	Leu	Glu	Lys	Glu	Lys	Ala	Thr	Val	Gly
			325						330					335	
Gly	Lys														

(2) INFORMATION FOR SEQ ID NO:4667:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 240 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...240
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4667:

Asn	Thr	Val	Ile	Leu	Asn	Ile	Lys	Glu	Phe	Asp	Met	Glu	Trp	Ile	Arg
1				5					10					15	
Leu	Ile	Gly	Ile	Ala	Ile	Ile	Val	Val	Gly	Phe	Ile	Leu	Lys	Phe	Asp
		20					25					30			
Thr	Ile	Ala	Thr	Val	Val	Leu	Ala	Gly	Leu	Val	Thr	Ala	Leu	Val	Ser
	35					40					45				
Gly	Val	Ser	Leu	Val	Glu	Phe	Leu	Glu	Ile	Leu	Gly	Lys	Glu	Phe	Ser
	50				55					60					
Asn	Gln	Arg	Val	Leu	Thr	Ile	Phe	Met	Val	Thr	Leu	Pro	Leu	Val	Gly
65				70					75					80	
Leu	Ser	Glu	Thr	Phe	Gly	Leu	Lys	Gln	Arg	Ser	Ile	Asp	Leu	Ile	Arg
			85					90					95		
Lys	Ile	Lys	Gly	Leu	Thr	Val	Gly	Asn	Phe	Tyr	Thr	Val	Tyr	Phe	Phe
	100						105					110			
Ile	Arg	Glu	Leu	Ala	Gly	Phe	Phe	Ser	Ile	Arg	Leu	Gly	Gly	His	Pro
	115					120					125				
Gln	Phe	Val	Arg	Pro	Leu	Val	Gln	Pro	Met	Gly	Glu	Ala	Ala	Ala	Glu
	130				135					140					
Ser	Gln	Leu	Gly	Arg	Lys	Leu	Thr	Glu	Val	Glu	Asp	Glu	Thr	Ile	Lys
145					150				155					160	
Ala	Arg	Ala	Ala	Ala	Asn	Glu	Asn	Phe	Gly	Asn	Phe	Phe	Ala	Gln	Asn
			165					170						175	

Thr	Phe	Val	Gly	Ala	Gly	Gly	Val	Leu	Leu	Ile	Gly	Gly	Thr	Leu	Asp
			180					185					190		
Gln	Leu	Gly	Tyr	Glu	Ser	Asn	Tyr	Ala	Gly	Ile	Ala	Ser	Thr	Ser	Ile
		195					200					205			
Ile	Val	Ala	Val	Ile	Thr	Leu	Ile	Val	Val	Gly	Ile	Tyr	Asn	Tyr	Leu
	210					215					220				
Phe	Asp	Lys	Lys	Leu	Ile	Ser	Lys	Lys	Thr	Arg	Gly	Gly	Glu	Gln	Lys
225					230					235					240

(2) INFORMATION FOR SEQ ID NO:4668:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4668:

Asn	Ser	Val	Met	Ser	Lys	Met	Tyr	Tyr	Ala	Glu	Asn	Pro	Asp	Ala	Ala
1				5					10					15	
His	Asp	Ile	His	Glu	Leu	Arg	Val	Asp	Leu	Leu	Gly	Gln	Lys	Met	Thr
			20					25					30		
Phe	Leu	Thr	Asp	Ala	Gly	Val	Phe	Ser	Lys	Lys	Ile	Val	Asp	Phe	Gly
		35					40					45			
Ser	Gln	Leu	Leu	Leu	Lys	Cys	Leu	Glu	Val	Asn	Gln	Gly	Glu	Thr	Val
		50				55					60				
Leu	Asp	Val	Gly	Cys	Gly	Tyr	Gly	Pro	Leu	Gly	Leu	Ser	Leu	Ala	Lys
65					70					75				80	
Ala	Tyr	Gly	Val	Gln	Ala	Thr	Met	Val	Asp	Ile	Asn	Thr	Arg	Ala	Leu
				85					90					95	
Asp	Leu	Ala	Arg	Arg	Asn	Ala	Glu	Lys	Asn	Asn	Ala	Lys	Ala	Thr	Ile
			100					105					110		
Phe	Gln	Ser	Asn	Ile	Tyr	Glu	Gln	Val	Glu	Gly	His	Phe	Asp	His	Val
		115					120					125			
Ile	Ser	Asn	Pro	Pro	Ile	Arg	Ala	Gly	Lys	Gln	Val	Val	His	Glu	Ile
	130					135					140				
Ile	Glu	Lys	Ser	Lys	Asp	Phe	Leu	Glu	Thr	Gly	Gly	Asp	Leu	Thr	Ile
145					150					155					160
Val	Ile	Gln	Lys	Lys	Thr	Arg	Gly	Ser	Lys	Cys					
				165						170					

(2) INFORMATION FOR SEQ ID NO:4669:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 473 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...473

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4669:

Gly	Leu	Val	Met	Glu	Asn	Leu	Gln	Phe	Lys	Ala	Leu	Pro	Lys	Glu	Phe
1				5				10						15	
Leu	Leu	Gly	Ala	Ala	Thr	Ala	Ala	Tyr	Gln	Val	Glu	Gly	Ala	Thr	Arg
			20					25					30		
Val	Asp	Gly	Lys	Gly	Ile	Asn	Met	Trp	Asp	Val	Tyr	Leu	Gln	Glu	Asn
	35					40						45			
Ser	Pro	Phe	Leu	Pro	Asp	Pro	Ala	Ser	Asp	Phe	Tyr	Tyr	Arg	Tyr	Glu
	50					55					60				
Glu	Asp	Ile	Ala	Leu	Ala	Ala	Glu	His	Gly	Leu	Gln	Ala	Leu	Arg	Leu
65				70					75					80	
Ser	Ile	Ser	Trp	Val	Arg	Ile	Phe	Pro	Asp	Ile	Asp	Gly	Asp	Ala	Asn
				85				90					95		
Ile	Leu	Ala	Val	Arg	Tyr	Tyr	His	Arg	Val	Phe	Gln	Ser	Cys	Leu	Lys
			100					105					110		
His	Asn	Val	Ile	Pro	Phe	Val	Ser	Leu	His	His	Phe	Asp	Ser	Pro	Gln
	115						120					125			
Lys	Met	Leu	Glu	Thr	Gly	Asp	Trp	Leu	Asp	Arg	Glu	Asn	Ile	Asp	His
	130					135					140				
Phe	Ile	Arg	Tyr	Ala	Arg	Phe	Cys	Phe	Gln	Glu	Phe	Thr	Glu	Val	Lys
145				150					155					160	
His	Trp	Phe	Thr	Ile	Asn	Glu	Leu	Met	Ser	Leu	Ala	Ala	Gly	Gln	Tyr
			165					170					175		
Ile	Gly	Gly	Gln	Phe	Pro	Pro	Asn	His	His	Phe	Gln	Leu	Ser	Glu	Ala
	180						185						190		
Ile	Gln	Ala	Asn	His	Asn	Met	Leu	Leu	Ala	His	Ala	Leu	Ala	Val	Leu
	195					200						205			
Glu	Phe	His	Gln	Leu	Gly	Ile	Glu	Gly	Glu	Ile	Gly	Cys	Ile	His	Ala
	210					215				220					
Leu	Lys	Pro	Gly	Tyr	Pro	Ile	Asp	Gly	Gln	Lys	Glu	Asn	Ile	Leu	Ala
225					230				235					240	
Ala	Lys	Arg	Tyr	Asp	Val	Tyr	Asn	Asn	Lys	Phe	Leu	Leu	Asp	Gly	Thr
			245						250					255	
Phe	Leu	Gly	Tyr	Tyr	Ser	Glu	Asp	Thr	Leu	Phe	His	Leu	Asn	Gln	Ile
			260					265					270		
Leu	Glu	Ala	Asn	Asn	Ser	Ser	Phe	Ile	Ile	Glu	Asp	Gly	Asp	Leu	Glu
	275						280					285			
Ile	Met	Lys	Arg	Ala	Ala	Pro	Leu	Asn	Thr	Met	Phe	Gly	Met	Asn	Tyr
	290					295					300				
Tyr	Arg	Ser	Glu	Phe	Ile	Arg	Glu	Tyr	Lys	Gly	Glu	Asn	Arg	Gln	Glu
305				310						315				320	
Phe	Asn	Ser	Thr	Gly	Ile	Lys	Gly	Gln	Ser	Ser	Phe	Lys	Leu	Asn	Ala
			325					330					335		

Leu Gly Glu Phe Val Lys Lys Thr Gly Ile Pro Thr Thr Asp Trp Asp
 340 345 350
 Trp Asn Ile Tyr Pro Gln Gly Leu Phe Asp Met Leu Leu Arg Ile Lys
 355 360 365
 Glu Glu Tyr Pro Gln His Pro Val Ile Tyr Leu Thr Glu Asn Gly Thr
 370 375 380
 Ala Leu Lys Glu Val Lys Pro Glu Gly Glu Asn Asp Ile Ile Asp Asp
 385 390 395 400
 Ser Lys Arg Ile Arg Tyr Ile Glu Gln His Leu His Lys Val Leu Glu
 405 410 415
 Ala Arg Asp Arg Gly Val Asn Ile Gln Gly Tyr Phe Ile Trp Ser Leu
 420 425 430
 Gln Asp Gln Phe Ser Trp Ala Asn Gly Tyr Asn Lys Arg Tyr Gly Leu
 435 440 445
 Phe Phe Val Asp Tyr Glu Thr Gln Lys Arg Tyr Ile Lys Lys Ser Ala
 450 455 460
 Leu Trp Val Lys Gly Leu Lys Arg Asn
 465 470

(2) INFORMATION FOR SEQ ID NO:4670:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...63
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4670:

Lys Gln Val Ile Lys Thr Arg Glu Cys Ser His Thr Leu Thr Ala Lys
 1 5 10 15
 Lys Glu Asn Val Ala Pro Arg Asp Gln Glu Phe Tyr Asp Lys Ala Tyr
 20 25 30
 Asn Leu Leu Thr Glu Ala His Lys Ala Ser Phe Glu Asn Lys Gly Arg
 35 40 45
 Asn Ser Asp Ser Lys Thr Leu Arg Gln Ile Ile Arg Thr Leu Glu
 50 55 60

(2) INFORMATION FOR SEQ ID NO:4671:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 162 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...162

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4671:

Asn	Arg	Val	Met	Lys	Ile	Lys	Val	Val	Thr	Val	Gly	Lys	Leu	Lys	Glu
1				5					10					15	
Lys	Tyr	Leu	Lys	Asp	Gly	Ile	Ala	Glu	Tyr	Ser	Lys	Arg	Ile	Ser	Arg
			20					25					30		
Phe	Ala	Lys	Phe	Glu	Met	Ile	Glu	Leu	Ser	Asp	Glu	Lys	Thr	Pro	Asp
			35				40					45			
Lys	Ala	Ser	Glu	Ser	Glu	Asn	Gln	Lys	Ile	Leu	Glu	Ile	Glu	Gly	Gln
			50			55					60				
Arg	Ile	Leu	Ser	Lys	Ile	Ala	Asp	Arg	Asp	Phe	Val	Ile	Val	Leu	Ala
65					70				75					80	
Ile	Glu	Gly	Lys	Thr	Phe	Phe	Ser	Glu	Glu	Phe	Ser	Lys	Gln	Leu	Glu
				85				90					95		
Glu	Thr	Ser	Ile	Lys	Gly	Phe	Ser	Thr	Leu	Thr	Phe	Ile	Ile	Gly	Gly
			100					105					110		
Ser	Leu	Gly	Leu	Ser	Ser	Ser	Val	Lys	Asn	Arg	Ala	Asn	Leu	Ser	Val
			115				120					125			
Ser	Phe	Gly	Arg	Leu	Thr	Leu	Pro	His	Gln	Leu	Met	Arg	Leu	Val	Leu
			130			135					140				
Val	Glu	Gln	Ile	Tyr	Arg	Ala	Phe	Thr	Ile	Gln	Gln	Gly	Phe	Pro	Tyr
145					150					155					160
His	Lys														

(2) INFORMATION FOR SEQ ID NO:4672:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 287 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...287

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4672:

Lys	Leu	Val	Ile	Gly	Glu	Ile	Phe	Ile	Lys	Leu	Lys	Leu	Ser	Asn	Asn
1				5					10					15	
Ser	Ile	Glu	Ser	Lys	Glu	Ser	Lys	Asn	Leu	Lys	Lys	Lys	Trp	Phe	Phe


```

1           5           10           15
His Phe Lys Glu Leu Tyr Lys Glu Lys Arg Leu Gln Leu Gln Gly Gln
20           25           30
Gly Gln Asn Gly Lys Gly Tyr Ser Gln Ala Phe Leu Leu Gly Leu Thr
35           40           45
Phe Ser Phe Ala Trp Thr Pro Cys Val Gly Pro Val Leu Gly Ser Val
50           55           60
Leu Ala Leu Ala Ala Ser Gly Gly Ser Arg Ala Trp Gln Gly Ala Gly
65           70           75           80
Leu Met Leu Val Tyr Thr Leu Gly Leu Ala Leu Pro Phe Leu Leu Leu
85           90           95
Ala Leu Thr Ser Ser Tyr Val Leu Lys His Phe Arg Lys Leu His Pro
100          105          110
Tyr Leu Gly Ile Leu Lys Lys Val Gly Gly Phe Leu Ile Ile Val Met
115          120          125
Gly Leu Leu Val Leu Phe Gly Asn Ala Ser Ile Leu Ser Gln Leu Phe
130          135          140
Glu
145

```

(2) INFORMATION FOR SEQ ID NO:4675:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 446 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...446

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4675:

```

Gly Asp Ser Met Lys Ile Asp Ile Thr Asn Gln Val Lys Asp Glu Phe
1           5           10           15
Leu Ile Ser Leu Lys Thr Leu Ile Ser Tyr Pro Ser Val Leu Asn Glu
20           25           30
Gly Glu Asn Gly Thr Pro Phe Gly Gln Ala Ile Gln Asp Val Leu Glu
35           40           45
Lys Thr Leu Glu Ile Cys Arg Asp Ile Gly Phe Thr Thr Tyr Leu Asp
50           55           60
Pro Lys Gly Tyr Tyr Gly Tyr Ala Glu Ile Gly Gln Gly Ala Glu Leu
65           70           75           80
Leu Ala Ile Leu Cys His Leu Asp Val Val Pro Ser Gly Asp Glu Ala
85           90           95
Asp Trp Gln Thr Pro Pro Phe Glu Ala Thr Ile Lys Asp Gly Trp Val
100          105          110
Phe Gly Arg Gly Val Gln Asp Asp Lys Gly Pro Ser Leu Ala Ala Leu
115          120          125
Tyr Ala Val Lys Ser Leu Leu Asp Gln Gly Ile Gln Phe Lys Lys Arg

```


130		135		140													
Val	Arg	Phe	Ile	Phe	Gly	Thr	Asp	Glu	Glu	Thr	Leu	Trp	Arg	Cys	Met		
145					150					155					160		
Ala	Arg	Tyr	Asn	Thr	Ile	Glu	Glu	Gln	Ala	Ser	Met	Gly	Phe	Ala	Pro		
				165						170					175		
Asp	Ser	Ser	Phe	Pro	Leu	Thr	Tyr	Ala	Glu	Lys	Gly	Leu	Leu	Gln	Val		
			180						185					190			
Lys	Leu	His	Gly	Pro	Gly	Ser	Asp	Gln	Leu	Glu	Leu	Glu	Val	Gly	Gly		
		195					200						205				
Ala	Phe	Asn	Val	Val	Pro	Asp	Lys	Ala	Asn	Tyr	Gln	Gly	Pro	Leu	Tyr		
		210				215					220						
Glu	Gln	Val	Cys	Asn	Asp	Leu	Lys	Glu	Ala	Gly	Tyr	Asp	Tyr	Gln	Ser		
225					230					235					240		
Thr	Glu	Gln	Thr	Val	Thr	Val	Leu	Gly	Val	Pro	Lys	His	Ala	Lys	Asp		
				245					250					255			
Ala	Ser	Gln	Gly	Ile	Asn	Ala	Val	Ile	Arg	Leu	Ala	Thr	Ile	Leu	Ala		
			260					265					270				
Pro	Leu	Gln	Glu	His	Pro	Ala	Leu	Ser	Phe	Leu	Ala	Thr	Gln	Ala	Gly		
		275					280					285					
Gln	Asp	Gly	Thr	Gly	Arg	Gln	Ile	Phe	Gly	Asp	Ile	Ala	Asp	Glu	Pro		
290					295					300							
Ser	Gly	His	Leu	Ser	Phe	Asn	Val	Ala	Gly	Leu	Met	Ile	Asn	His	Glu		
305					310					315					320		
Arg	Ser	Glu	Ile	Arg	Ile	Asp	Ile	Arg	Thr	Pro	Val	Leu	Ala	Asp	Lys		
				325					330					335			
Glu	Glu	Leu	Val	Lys	Leu	Leu	Thr	Arg	Cys	Ala	Gln	Asn	Tyr	Gln	Leu		
		340						345				350					
Arg	Tyr	Glu	Glu	Phe	Asp	Tyr	Leu	Ala	Pro	Leu	Tyr	Val	Ala	Lys	Asp		
		355					360					365					
Ser	Lys	Leu	Val	Ser	Thr	Leu	Met	Gln	Ile	Tyr	Gln	Glu	Lys	Thr	Gly		
		370				375				380							
Asp	Asn	Ser	Pro	Ala	Ile	Ser	Ser	Gly	Gly	Ala	Thr	Phe	Ala	Arg	Thr		
385					390					395					400		
Met	Pro	Asn	Cys	Val	Ala	Phe	Gly	Ala	Leu	Phe	Pro	Gly	Ala	Lys	Gln		
				405					410					415			
Thr	Glu	His	Gln	Ala	Asn	Glu	Cys	Ala	Val	Leu	Glu	Asp	Leu	Tyr	Arg		
			420					425					430				
Ala	Met	Asp	Ile	Tyr	Ala	Glu	Ala	Val	Tyr	Arg	Leu	Ala	Thr				
		435					440					445					

(2) INFORMATION FOR SEQ ID NO:4676:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...71

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4676:

Gly	Cys	Ser	Ile	Leu	Cys	Arg	Gly	Pro	Glu	Ser	Asn	Arg	Tyr	Asp	Arg
1				5				10						15	
Tyr	Gln	Ser	Gln	Asp	Phe	Lys	Ser	Cys	Ala	Ser	Ala	Ser	Ser	Ala	Thr
			20					25					30		
Pro	Ala	Ser	Leu	Ser	Glu	Arg	Arg	Asp	Ser	Asn	Pro	Arg	Pro	Pro	Pro
		35					40					45			
Trp	Gln	Gly	Gly	Val	Leu	Pro	Leu	Asn	Tyr	Val	Arg	Thr	Val	Phe	Phe
	50					55					60				
Tyr	Leu	Lys	Met	Pro	Ala	Thr									
65						70									

(2) INFORMATION FOR SEQ ID NO:4677:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...71

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4677:

Gly	Cys	Ser	Ile	Leu	Cys	Arg	Gly	Pro	Glu	Ser	Asn	Arg	Tyr	Asp	Arg
1				5				10					15		
Tyr	Gln	Ser	Gln	Asp	Phe	Lys	Ser	Cys	Ala	Ser	Ala	Ser	Ser	Ala	Thr
			20					25					30		
Pro	Ala	Ser	Leu	Ser	Glu	Arg	Arg	Asp	Ser	Asn	Pro	Arg	Pro	Pro	Pro
		35					40					45			
Trp	Gln	Gly	Gly	Val	Leu	Pro	Leu	Asn	Tyr	Val	Arg	Thr	Val	Phe	Phe
	50					55					60				
Tyr	Leu	Lys	Met	Pro	Ala	Thr									
65						70									

(2) INFORMATION FOR SEQ ID NO:4678:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4678:

```

Asp Val Pro Met Glu Ile Pro Ile Lys Ile Ile Gln Ala Ser Lys Ser
1          5          10          15
Asp Leu Pro Glu Ile Gly Ala Leu Gln Thr Ser Ser Phe Pro Ala Glu
          20          25          30
Lys Gln Gln Leu Ser His Ile Leu Glu Glu Ser Ile Arg Lys Cys Ala
          35          40          45
Asp Thr Phe Leu Leu Ala Arg Asp Glu Asn Gln Leu Leu Gly Tyr Ile
          50          55          60
Leu Ser Ser Pro Gln Ser Asp Asn Pro Gln Cys Leu Lys Val His Ser
65          70          75          80
Leu Val Ile Glu Ser Asp His Gln Arg Gln Gly Leu Gly Thr Leu Leu
          85          90          95
Leu Ala Ala Leu Lys Glu Val Ala Val Glu Leu Asp Tyr Lys Gly Phe
          100         105         110
Val Trp Arg Ser Cys Gly Val Phe
          115         120

```

(2) INFORMATION FOR SEQ ID NO:4679:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 116 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4679:

```

Ala Asn Pro Ile Gly Thr Lys Val Leu Ser Asn Pro Ile Val Ile Asp
1          5          10          15
Leu Leu Asp Trp Tyr Phe Asp Gln Leu Ser Pro Leu Val Ser Leu Glu
          20          25          30
Phe Phe Pro Gln Ala Thr Lys Asn Lys Ala Val Ile Arg Leu Thr Asn
          35          40          45
Thr Ser Ile His Phe Phe Ile His Phe Phe Ile His Phe Ser Ser Tyr
          50          55          60
Leu Gly Ser Thr Phe Asn Asn Thr Ser Ala Ile Phe Ser Ala Asn Cys
65          70          75          80
Lys Ser Trp Val Thr Thr Ile Trp Val Ile Pro Ser Ser Leu Phe Cys

```

			85					90					95			
Lys	Ile	Ser	Phe	Ser	Thr	Ser	Lys	Arg	Asn	Ser	Gly	Ser	Arg	Ala	Glu	
			100					105					110			
Val	Gly	Ser	Ser													
			115													

(2) INFORMATION FOR SEQ ID NO:4680:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 499 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...499

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4680:

Glu	Asp	Pro	Met	Ser	Thr	Glu	His	Met	Glu	Glu	Leu	Asn	Asp	Gln	Gln	
1				5				10						15		
Ile	Val	Arg	Arg	Glu	Lys	Met	Ala	Ala	Leu	Arg	Glu	Gln	Gly	Ile	Asp	
			20				25						30			
Pro	Phe	Gly	Lys	Arg	Phe	Glu	Arg	Thr	Ala	Asn	Ser	Gln	Glu	Leu	Lys	
		35				40					45					
Asp	Lys	Tyr	Ala	Asn	Leu	Asp	Lys	Glu	Gln	Leu	His	Asp	Lys	Asn	Glu	
	50				55					60						
Thr	Ala	Thr	Ile	Ala	Gly	Arg	Leu	Val	Thr	Lys	Arg	Gly	Lys	Gly	Lys	
65					70					75					80	
Val	Gly	Phe	Ala	His	Leu	Gln	Asp	Arg	Glu	Gly	Gln	Ile	Gln	Ile	Tyr	
			85					90					95			
Val	Arg	Lys	Asp	Ala	Val	Gly	Glu	Glu	Asn	Tyr	Glu	Ile	Phe	Lys	Lys	
		100					105						110			
Ala	Asp	Leu	Gly	Asp	Phe	Leu	Gly	Val	Glu	Gly	Glu	Val	Met	Arg	Thr	
		115				120						125				
Asp	Met	Gly	Glu	Leu	Ser	Ile	Lys	Ala	Thr	His	Ile	Thr	His	Leu	Ser	
	130					135					140					
Lys	Ala	Leu	Arg	Pro	Leu	Pro	Glu	Lys	Phe	His	Gly	Leu	Thr	Asp	Val	
145					150					155					160	
Glu	Thr	Ile	Tyr	Arg	Lys	Arg	Tyr	Leu	Asp	Leu	Ile	Ser	Asn	Arg	Glu	
			165						170					175		
Ser	Phe	Glu	Arg	Phe	Val	Thr	Arg	Ser	Lys	Ile	Ile	Ser	Glu	Ile	Arg	
		180					185						190			
Arg	Tyr	Leu	Asp	Gln	Lys	Gly	Phe	Leu	Glu	Val	Glu	Thr	Pro	Val	Leu	
		195				200						205				
His	Asn	Glu	Ala	Gly	Gly	Ala	Ala	Ala	Arg	Pro	Phe	Ile	Thr	His	His	
	210					215					220					
Asn	Ala	Gln	Asn	Ile	Asp	Met	Val	Leu	Arg	Ile	Ala	Thr	Glu	Leu	His	
225					230				235					240		
Leu	Lys	Arg	Leu	Ile	Val	Gly	Gly	Met	Glu	Arg	Val	Tyr	Glu	Ile	Gly	

Arg	Asn	Ser	Arg	Ile	Gly	Ile	Ser	Phe	Gly	Gly	Gly	Arg	Val	Met	Asn
			20					25					30		
Lys	Tyr	Lys	Val	Ile	Tyr	Tyr	Val	Val	Val	Ile	Ala	Leu	Leu	Val	Ser
		35					40					45			
Val	Phe	Leu	Leu	Ile	Gly	Met	Asp	Leu	Ser	Trp	Phe	Asn	Pro	Tyr	Gln
	50					55					60				
Ser	Asp	Gln	Phe	Val	Trp	Val	Tyr	Phe	Ala	Leu	Ile	Pro	Val	Ile	Glu
65					70					75					80
Trp	Ile	Glu	Lys	Lys	Ser	Lys	Asn	Leu	Ala	Ser	Glu	Lys	Gly	Glu	
				85					90					95	

(2) INFORMATION FOR SEQ ID NO:4682:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 197 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4682:

Glu	Asn	Thr	Met	Ser	Tyr	Lys	Asp	Thr	Val	Gln	Lys	Ile	Leu	Asp	Val
1				5					10					15	
Ile	Gly	Gly	Glu	Lys	Asn	Val	Asn	Arg	Val	Thr	His	Cys	Val	Thr	Arg
			20					25					30		
Leu	Arg	Leu	Glu	Leu	Lys	Asp	Glu	Asn	Leu	Val	Asn	Asp	Asp	Asp	Val
		35					40					45			
Lys	Lys	Ile	Pro	Gly	Val	Ile	Gly	Ile	Met	Lys	Lys	Asn	Gly	Gln	Tyr
	50					55					60				
Gln	Ile	Ile	Leu	Gly	Asn	Asp	Val	Ala	Asn	Tyr	Tyr	Lys	Glu	Phe	Val
65					70					75					80
Lys	Leu	Gly	Asn	Phe	Glu	Ser	Asp	Ser	Val	Val	Gln	Gly	His	Lys	Gly
			85						90					95	
Asn	Ile	Leu	Glu	Arg	Ile	Ile	Glu	Tyr	Ile	Ala	Gly	Ser	Met	Thr	Pro
			100					105					110		
Ile	Ile	Pro	Ala	Met	Leu	Gly	Gly	Gly	Met	Leu	Lys	Val	Leu	Val	Ile
		115					120					125			
Ile	Leu	Pro	Met	Leu	Gly	Ile	Leu	Gln	Ser	Asp	Ser	Gln	Thr	Ile	Ala
	130					135					140				
Phe	Leu	Thr	Phe	Phe	Gly	Asp	Ala	Pro	Tyr	Tyr	Phe	Leu	Pro	Leu	Leu
145					150					155					160
Leu	Ala	Tyr	Ser	Ala	Ser	Gln	Lys	Leu	Lys	Val	Thr	Ser	Thr	Ile	Ala
			165						170					175	
Met	Ser	Val	Ala	Gly	Asp	Phe	Ser	Ile	Gln	Ile	Leu	Phe	Lys	Trp	Cys
			180					185					190		
Asn	Gln	Glu	Ser	Ser											
			195												

(2) INFORMATION FOR SEQ ID NO:4683:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...74
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4683:

Arg	Pro	Thr	Ile	Leu	Val	His	Val	Cys	Cys	Ala	Pro	Cys	Ser	Thr	Tyr
1				5				10						15	
Thr	Leu	Glu	Tyr	Leu	Thr	Lys	Tyr	Ala	Asp	Val	Thr	Ile	Tyr	Phe	Ala
			20					25					30		
Asn	Ser	Asn	Ile	His	Pro	Lys	Ala	Glu	Tyr	His	Lys	Arg	Val	Tyr	Val
		35				40					45				
Thr	Lys	Lys	Phe	Val	Ser	Asp	Phe	Asn	Glu	Arg	Thr	Gly	Asn	Thr	Val
	50					55					60				
Gln	Tyr	Leu	Glu	Ala	Pro	Tyr	Glu	Pro	Asn						
65						70									

(2) INFORMATION FOR SEQ ID NO:4684:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 182 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...182
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4684:

Glu	Arg	Thr	Met	Ser	Leu	Lys	Asp	Arg	Phe	Asp	Arg	Phe	Ile	Asp	Tyr
1				5				10					15		
Phe	Thr	Glu	Asp	Glu	Asp	Ser	Ser	Leu	Pro	Tyr	Glu	Lys	Arg	Asp	Glu
			20					25					30		
Pro	Val	Phe	Thr	Ser	Val	Asn	Ser	Ser	Gln	Glu	Pro	Ala	Leu	Pro	Met

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4686:

Leu	Leu	Ala	Ile	Leu	Lys	Lys	Asn	Phe	Val	Pro	Ser	Tyr	Asp	Val	Glu
1				5					10					15	
Ser	Phe	Val	Asn	Ser	Ile	Glu	Lys	Pro	Arg	Arg	Ile	Met	Leu	Met	Val
			20					25					30		
Gln	Ala	Gly	Pro	Gly	Thr	Asp	Ala	Thr	Ile	Gln	Ala	Leu	Leu	Pro	His
		35					40					45			
Leu	Asp	Lys	Gly	Asp	Ile	Leu	Ile	Asp	Gly	Gly	Asn	Thr	Phe	Tyr	Lys
	50					55					60				
Asp	Thr	Ile	Arg	Arg	Asn	Glu	Glu	Leu	Ala	Asn	Ser	Gly	Ile	Asn	Phe
65					70					75				80	
Ile	Gly	Thr	Gly	Val	Ser	Gly	Gly	Glu	Lys	Gly	Ala	Leu	Glu	Gly	Pro
			85						90					95	
Ser	Ile	Met	Pro	Gly	Gly	Gln	Lys	Glu	Ala	Tyr	Glu	Leu	Val	Ser	Asp
			100					105					110		
Val	Leu	Glu	Glu	Ile	Ser	Ala	Lys	Ala	Pro	Glu	Asp	Gly	Lys	Pro	Cys
		115					120					125			
Val	Thr	Tyr	Ile	Gly	Pro	Asp	Gly	Ala	Gly	His	Tyr	Val	Lys	Met	Val
	130					135					140				
His	Asn	Gly	Ile	Glu	Tyr	Gly	Asp	Met	Gln	Leu	Ile	Ala	Glu	Ser	Tyr
145					150					155				160	
Asp	Leu	Met	Gln	His	Leu	Leu	Gly	Leu	Ser	Ala	Glu	Asp	Met	Ala	Glu
			165						170					175	
Ile	Phe	Thr	Glu	Trp	Asn	Lys	Gly	Glu	Leu	Asp	Ser	Tyr	Leu	Ile	Glu
			180					185					190		
Ile	Thr	Ala	Asp	Ile	Leu	Ser	Arg	Lys	Asp	Asp	Glu	Asp	Gln	Asp	Gly
	195						200					205			
Pro	Ile	Val	Asp	Tyr	Ile	Leu	Asp	Ala	Ala	Gly	Asn	Lys	Gly	Thr	Gly
	210					215					220				
Lys	Trp	Thr	Ser	Gln	Ser	Ser	Leu	Asp	Leu	Gly	Val	Pro	Leu	Ser	Leu
225					230					235				240	
Ile	Thr	Glu	Ser	Val	Phe	Ala	Arg	Tyr	Ile	Ser	Thr	Tyr	Lys	Glu	Glu
			245						250					255	
Arg	Val	His	Ala	Ser	Lys	Val	Leu	Pro	Lys	Pro	Ala	Ala	Phe	Asn	Phe
			260					265					270		
Glu	Gly	Asp	Lys	Ala	Glu	Leu	Ile	Glu	Lys	Ile	Arg	Gln	Ala	Leu	Tyr
		275					280					285			
Phe	Ser	Lys	Ile	Ile	Ser	Tyr	Ala	Gln	Gly	Phe	Ala	Gln	Leu	Arg	Val
	290					295					300				
Ala	Ser	Lys	Glu	Asn	Asn	Trp	Asn	Leu	Pro	Phe	Ala	Asp	Ile	Ala	Ser
305					310					315				320	
Ile	Trp	Arg	Asp	Gly	Cys	Ile	Ile	Pro	Ser	Ser	Phe	Leu	Ala	Lys	Asp
			325						330					335	
Tyr	Arg	Cys	Leu	Gln	Pro	Arg	Cys	Arg	Ser	Cys	Pro	Pro	Ser	Phe	Gly
			340					345					350		
Arg	Val	Leu	Leu	Gly	Cys	Tyr	Cys								

(2) INFORMATION FOR SEQ ID NO:4687:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4687:

```

Glu Ala Ala Met Leu Glu Leu Arg Asn Ile Asn Lys Val Phe Gly Asp
1          5          10          15
Lys Gln Ile Leu Ser Asn Phe Ser Leu Ser Ile Pro Glu Lys Gln Ile
          20          25          30
Leu Ala Ile Val Gly Pro Ser Gly Gly Gly Lys Thr Thr Leu Leu Arg
          35          40          45
Met Leu Ala Gly Leu Glu Thr Ile Asp Ser Gly Gln Ile Phe Tyr Asn
          50          55          60
Gly Gln Pro Leu Glu Leu Asp Glu Leu Gln Lys Arg Asn Leu Leu Gly
65          70          75          80
Phe Val Phe Gln Asp Phe Gln Leu Phe Pro His Leu Ser Val Leu Glu
          85          90          95
Asn Leu Thr Leu Ser Pro Val Lys Thr His Gly Asn Glu Ala Gly Arg
          100          105          110
Gly

```

(2) INFORMATION FOR SEQ ID NO:4688:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 82 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...82

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4688:

Leu	Ser	Ala	Ile	Ile	Ser	Leu	Phe	Phe	Ser	Ser	Leu	Asn	Leu	Phe	Asn
1				5					10					15	
Tyr	Ser	Ile	Asn	Ile	Asp	Phe	Ile	Gln	Ser	Tyr	Ile	Asp	Leu	Val	Ile
		20						25					30		
Cys	Phe	Arg	Glu	Phe	Val	Val	Leu	Phe	Arg	Pro	Tyr	Phe	Ala	Ile	Asn
		35					40					45			
Cys	Phe	Lys	Trp	Asp	Leu	Leu	Ser	Leu	Pro	Phe	Leu	Pro	Pro	Asn	Phe
	50					55					60				
Glu	Tyr	Lys	Lys	Asp	Asp	Arg	Val	Phe	Asn	Phe	Tyr	Arg	Leu	Arg	Phe
65					70				75						80
Thr	Tyr														

(2) INFORMATION FOR SEQ ID NO:4689:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 126 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...126

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4689:

Leu	Ile	Val	Phe	Glu	Asn	Leu	Phe	Lys	Pro	Arg	Gln	Arg	Arg	Leu	Thr
1				5					10					15	
Val	Tyr	Met	Leu	Leu	Thr	Ser	Ser	Val	Leu	Ser	Ala	Thr	Ser	Lys	Pro
		20						25					30		
Cys	Phe	Glu	Leu	Thr	Ser	Ser	Val	Ser	Ser	Ala	Thr	Ser	Lys	Pro	Cys
		35					40					45			
Phe	Glu	Leu	Thr	Ser	Ser	Val	Ser	Ser	Thr	Thr	Ser	Lys	Pro	Cys	Phe
	50					55					60				
Glu	Leu	Thr	Ser	Ser	Val	Leu	Ser	Thr	Thr	Ser	Lys	Gln	Cys	Phe	Glu
65					70				75						80
Gln	Pro	Ala	Ala	Ser	Phe	Leu	Val	Cys	Thr	Leu	Ile	Phe	Ile	Glu	Tyr
				85					90					95	
Lys	Lys	Ile	Leu	Gly	Lys	Asp	Ser	Ile	Ser	Val	Glu	Lys	Glu	Val	Asn
		100						105					110		
Leu	Pro	Thr	Ile	Lys	Arg	Ile	Val	Ser	Ser	Phe	Phe	Asn	Thr		
		115					120					125			

(2) INFORMATION FOR SEQ ID NO:4690:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 69 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...69

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4690:

Lys	Lys	Val	Phe	Lys	Ile	Ile	Lys	Arg	Ile	Ile	Ser	Ser	Phe	Phe	Lys
1				5					10					15	
Asn	Leu	Asp	Met	Met	Arg	Phe	Ile	Val	Gly	Ile	Phe	Ile	Ser	Phe	Ser
			20					25					30		
Thr	Lys	Ile	Met	Phe	Leu	Asn	Asn	Leu	Tyr	Leu	Ser	Ser	Leu	Tyr	Asn
		35				40						45			
Pro	Pro	Gln	Ser	Ala	Phe	Thr	Ile	Ser	Phe	Asn	Thr	Met	Thr	Ile	Pro
	50					55					60				
Phe	Leu	His	Phe	Phe											
65															

(2) INFORMATION FOR SEQ ID NO:4691:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 208 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...208

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4691:

Gly	Val	Tyr	Met	Ser	Gln	Asp	Lys	Gln	Met	Lys	Ala	Val	Ser	Pro	Leu
1				5					10					15	
Leu	Gln	Arg	Val	Ile	Asn	Ile	Ser	Ser	Ile	Val	Gly	Gly	Val	Gly	Ser
			20					25					30		
Leu	Ile	Phe	Cys	Ile	Trp	Ala	Tyr	Gln	Ala	Gly	Ile	Leu	Gln	Ser	Lys
		35				40						45			
Glu	Thr	Leu	Ser	Ala	Phe	Ile	Gln	Gln	Ala	Gly	Ile	Trp	Gly	Pro	Pro
	50					55					60				
Leu	Phe	Ile	Phe	Leu	Gln	Ile	Leu	Gln	Thr	Val	Val	Pro	Ile	Ile	Pro
65					70					75					80

Gly	Ala	Leu	Thr	Ser	Val	Ala	Gly	Val	Phe	Ile	Tyr	Gly	His	Ile	Ile
				85					90					95	
Gly	Thr	Ile	Tyr	Asn	Tyr	Ile	Gly	Ile	Val	Ile	Gly	Cys	Ala	Ile	Ile
			100					105					110		
Phe	Tyr	Leu	Val	Arg	Leu	Tyr	Gly	Ala	Ala	Phe	Val	Gln	Ser	Val	Val
		115					120					125			
Ser	Lys	Arg	Thr	Tyr	Asp	Lys	Tyr	Ile	Gly	Trp	Leu	Asp	Lys	Gly	Asn
	130					135					140				
Arg	Phe	Asp	Arg	Phe	Phe	Ile	Phe	Met	Met	Ile	Trp	Pro	Ile	Ser	Pro
145					150					155					160
Ala	Asp	Phe	Leu	Cys	Met	Leu	Ala	Ala	Leu	Thr	Lys	Met	Ser	Phe	Lys
				165					170					175	
Arg	Tyr	Met	Thr	Ile	Ile	Ile	Leu	Thr	Lys	Pro	Phe	Thr	Leu	Val	Val
			180					185					190		
Tyr	Thr	Tyr	Gly	Leu	Thr	Tyr	Ile	Ile	Asp	Phe	Phe	Trp	Gln	Met	Leu
		195					200					205			

(2) INFORMATION FOR SEQ ID NO:4692:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 212 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4692:

Glu	Asn	Tyr	Met	Thr	Lys	Ser	Asp	Thr	Ile	Ile	Glu	Leu	Lys	Lys	Gln
1				5					10					15	
Lys	Ile	Val	Ala	Val	Ile	Arg	Gly	Asn	Thr	Lys	Glu	Glu	Gly	Leu	Gln
			20					25					30		
Ala	Ser	Ile	Ala	Cys	Ile	Lys	Gly	Gly	Ile	Lys	Ala	Ile	Glu	Ile	Ala
		35					40					45			
Tyr	Thr	Asn	Gln	Tyr	Ala	Gly	Gln	Ile	Ile	Lys	Glu	Leu	Val	Asp	Leu
	50					55				60					
Tyr	Gln	Asp	Asp	Gln	Ser	Val	Cys	Ile	Gly	Ala	Gly	Thr	Val	Leu	Asp
65					70				75					80	
Ala	Val	Thr	Ala	Arg	Asp	Ala	Ile	Leu	Ala	Gly	Ala	Asn	Tyr	Val	Val
				85					90					95	
Ser	Pro	Ser	Phe	His	Ala	Glu	Thr	Ala	Lys	Met	Cys	Asn	Leu	Tyr	Ser
			100					105					110		
Thr	Pro	Tyr	Ile	Pro	Gly	Cys	Ile	Thr	Leu	Thr	Glu	Ile	Thr	Thr	Ala
		115				120						125			
Leu	Glu	Ala	Gly	Ser	Glu	Ile	Ile	Lys	Leu	Phe	Pro	Gly	Ser	Thr	Leu
	130					135					140				
Ser	Pro	Ala	Tyr	Ile	Ser	Ala	Val	Lys	Ala	Pro	Ile	Pro	Gln	Val	Ser

145		150		155		160									
Val	Met	Val	Thr	Gly	Gly	Val	Gly	Leu	Asn	Asn	Ile	Pro	Gln	Trp	Phe
		165		170		175									
Ala	Ala	Gly	Ala	Asp	Ala	Val	Gly	Ile	Gly	Gly	Glu	Leu	Asn	Lys	Leu
		180		185		190									
Ala	Ser	Gln	Gly	Asn	Phe	Asp	Arg	Ile	Ser	Glu	Ile	Ala	Gln	Gln	Tyr
		195		200		205									
Ile	Thr	Leu	Arg												
	210														

(2) INFORMATION FOR SEQ ID NO:4693:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 388 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...388

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4693:

Phe	Leu	Val	Phe	Leu	Phe	Ala	Leu	Ser	His	Tyr	Ile	Ile	Asn	Leu	Gln
1			5						10					15	
Lys	Gln	Phe	Lys	Arg	Arg	Thr	Ile	Met	Glu	Val	Val	Ser	Ser	Val	Leu
			20					25					30		
Asn	Trp	Phe	Ser	Ser	Asn	Ile	Leu	Gln	Asn	Pro	Ala	Phe	Phe	Val	Gly
		35				40						45			
Leu	Leu	Val	Leu	Ile	Gly	Tyr	Ala	Leu	Leu	Lys	Lys	Pro	Ala	His	Asp
	50				55						60				
Val	Phe	Ser	Gly	Phe	Val	Lys	Ala	Thr	Val	Gly	Tyr	Met	Leu	Leu	Asn
65				70					75					80	
Val	Gly	Ala	Gly	Gly	Leu	Val	Thr	Thr	Phe	Arg	Pro	Ile	Leu	Ala	Ala
			85					90					95		
Leu	Asn	Tyr	Lys	Phe	Gln	Ile	Gly	Ala	Ala	Val	Ile	Asp	Pro	Tyr	Phe
		100					105					110			
Gly	Leu	Ala	Ala	Ala	Asn	Asn	Lys	Ile	Val	Ala	Glu	Phe	Pro	Asp	Phe
	115					120					125				
Val	Gly	Thr	Ala	Thr	Thr	Ala	Leu	Leu	Ile	Gly	Phe	Gly	Ile	Asn	Ile
	130				135					140					
Leu	Leu	Val	Ala	Leu	Arg	Lys	Ile	Thr	Lys	Val	Arg	Thr	Leu	Phe	Ile
145				150					155					160	
Thr	Gly	His	Ile	Met	Val	Gln	Gln	Ala	Ala	Thr	Val	Ser	Leu	Met	Val
			165					170					175		
Leu	Phe	Leu	Val	Pro	Gln	Leu	Arg	Asn	Ala	Tyr	Gly	Thr	Ala	Ala	Ile
		180				185						190			
Gly	Ile	Ile	Cys	Gly	Leu	Tyr	Trp	Ala	Val	Ser	Ser	Asn	Met	Thr	Val
	195				200					205					
Glu	Ala	Thr	Gln	Arg	Leu	Thr	Gly	Gly	Gly	Gly	Phe	Ala	Ile	Gly	His

210		215		220											
Gln	Gln	Gln	Phe	Ala	Ile	Trp	Phe	Val	Asp	Lys	Val	Ala	Gly	Arg	Phe
225		230		235		240									
Gly	Lys	Lys	Glu	Glu	Ser	Leu	Asp	Asn	Leu	Lys	Leu	Pro	Lys	Phe	Leu
		245		250		255									
Ser	Ile	Phe	His	Asp	Thr	Val	Val	Ala	Ser	Ala	Thr	Leu	Met	Leu	Val
		260		265		270									
Phe	Phe	Gly	Ala	Ile	Leu	Leu	Ile	Leu	Gly	Pro	Asp	Ile	Met	Ser	Asn
		275		280		285									
Lys	Glu	Val	Ile	Thr	Ser	Gly	Thr	Leu	Phe	Asn	Pro	Ala	Lys	Gln	Asp
		290		295		300									
Phe	Phe	Met	Tyr	Ile	Ile	Gln	Thr	Ala	Phe	Thr	Phe	Ser	Val	Tyr	Leu
305				310		315									
Phe	Val	Leu	Met	Gln	Gly	Val	Arg	Met	Phe	Val	Ser	Glu	Leu	Thr	Asn
		325		330		335									
Ala	Phe	Gln	Gly	Ile	Ser	Asn	Lys	Leu	Leu	Pro	Gly	Ser	Phe	Pro	Ala
		340		345		350									
Val	Asp	Val	Ala	Ala	Ser	Tyr	Gly	Phe	Gly	Ser	Pro	Asn	Ala	Val	Leu
		355		360		365									
Ser	Gly	Phe	Thr	Phe	Gly	Phe	Asp	Trp	Ser	Ile	Asp	Tyr	Asn	Cys	Phe
370				375		380									
Ala	His	Arg	Leu												
385															

(2) INFORMATION FOR SEQ ID NO:4694:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4694:

Ile	Met	Val	Leu	Ser	Lys	Lys	Arg	Ala	Arg	Lys	Val	Leu	Glu	Glu	Ile
1			5				10				15				
Ile	Ala	Leu	Phe	Pro	Asp	Ala	Lys	Pro	Ser	Leu	Asp	Phe	Thr	Asn	His
		20				25					30				
Phe	Glu	Leu	Leu	Val	Ala	Val	Met	Leu	Ser	Ala	Gln	Thr	Thr	Asp	Ala
		35				40					45				
Ala	Val	Asn	Lys	Ala	Thr	Pro	Gly	Leu	Phe	Val	Ala	Phe	Pro	Thr	Pro
		50				55					60				
Gln	Ala	Met	Ser	Val	Ala	Thr	Glu	Ser	Glu	Ile	Ala	Ser	His	Ile	Ser
65				70					75					80	
Arg	Leu	Gly	Leu	Tyr	Arg	Asn	Lys	Ala	Lys	Phe	Leu	Lys	Lys	Cys	Ala
		85				90								95	
Gln	Gln	Leu	Leu	Asp	Asp	Phe	Asp	Gly	Gln	Val	Pro	Gln	Thr	Arg	Glu

			100					105				110					
Glu	Leu	Glu	Ser	Leu	Ala	Gly	Val	Gly	Arg	Lys	Thr	Ala	Asn	Val	Val		
		115						120				125					
Met	Ser	Val	Gly	Phe	Gly	Ile	Pro	Ala	Phe	Ala	Val	Asp	Thr	His	Val		
		130						135				140					
Glu	Arg	Ile	Cys	Lys	His	His	Asp	Ile	Val	Lys	Lys	Ser	Ala	Thr	Pro		
		145					150				155				160		
Leu	Glu	Val	Glu	Lys	Arg	Val	Met	Asp	Ile	Leu	Pro	Pro	Glu	Gln	Trp		
				165					170					175			
Leu	Asp	Ala	His	Gln	Ala	Met	Ile	Tyr	Phe	Gly	Arg	Ala	Ile	Cys	His		
		180						185					190				
Pro	Lys	Asn	Pro	Glu	Cys	Asp	Gln	Tyr	Pro	Gln	Leu	Tyr	Asp	Phe	Ser		
		195					200					205					
Asn	Leu																
		210															

(2) INFORMATION FOR SEQ ID NO:4695:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 117 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4695:

Gly	Glu	His	Met	Ile	Gln	Ala	Val	Phe	Glu	Arg	Ala	Glu	Asp	Gly	Glu		
1				5				10						15			
Leu	Arg	Ser	Ala	Glu	Ile	Thr	Gly	His	Ala	Glu	Ser	Gly	Glu	Tyr	Gly		
		20					25					30					
Leu	Asp	Val	Val	Cys	Ala	Ser	Val	Thr	Leu	Ala	Ile	Asn	Phe	Ile			
		35					40				45						
Asn	Ser	Ile	Glu	Lys	Phe	Ala	Gly	Tyr	Glu	Pro	Ile	Leu	Glu	Leu	Asn		
		50				55				60							
Glu	Asp	Glu	Gly	Gly	Tyr	Leu	Met	Val	Glu	Ile	Pro	Lys	Asp	Leu	Pro		
65				70					75					80			
Ser	His	Gln	Arg	Glu	Met	Thr	Gln	Leu	Phe	Phe	Glu	Ser	Phe	Phe	Leu		
		85					90						95				
Gly	Met	Ala	Asn	Leu	Ser	Glu	Asn	Ser	Ser	Glu	Phe	Val	Gln	Thr	Arg		
		100					105					110					
Val	Ile	Thr	Glu	Asn													
		115															

(2) INFORMATION FOR SEQ ID NO:4696:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 123 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4696:

Lys	Val	Asn	Ile	Pro	Asn	Ser	Glu	Ser	Thr	Lys	Pro	Lys	Thr	Phe	Glu
1				5					10					15	
Ile	Asp	Cys	Leu	Val	Gly	Glu	Lys	His	Ala	Tyr	Glu	Ile	Lys	Trp	Trp
		20						25					30		
Asp	Ala	Thr	Thr	Asp	Gly	Asp	His	Ile	Thr	Lys	Glu	His	Thr	Arg	Ile
		35					40					45			
Lys	Val	Ile	His	Asn	Lys	Gly	Tyr	Ile	Pro	Ile	Arg	Leu	Met	Phe	Tyr
		50				55					60				
Tyr	Pro	Asn	Arg	Thr	Gln	Ala	Ile	Lys	Ile	Gln	Gln	Thr	Leu	Glu	Thr
65					70					75				80	
Leu	Tyr	Asn	Gly	Ile	Gly	Gly	Lys	Tyr	Tyr	Gly	Asp	Ser	Ala	Trp	Glu
			85						90					95	
His	Leu	Arg	Ala	Val	Thr	Gly	Ile	Asp	Leu	Leu	Ser	Ile	Leu	Thr	Asp
			100					105						110	
Ile	Ala	Asn	Lys	Lys	Thr	Gly	Val	Lys	Ser	Lys					
			115					120							

(2) INFORMATION FOR SEQ ID NO:4697:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 71 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...71

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4697:

Val	Cys	Asn	Met	Gln	Leu	Lys	Asn	Arg	Leu	Lys	Glu	Leu	Arg	Ala	Arg
1				5					10					15	

Glu	Trp	Ser	Gln	Ser	Asn	Arg	Pro	Ser	Gln	Thr	Gly	Arg	Gly	Phe	Arg
			20					25					30		
Gln	Thr	Ile	Ser	Leu	Leu	Glu	Arg	Asp	Glu	Tyr	Thr	Pro	Ser	Ile	Ile
		35				40					45				
Ile	Ala	Leu	Lys	Ile	Ser	Gln	Ile	Phe	Asn	Glu	Thr	Val	Glu	Ser	Val
	50					55					60				
Phe	Arg	Leu	Glu	Glu	Asp	Glu									
65					70										

(2) INFORMATION FOR SEQ ID NO:4698:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 540 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...540

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4698:

Gly	Lys	Asn	Met	Glu	Ile	Met	Ser	Leu	Ala	Ile	Ala	Val	Phe	Ala	Val
1				5					10					15	
Ile	Ile	Gly	Leu	Val	Ile	Gly	Tyr	Val	Ser	Ile	Ser	Ala	Lys	Met	Lys
			20					25					30		
Ser	Ser	Gln	Glu	Ala	Ala	Glu	Leu	Met	Leu	Leu	Asn	Ala	Glu	Gln	Glu
		35					40					45			
Ala	Thr	Asn	Leu	Arg	Gly	Gln	Ala	Glu	Arg	Glu	Ala	Asp	Leu	Leu	Val
	50					55					60				
Asn	Glu	Ala	Lys	Arg	Glu	Ser	Lys	Ser	Leu	Lys	Lys	Glu	Ala	Leu	Leu
65					70					75				80	
Glu	Ala	Lys	Glu	Glu	Ala	Arg	Lys	Tyr	Arg	Glu	Glu	Val	Asp	Ala	Glu
			85						90					95	
Phe	Lys	Ser	Glu	Arg	Gln	Glu	Leu	Lys	Gln	Ile	Glu	Ser	Arg	Leu	Thr
			100					105					110		
Glu	Arg	Ala	Thr	Ser	Leu	Asp	Arg	Lys	Asp	Asp	Asn	Leu	Thr	Ser	Lys
		115					120					125			
Glu	Gln	Thr	Leu	Glu	Gln	Lys	Glu	Gln	Ser	Ile	Ser	Asp	Arg	Ala	Lys
	130					135					140				
Asn	Leu	Asp	Ala	Arg	Glu	Glu	Gln	Leu	Glu	Glu	Val	Glu	Arg	Gln	Lys
145					150					155					160
Glu	Ala	Glu	Leu	Glu	Arg	Ile	Gly	Ala	Leu	Ser	Gln	Ala	Glu	Ala	Arg
			165					170						175	
Asp	Ile	Ile	Leu	Ala	Gln	Thr	Glu	Glu	Asn	Leu	Thr	Arg	Glu	Ile	Ala
			180					185					190		
Ser	Arg	Ile	Arg	Glu	Ala	Glu	Gln	Glu	Val	Lys	Glu	Arg	Ser	Asp	Lys
		195					200					205			
Met	Ala	Lys	Asp	Ile	Leu	Val	Gln	Ala	Met	Gln	Arg	Ile	Ala	Gly	Glu
	210					215					220				

Tyr	Val	Ala	Glu	Ser	Thr	Asn	Ser	Thr	Val	His	Leu	Pro	Asp	Asp	Thr
225					230					235					240
Met	Lys	Gly	Arg	Ile	Ile	Gly	Arg	Glu	Gly	Arg	Asn	Ile	Arg	Thr	Phe
				245					250						255
Glu	Ser	Leu	Thr	Gly	Val	Asp	Val	Ile	Ile	Asp	Asp	Thr	Pro	Glu	Val
			260					265					270		
Val	Thr	Leu	Ser	Gly	Phe	Asp	Pro	Ile	Arg	Arg	Glu	Ile	Ala	Arg	Met
	275						280					285			
Thr	Met	Glu	Met	Leu	Leu	Lys	Asp	Gly	Arg	Ile	His	Pro	Ala	Arg	Ile
290						295					300				
Glu	Glu	Leu	Val	Glu	Lys	Asn	Arg	Gln	Glu	Ile	Asp	Asn	Lys	Ile	Arg
305				310						315					320
Glu	Tyr	Gly	Glu	Ala	Ala	Ala	Tyr	Glu	Ile	Gly	Ala	Pro	Asn	Leu	His
				325					330					335	
Pro	Asp	Leu	Met	Lys	Ile	Met	Gly	Arg	Leu	Gln	Phe	Arg	Thr	Ser	Tyr
		340					345						350		
Gly	Gln	Asn	Val	Leu	Arg	His	Ser	Ile	Glu	Val	Ala	Lys	Leu	Ala	Gly
	355						360					365			
Ile	Met	Ala	Ser	Glu	Leu	Gly	Glu	Asn	Ala	Ala	Leu	Ala	Arg	Arg	Ala
370						375					380				
Gly	Phe	Leu	His	Asp	Ile	Gly	Lys	Ala	Ile	Asp	His	Glu	Val	Glu	Gly
385				390						395					400
Ser	His	Val	Glu	Ile	Gly	Met	Glu	Leu	Ala	Arg	Lys	Tyr	Lys	Glu	Pro
			405						410					415	
Pro	Val	Val	Val	Asn	Thr	Ile	Ala	Ser	His	His	Gly	Asp	Val	Glu	Ala
		420					425					430			
Glu	Ser	Val	Ile	Ala	Val	Ile	Val	Ala	Ala	Ala	Asp	Ala	Leu	Ser	Ala
	435						440					445			
Ala	Arg	Pro	Gly	Ala	Arg	Ser	Glu	Ser	Leu	Glu	Ser	Tyr	Ile	Lys	Arg
450						455					460				
Leu	His	Asp	Leu	Glu	Glu	Ile	Ala	Asn	Gly	Phe	Glu	Gly	Val	Gln	Thr
465				470						475					480
Ser	Phe	Ala	Leu	Gln	Ala	Gly	Arg	Glu	Ile	Arg	Ile	Met	Val	Asn	Pro
			485					490						495	
Gly	Lys	Ile	Lys	Asp	Asp	Lys	Val	Thr	Ile	Leu	Ala	His	Lys	Val	Arg
		500					505					510			
Lys	Lys	Ile	Glu	Asn	Asn	Leu	Asp	Tyr	Pro	Gly	Asn	Ile	Lys	Val	Thr
	515					520					525				
Val	Ile	Arg	Glu	Leu	Arg	Ala	Val	Asp	Tyr	Ala	Lys				
530						535					540				

(2) INFORMATION FOR SEQ ID NO:4699:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 418 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...418

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4699:

Glu	Lys	Asn	Ile	Glu	Ser	Lys	Tyr	Met	Ala	Leu	Thr	Thr	Leu	Thr	Lys	1	5	10	15
Glu	Glu	Phe	Gln	Thr	Tyr	Ser	Asp	Gln	Val	Ser	Ser	Arg	Ser	Phe	Met	20	25	30	
Gln	Ser	Val	Gln	Met	Gly	Asp	Leu	Leu	Glu	Lys	Arg	Gly	Ala	Arg	Ile	35	40	45	
Val	Tyr	Leu	Ala	Leu	Lys	Gln	Glu	Gly	Glu	Ile	Gln	Val	Ala	Ala	Leu	50	55	60	
Val	Tyr	Ser	Leu	Pro	Met	Leu	Gly	Gly	Leu	His	Met	Glu	Leu	Asn	Ser	65	70	75	80
Gly	Pro	Ile	Tyr	Thr	Gln	Gln	Asp	Ala	Leu	Pro	Val	Phe	Tyr	Ala	Glu	85	90	95	
Leu	Lys	Glu	Tyr	Ala	Lys	Gln	Asn	Gly	Val	Leu	Glu	Leu	Leu	Val	Lys	100	105	110	
Pro	Tyr	Glu	Thr	Tyr	Gln	Thr	Phe	Asp	Ser	Gln	Gly	Asn	Pro	Ile	Asp	115	120	125	
Ala	Glu	Lys	Lys	Ser	Ile	Ile	Gln	Gly	Leu	Thr	Asp	Leu	Gly	Tyr	Gln	130	135	140	
Phe	Asp	Gly	Leu	Thr	Thr	Gly	Tyr	Pro	Gly	Gly	Glu	Pro	Asp	Trp	Leu	145	150	155	160
Tyr	Tyr	Lys	Asp	Leu	Thr	Glu	Leu	Thr	Glu	Lys	Ser	Leu	Leu	Lys	Ser	165	170	175	
Phe	Ser	Lys	Lys	Gly	Lys	Pro	Leu	Val	Lys	Lys	Ala	Glu	Thr	Phe	Gly	180	185	190	
Ile	Arg	Leu	Lys	Lys	Leu	Lys	Arg	Glu	Glu	Leu	Ser	Ile	Phe	Lys	Asn	195	200	205	
Ile	Thr	Lys	Glu	Thr	Ser	Glu	Arg	Arg	Glu	Tyr	Ser	Asp	Lys	Ser	Leu	210	215	220	
Glu	Tyr	Tyr	Glu	His	Phe	Tyr	Asp	Thr	Phe	Gly	Glu	Gln	Ala	Glu	Phe	225	230	235	240
Leu	Ile	Ala	Ser	Leu	Asn	Phe	Ser	Glu	Tyr	Met	Ser	Lys	Leu	Gln	Gly	245	250	255	
Glu	Gln	Ser	Lys	Leu	Glu	Glu	Lys	Leu	Asp	Lys	Leu	Arg	Leu	Asp	Leu	260	265	270	
Ser	Lys	Asn	Pro	His	Ser	Glu	Lys	Lys	Gln	Asn	Gln	Leu	Arg	Glu	Tyr	275	280	285	
Ser	Ser	Gln	Phe	Glu	Thr	Phe	Glu	Val	Arg	Lys	Ala	Glu	Ala	Arg	Asp	290	295	300	
Leu	Ile	Glu	Lys	Tyr	Gly	Glu	Glu	Asp	Ile	Val	Leu	Ala	Gly	Ser	Leu	305	310	315	320
Phe	Val	Tyr	Met	Pro	Gln	Glu	Thr	Thr	Tyr	Leu	Phe	Ser	Gly	Ser	Tyr	325	330	335	
Thr	Glu	Phe	Asn	Lys	Phe	Tyr	Ala	Pro	Ala	Leu	Leu	Gln	Lys	Tyr	Val	340	345	350	
Met	Leu	Glu	Ser	Ile	Lys	Arg	Gly	Ile	Pro	Lys	Tyr	Asn	Phe	Leu	Gly	355	360	365	
Ile	Gln	Gly	Ile	Phe	Asp	Gly	Ser	Asp	Gly	Val	Leu	Arg	Phe	Lys	Gln	370	375	380	
Asn	Phe	Asn	Gly	Tyr	Ile	Val	Arg	Lys	Ala	Gly	Thr	Phe	Arg	Tyr	His	385	390	395	400
Pro	Ser	Pro	Leu	Lys	Tyr	Lys	Ala	Ile	Gln	Leu	Leu	Lys	Lys	Ile	Val	405	410	415	
Gly	Arg																		

(2) INFORMATION FOR SEQ ID NO:4700:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 334 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...334

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4700:

Gly	Lys	Asn	Met	Asn	Val	Lys	Lys	Ile	Met	Ser	Ile	Phe	Gln	Ser	Phe	
1				5					10					15		
Tyr	Val	Asp	Val	Ser	Ile	Glu	Glu	Leu	Thr	Leu	Thr	Leu	Pro	Ile	Ser	
			20					25					30			
Phe	Val	Lys	Arg	Phe	Glu	Tyr	Thr	Gln	Met	Thr	Phe	His	Lys	Glu	Ser	
		35					40					45				
Phe	Leu	Leu	Ile	Lys	Glu	Lys	Arg	Arg	Gly	Ser	Leu	Ser	Ser	Phe	Val	
	50					55					60					
Thr	Gln	Ala	Arg	Thr	Met	Gly	Glu	Lys	Ala	Asn	Met	Asp	Val	Val	Leu	
65					70					75					80	
Val	Phe	Ser	Lys	Leu	Ser	Asp	Ser	Glu	Lys	Lys	Gln	Leu	Leu	Gln	Ala	
			85					90						95		
Arg	Val	Pro	Phe	Val	Asp	Phe	Lys	Gly	Asn	Leu	Phe	Phe	Pro	Pro	Leu	
		100						105					110			
Gly	Leu	Val	Leu	Asn	Ala	Asn	Asp	Thr	Glu	Ile	Pro	Lys	Glu	Leu	Thr	
	115					120						125				
Pro	Ser	Glu	Gln	Leu	Thr	Trp	Ile	Ala	Phe	Leu	Leu	Pro	Lys	Gly	Gln	
	130					135					140					
Lys	Val	Val	Asn	Val	Asp	Leu	Leu	Ser	His	Val	Thr	Gly	Leu	Pro	Asn	
145				150					155					160		
Ser	Thr	Ile	Tyr	Arg	Cys	Leu	Arg	Thr	Phe	Lys	Ala	Leu	Tyr	Trp	Leu	
			165					170						175		
Asn	Lys	Gln	Asn	Lys	Leu	Tyr	Thr	Tyr	Thr	Val	Ser	Lys	Lys	Glu	Leu	
		180					185						190			
Phe	Leu	Lys	Ser	Val	Ser	Cys	Leu	Phe	Asn	Pro	Ile	Lys	Lys	Arg	Ile	
	195					200					205					
Leu	Leu	Pro	Asp	Gly	Asp	Ile	Lys	Gln	Ile	Lys	Ser	Val	Ser	Asn	Leu	
	210				215						220					
Leu	Tyr	Gly	Gly	Ala	Tyr	Ala	Leu	Ser	His	Ser	Thr	Phe	Leu	Ala	Glu	
225				230					235					240		
Thr	Asp	Glu	Asn	Thr	Ser	Tyr	Val	Ile	Trp	Gln	Arg	Lys	Phe	Asn	Gln	
			245					250					255			
Leu	Ser	Leu	Pro	Leu	Ser	Gln	His	Val	Leu	Lys	Gly	Lys	Met	Leu	Glu	
		260				265						270				
Ile	Trp	Lys	Tyr	Arg	Pro	Phe	Val	Ser	Glu	Phe	Trp	Asn	Asp	Phe	Lys	

	275					280				285					
Asn	Asn	His	Asp	Lys	Gln	Phe	Val	Asp	Pro	Ile	Ser	Leu	Tyr	Leu	Thr
	290					295					300				
Leu	Lys	Asp	Asp	Asp	Asp	Pro	Arg	Ile	Glu	Glu	Glu	Ser	Glu	Ala	Leu
305					310					315					320
Glu	Asn	Met	Ile	Leu	Gln	Tyr	Leu	Gly	Glu	Asp	Asp	Ala	Ser		
			325						330						

(2) INFORMATION FOR SEQ ID NO:4701:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4701:

Thr	Glu	Asn	Ile	Pro	Glu	Ser	Asp	Lys	Thr	Leu	Glu	Cys	Phe	Gly	Ser
1				5					10					15	
Ile	Ile	Ser	Val	Val	Gly	Asn	Pro	Thr	Pro	Gly	Ile	Ile	Gly	Ser	Phe
			20					25					30		
Leu	Val	Glu	Lys	Lys	Pro	His	Met	Thr	Tyr	Asn	Glu	Lys	Arg	Leu	Thr
			35				40					45			
Asn	Ser	Leu	Glu	Arg	Val	His	Met	Glu	Gln	Leu	Lys	Asn	Thr	Thr	Asp
50						55					60				
Leu	Leu	Gly	Leu	Glu	Asp	Lys	Asn	Ile	Lys	Ile	Leu	Ser	Val	Leu	Lys
65					70					75				80	
Tyr	Gln	Thr	His	Leu	Val	Val	Gln	Pro	Lys	Leu	Asp	Ser	Pro	Ala	Pro
			85					90						95	
Pro	Cys	Pro	His	Cys	Gln	Gly	Lys	Met	Ile	Lys	Tyr	Asp	Phe	Gln	Lys
			100					105						110	
Ala	Ser	Lys	Ile	Pro	Leu	Leu	Asp	Cys	Gln	Gly	Leu	Pro	Thr	Val	Leu
			115				120					125			
His	Leu	Lys	Lys	Arg	Arg	Phe	Gln	Cys	Lys	Asn	Cys	Leu	Lys	Val	Val
130						135					140				
Val	Ser	Gln	Thr	Ser	Ile	Val	Lys	Lys	Asn	Cys	Gln	Ile	Ser	Asn	Met
145					150					155					160
Val	Arg	Gln	Lys	Ile	Ala	Gln	Leu	Leu	Leu	Glu	Lys	Gln	Ser	Met	Thr
			165					170						175	
Glu	Ile	Ala	His	Arg	Leu	Ala	Val	Ser	Thr	Ser	Thr	Val	Ile	Arg	Lys
			180					185					190		
Leu	Arg	Glu	Phe	Lys	Phe	Glu	Thr	Asp	Trp	Thr	Lys	Leu	Pro	Lys	Val
			195				200					205			
Met	Ser	Trp	Asp	Glu	Tyr	Ser	Phe	Lys	Lys	Ser	Lys	Met	Ser	Phe	Ile
210						215					220				
Ala	Gln	Asp	Phe	Glu	Ser	Lys	Ser	Ile	Leu	Ala	Ile	Leu	Asp	Gly	Arg

225		230		235		240									
Thr	His	Ala	Val	Ile	Arg	Asn	His	Phe	Gln	Arg	Tyr	Gln	Arg	Glu	Val
		245		250		255									
Arg	Glu	Leu	Val	Glu	Val	Ile	Thr	Met	Asp	Met	Tyr	Ser	Pro	Tyr	Tyr
		260		265		270									
Arg	Leu	Ala	Lys	Gln	Leu	Phe	Pro	Lys	Ala	Lys	Ile	Val	Leu	Asp	Arg
		275		280		285									
Phe	His	Ile	Val	Gln	His	Leu	Ser	Arg	Ala	Met	Asn	Arg	Val	Arg	Ile
		290		295		300									
Gln	Ile	Met	Asn	Gln	Phe	Asp	Arg	Lys	Ser	Leu	Glu	Tyr	Arg	Ala	Leu
305				310		315									
Lys	Arg	Phe	Trp	Asn	Pro	Arg	Phe	Phe	Val	Ser	Arg	Leu	Gly	Leu	Asn
				325		330									
Gln	Ser	Thr	Gly	Leu	Ile	Tyr	Tyr	Thr	Arg	Ile	Ala	Ser	Ser	Ser	Val
				340		345									
Arg	Asn	Asp	Ser	Ile	Ser	Pro	Arg	Phe	Glu	Cys	Thr				
		355				360									

(2) INFORMATION FOR SEQ ID NO:4702:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 640 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...640

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4702:

Glu	Arg	Asn	Met	Ile	Tyr	His	Phe	Thr	Glu	Glu	Tyr	Asp	Ile	Ile	Val
1			5					10					15		
Ile	Gly	Ala	Gly	His	Ala	Gly	Val	Glu	Ala	Ser	Leu	Ala	Ala	Ser	Arg
		20						25				30			
Met	Gly	Cys	Lys	Val	Leu	Leu	Ala	Thr	Ile	Asn	Ile	Glu	Met	Leu	Ala
		35				40					45				
Phe	Met	Pro	Cys	Asn	Pro	Ser	Ile	Gly	Gly	Ser	Ala	Lys	Gly	Ile	Val
		50			55					60					
Val	Arg	Glu	Val	Asp	Ala	Leu	Gly	Gly	Glu	Met	Ala	Lys	Thr	Ile	Asp
65				70					75					80	
Lys	Thr	Tyr	Ile	Gln	Met	Lys	Met	Leu	Asn	Thr	Gly	Lys	Gly	Pro	Ala
			85					90						95	
Val	Arg	Ala	Leu	Arg	Ala	Gln	Ala	Asp	Lys	Glu	Leu	Tyr	Ser	Lys	Glu
		100					105					110			
Met	Arg	Lys	Thr	Val	Glu	Asn	Gln	Glu	Asn	Leu	Thr	Leu	Arg	Gln	Thr
		115				120					125				
Met	Ile	Asp	Glu	Ile	Leu	Val	Glu	Asp	Gly	Lys	Ala	Val	Gly	Val	Arg
130					135				140						
Thr	Ala	Thr	His	Gln	Glu	Tyr	Ala	Ala	Lys	Ala	Val	Ile	Val	Thr	Thr

145					150					155				160
Gly	Thr	Ala	Leu	Arg	Gly	Glu	Ile	Ile	Ile	Gly	Asp	Leu	Lys	Tyr
				165					170					175
Ser	Gly	Pro	Asn	His	Ser	Leu	Ala	Ser	Ile	Asn	Leu	Ala	Asp	Asn
			180					185					190	
Lys	Glu	Leu	Gly	Leu	Glu	Ile	Gly	Arg	Phe	Lys	Thr	Gly	Thr	Pro
		195					200					205		
Arg	Val	Lys	Ala	Ser	Ser	Ile	Asn	Tyr	Asp	Val	Thr	Glu	Ile	Gln
	210					215					220			
Gly	Asp	Glu	Val	Pro	Asn	His	Phe	Ser	Tyr	Thr	Ser	Arg	Asp	Glu
225					230					235				240
Tyr	Val	Lys	Asp	Gln	Val	Pro	Cys	Trp	Leu	Thr	Tyr	Thr	Asn	Gly
			245					250						255
Ser	His	Glu	Ile	Ile	Gln	Asn	Asn	Leu	His	Arg	Ala	Pro	Met	Phe
		260					265					270		
Gly	Val	Val	Lys	Gly	Val	Gly	Pro	Arg	Tyr	Cys	Pro	Ser	Ile	Glu
	275					280					285			
Lys	Ile	Val	Arg	Phe	Ala	Asp	Lys	Glu	Arg	His	Gln	Leu	Phe	Leu
	290					295				300				
Pro	Glu	Gly	Arg	Asn	Thr	Glu	Glu	Val	Tyr	Val	Gln	Gly	Leu	Ser
305				310					315					320
Ser	Leu	Pro	Glu	Asp	Val	Gln	Arg	Asp	Leu	Val	His	Ser	Ile	Lys
			325					330						335
Leu	Glu	Asn	Ala	Glu	Met	Met	Arg	Thr	Gly	Tyr	Ala	Ile	Glu	Tyr
		340					345					350		
Met	Val	Leu	Pro	His	Gln	Leu	Arg	Ala	Thr	Leu	Glu	Thr	Lys	Lys
	355					360					365			
Ser	Gly	Leu	Phe	Thr	Ala	Gly	Gln	Thr	Asn	Gly	Thr	Ser	Gly	Tyr
	370					375				380				
Glu	Ala	Ala	Gly	Gln	Gly	Ile	Ile	Ala	Gly	Ile	Asn	Ala	Ala	Leu
385				390					395					400
Ile	Gln	Gly	Lys	Pro	Glu	Leu	Ile	Leu	Lys	Arg	Ser	Asp	Gly	Tyr
			405					410					415	
Gly	Val	Met	Ile	Asp	Asp	Leu	Val	Thr	Lys	Gly	Thr	Ile	Glu	Pro
	420						425					430		
Arg	Leu	Leu	Thr	Ser	Arg	Ala	Glu	Tyr	Arg	Leu	Ile	Leu	Arg	His
	435					440					445			
Asn	Ala	Asp	Met	Arg	Leu	Thr	Glu	Met	Gly	Arg	Glu	Ile	Gly	Leu
	450				455				460					
Asp	Asp	Glu	Arg	Trp	Ala	Arg	Phe	Glu	Ile	Lys	Lys	Asn	Gln	Phe
465				470					475					480
Asn	Glu	Met	Lys	Arg	Leu	Asp	Ser	Ile	Lys	Leu	Lys	Pro	Val	Lys
			485					490						495
Thr	Asn	Ala	Lys	Val	Glu	Glu	Met	Gly	Phe	Lys	Pro	Leu	Thr	Asp
		500					505					510		
Val	Thr	Ala	Lys	Glu	Phe	Leu	Arg	Arg	Pro	Glu	Val	Ser	Tyr	Gln
	515					520					525			
Val	Val	Ala	Phe	Ile	Gly	Pro	Ala	Ala	Glu	Glu	Leu	Asp	Asp	Lys
	530				535					540				
Ile	Glu	Leu	Ile	Glu	Thr	Glu	Ile	Lys	Tyr	Glu	Gly	Tyr	Ile	Ser
545				550					555					560
Ala	Met	Asp	Gln	Val	Ala	Lys	Met	Lys	Arg	Met	Glu	Glu	Lys	Arg
			565					570						575
Pro	Ala	Asn	Ile	Asp	Trp	Asp	Asp	Ile	Asp	Ser	Ile	Ala	Thr	Glu
		580					585					590		
Arg	Gln	Lys	Phe	Lys	Leu	Ile	Asn	Pro	Glu	Thr	Ile	Gly	Gln	Ala
	595					600						605		

Arg	Ile	Ser	Gly	Val	Asn	Pro	Ala	Asp	Ile	Ser	Ile	Leu	Met	Val	Tyr
610						615					620				
Leu	Glu	Gly	Lys	Asn	Arg	Ser	Ile	Ser	Lys	Thr	Leu	Gln	Lys	Ser	Lys
625					630					635					640

(2) INFORMATION FOR SEQ ID NO:4703:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 303 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4703:

Lys	Met	Asn	Ile	Gln	Gln	Leu	Arg	Tyr	Val	Val	Ala	Ile	Ala	Asn	Ser
1				5					10					15	
Gly	Thr	Phe	Arg	Glu	Ala	Ala	Glu	Lys	Met	Tyr	Val	Ser	Gln	Pro	Ser
			20					25					30		
Leu	Ser	Ile	Ser	Val	Arg	Asp	Leu	Glu	Lys	Glu	Leu	Gly	Phe	Lys	Ile
		35				40						45			
Phe	Arg	Arg	Thr	Ser	Ser	Gly	Thr	Phe	Leu	Thr	Arg	Arg	Gly	Met	Glu
50						55					60				
Phe	Tyr	Glu	Lys	Ser	Gln	Glu	Leu	Val	Lys	Gly	Phe	Asp	Ile	Phe	Gln
65					70					75					80
Asn	Gln	Tyr	Ala	Asn	Pro	Glu	Glu	Glu	Lys	Asp	Glu	Phe	Ser	Val	Ala
				85					90					95	
Ser	Gln	His	Tyr	Asp	Phe	Leu	Pro	Pro	Thr	Ile	Thr	Ala	Phe	Ser	Glu
			100					105					110		
Arg	Tyr	Pro	Asp	Tyr	Lys	Asn	Phe	Arg	Ile	Phe	Glu	Ser	Thr	Thr	Val
		115					120					125			
Gln	Ile	Leu	Asp	Glu	Val	Ala	Gln	Gly	His	Ser	Glu	Ile	Gly	Ile	Ile
130						135					140				
Tyr	Leu	Asn	Asn	Gln	Asn	Lys	Lys	Gly	Ile	Met	Gln	Arg	Val	Glu	Lys
145					150					155					160
Leu	Gly	Leu	Glu	Val	Ile	Glu	Leu	Ile	Pro	Phe	His	Thr	His	Ile	Tyr
				165					170					175	
Leu	Arg	Glu	Gly	His	Pro	Leu	Ala	Gln	Lys	Glu	Glu	Leu	Val	Met	Glu
				180					185				190		
Asp	Leu	Ala	Asp	Leu	Pro	Thr	Val	Arg	Phe	Thr	Gln	Glu	Lys	Asp	Glu
		195					200					205			
Tyr	Leu	Tyr	Tyr	Ser	Glu	Asn	Phe	Val	Asp	Thr	Ser	Ala	Ser	Ser	Gln
210						215					220				
Met	Phe	Asn	Val	Thr	Asp	Arg	Ala	Thr	Leu	Asn	Gly	Ile	Leu	Glu	Arg
225					230					235					240
Thr	Asp	Ala	Tyr	Ala	Thr	Gly	Ser	Gly	Phe	Leu	Asp	Ser	Asp	Ser	Val
				245					250					255	

Asn	Gly	Ile	Thr	Val	Ile	Arg	Leu	Lys	Asp	Asn	Leu	Asp	Asn	Arg	Met
			260					265					270		
Val	Tyr	Val	Lys	Arg	Glu	Glu	Val	Glu	Leu	Ser	Gln	Ala	Gly	Thr	Leu
		275					280					285			
Phe	Val	Glu	Val	Met	Gln	Glu	Tyr	Phe	Asp	Gln	Lys	Arg	Lys	Ser	
	290					295					300				

(2) INFORMATION FOR SEQ ID NO:4704:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 71 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...71
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4704:

Asn	Lys	Asn	Met	Ala	Arg	Cys	Ser	Asn	Trp	Cys	Cys	Gly	Arg	Ser	Tyr
1			5					10					15		
Thr	Trp	Arg	Cys	Gly	Leu	Cys	Ser	Asp	Met	Leu	Val	Val	Ile	Met	Asp
		20					25					30			
Phe	Lys	Ser	Phe	Ile	Ile	Gly	Leu	Val	Val	Gly	Ile	Phe	Gly	Pro	Tyr
	35				40					45					
Met	Asp	Asp	Leu	Ile	Arg	Lys	Lys	Phe	Leu	Lys	Ser	Ser	Glu	Lys	Lys
	50				55					60					
Thr	Glu	Lys	Ser	Ile	Lys	Lys									
65					70										

(2) INFORMATION FOR SEQ ID NO:4705:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 482 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...482
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4705:

Leu	Asn	Asp	Ile	Ala	Gln	Ala	Ala	Thr	Ser	Phe	Asn	Arg	Gly	Asn	Gly
1				5					10					15	
Ser	Gln	Ala	Glu	Gln	Arg	Gly	Glu	Leu	Asp	Leu	Glu	Arg	Asp	Lys	Ala
		20						25					30		
Met	Lys	Ala	Val	Ser	Glu	Tyr	Val	Gly	Lys	Met	Val	Arg	Asp	Ala	Tyr
		35					40					45			
Val	Lys	Ser	Asp	Arg	Lys	Arg	His	Lys	Asn	Thr	Val	Ala	Leu	Val	Asn
	50					55					60				
Gln	Leu	Gly	Asn	Ile	Lys	Asn	Arg	Tyr	Leu	Asn	Glu	Ile	Val	His	Ser
65					70					75					80
Thr	Ser	Lys	Ser	Gln	Leu	Gln	Glu	Leu	Met	Met	Lys	Ser	Gln	Ser	Glu
				85					90					95	
Val	Asp	Glu	Ala	Val	Ser	Lys	Phe	Glu	Lys	Asp	Ser	Phe	Ser	Ser	Ser
			100					105					110		
Ser	Ser	Gly	Ser	Ser	Thr	Lys	Pro	Glu	Thr	Pro	Gln	Pro	Glu	Asn	Pro
		115					120					125			
Glu	His	Gln	Lys	Pro	Thr	Thr	Pro	Ser	Pro	Asp	Thr	Lys	Pro	Ser	Pro
	130					135					140				
Gln	Pro	Glu	Gly	Lys	Lys	Pro	Ser	Val	Pro	Asp	Ile	Asn	Gln	Glu	Lys
145					150					155					160
Glu	Lys	Ala	Lys	Leu	Ala	Val	Val	Thr	Tyr	Met	Ser	Lys	Ile	Leu	Asp
				165					170					175	
Asp	Ile	Gln	Lys	His	His	Leu	Gln	Lys	Glu	Lys	His	Arg	Gln	Ile	Val
			180					185					190		
Ala	Leu	Ile	Lys	Glu	Leu	Asp	Glu	Leu	Lys	Lys	Gln	Ala	Leu	Ser	Glu
		195					200					205			
Ile	Asp	Asn	Val	Asn	Thr	Lys	Val	Glu	Ile	Glu	Asn	Thr	Val	His	Lys
	210					215					220				
Ile	Phe	Ala	Asp	Met	Asp	Ala	Val	Val	Thr	Lys	Phe	Lys	Lys	Gly	Leu
225					230					235					240
Thr	Gln	Asp	Thr	Pro	Lys	Glu	Pro	Gly	Asn	Lys	Lys	Pro	Ser	Ala	Pro
				245					250					255	
Lys	Pro	Gly	Met	Gln	Pro	Ser	Pro	Gln	Pro	Glu	Val	Lys	Pro	Gln	Leu
			260					265					270		
Glu	Lys	Pro	Lys	Pro	Glu	Val	Lys	Pro	Gln	Pro	Glu	Lys	Pro	Lys	Pro
		275					280					285			
Glu	Val	Lys	Pro	Gln	Pro	Glu	Lys	Pro	Lys	Pro	Glu	Val	Lys	Pro	Gln
	290					295					300				
Pro	Glu	Lys	Pro	Lys	Pro	Glu	Val	Lys	Pro	Gln	Pro	Glu	Lys	Pro	Lys
305					310					315					320
Pro	Glu	Val	Lys	Pro	Gln	Pro	Glu	Lys	Pro	Lys	Pro	Glu	Val	Lys	Pro
				325					330					335	
Gln	Pro	Glu	Lys	Pro	Lys	Pro	Glu	Val	Lys	Pro	Gln	Pro	Glu	Lys	Pro
			340					345					350		
Lys	Pro	Glu	Val	Lys	Pro	Gln	Pro	Glu	Lys	Pro	Lys	Pro	Glu	Val	Lys
		355					360					365			
Pro	Gln	Pro	Glu	Lys	Pro	Lys	Pro	Glu	Val	Lys	Pro	Gln	Pro	Glu	Lys
	370					375					380				
Pro	Lys	Pro	Glu	Val	Lys	Pro	Gln	Pro	Glu	Lys	Pro	Lys	Pro	Glu	Val
385					390					395					400
Lys	Pro	Gln	Pro	Glu	Lys	Pro	Lys	Pro	Asp	Asn	Ser	Lys	Pro	Gln	Ala
				405					410					415	
Asp	Asp	Lys	Lys	Pro	Ser	Thr	Thr	Asn	Asn	Leu	Ser	Lys	Asp	Lys	Gln
			420					425					430		
Pro	Ser	Asn	Gln	Ala	Ser	Thr	Asn	Glu	Lys	Ala	Thr	Asn	Lys	Pro	Lys
		435					440					445			

Lys	Ser	Leu	Pro	Ser	Thr	Gly	Ser	Ile	Ser	Asn	Leu	Ala	Leu	Glu	Ile
450						455					460				
Ala	Gly	Leu	Leu	Thr	Leu	Ala	Gly	Ala	Thr	Ile	Leu	Ala	Lys	Lys	Arg
465					470					475					480
Met	Lys														

(2) INFORMATION FOR SEQ ID NO:4706:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 224 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...224
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4706:

Cys	Ile	Cys	Ile	Trp	Val	Phe	Ile	Arg	Gly	Ile	Met	Thr	Tyr	Leu	Asp
1				5					10					15	
Ala	Phe	Lys	Ser	Gly	Thr	Leu	Val	Leu	Pro	Ser	Ala	Leu	Leu	Leu	His
		20						25					30		
Phe	Lys	Glu	Leu	Phe	Pro	Ser	Ser	Asp	Asp	Phe	Leu	Val	Trp	Gln	Phe
		35				40						45			
Phe	Tyr	Leu	Gln	Asn	Thr	Thr	Gly	Leu	Glu	Glu	Met	Ser	Pro	Ser	Gln
	50					55					60				
Ile	Ala	Glu	Arg	Ile	Gly	Lys	Glu	Ile	Ser	Asp	Val	Asn	Gln	Ser	Ile
65					70					75				80	
Ser	Asn	Leu	Thr	Glu	Arg	Gly	Leu	Leu	Gln	Tyr	Arg	Thr	Ile	Glu	Leu
			85						90					95	
Asn	Gly	Glu	Ile	Glu	Leu	Leu	Phe	Asp	Ala	Ser	Leu	Ala	Leu	Glu	Arg
		100						105					110		
Leu	Asp	Asp	Leu	Phe	Gly	Ala	Val	His	Ser	Ser	Ser	Asp	Gln	Leu	Thr
	115						120					125			
Pro	Gln	Asn	Gln	Leu	Lys	Asp	Leu	Val	Glu	Thr	Phe	Gln	Gln	Glu	Leu
	130					135					140				
Gly	Arg	Leu	Leu	Thr	Pro	Phe	Glu	Ile	Glu	Asp	Leu	Thr	Lys	Thr	Leu
145					150					155					160
Lys	Glu	Asp	Gly	Thr	Ser	Ala	Asp	Leu	Ile	Lys	Glu	Ala	Leu	Arg	Glu
			165					170					175		
Ala	Val	Leu	Asn	Gly	Lys	Pro	Asn	Trp	Lys	Tyr	Ile	Gln	Ala	Ile	Leu
			180					185					190		
Arg	Asn	Trp	Arg	His	Glu	Gly	Ile	Lys	Ser	Val	Ala	Gln	Ile	Glu	Ala
	195					200						205			
Lys	Arg	Ala	Glu	Arg	Glu	Ala	Ser	Asn	Pro	Gln	Ser	Ser	Pro	Arg	Val
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:4707:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 730 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...730

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4707:

Asn	Lys	Arg	Met	Lys	Leu	Asp	Lys	Leu	Phe	Glu	Lys	Phe	Leu	Ser	Leu
1			5					10					15		
Phe	Lys	Lys	Glu	Thr	Ser	Glu	Leu	Glu	Asp	Ser	Asp	Ser	Thr	Ile	Leu
		20					25					30			
Arg	Arg	Ser	Arg	Ser	Asp	Arg	Lys	Lys	Leu	Ala	Gln	Val	Gly	Pro	Ile
		35					40				45				
Arg	Lys	Phe	Trp	Arg	Arg	Tyr	His	Leu	Thr	Lys	Ile	Ile	Leu	Ile	Leu
	50					55				60					
Gly	Leu	Ser	Ala	Gly	Leu	Leu	Val	Gly	Ile	Tyr	Leu	Phe	Ala	Val	Ala
65				70					75					80	
Lys	Ser	Thr	Asn	Val	Asn	Asp	Leu	Gln	Asn	Ala	Leu	Lys	Thr	Arg	Thr
			85					90						95	
Leu	Ile	Phe	Asp	Arg	Glu	Glu	Lys	Glu	Ala	Gly	Ala	Leu	Ser	Gly	Gln
			100				105					110			
Lys	Gly	Thr	Tyr	Val	Glu	Leu	Thr	Asp	Ile	Ser	Lys	Asn	Leu	Gln	Asn
		115					120					125			
Ala	Val	Ile	Ala	Thr	Glu	Asp	Arg	Ser	Phe	Tyr	Lys	Asn	Asp	Gly	Ile
	130					135					140				
Asn	Tyr	Gly	Arg	Phe	Phe	Leu	Ala	Ile	Val	Thr	Ala	Gly	Arg	Ser	Gly
145				150					155					160	
Gly	Gly	Ser	Thr	Ile	Thr	Gln	Gln	Leu	Ala	Lys	Asn	Ala	Tyr	Leu	Ser
			165					170						175	
Gln	Asp	Gln	Thr	Val	Glu	Arg	Lys	Ala	Lys	Glu	Phe	Phe	Leu	Ala	Leu
		180					185						190		
Glu	Leu	Ser	Lys	Lys	Tyr	Ser	Lys	Glu	Gln	Ile	Leu	Thr	Met	Tyr	Leu
	195						200					205			
Asn	Asn	Ala	Tyr	Phe	Gly	Asn	Gly	Val	Trp	Gly	Val	Glu	Asp	Ala	Ser
	210					215					220				
Lys	Lys	Tyr	Phe	Gly	Val	Ser	Ala	Ser	Glu	Val	Ser	Leu	Asp	Gln	Ala
225				230						235				240	
Ala	Thr	Leu	Ala	Gly	Met	Leu	Lys	Gly	Pro	Glu	Leu	Tyr	Asn	Pro	Leu
			245					250						255	
Asn	Ser	Val	Glu	Asp	Ser	Thr	Asn	Arg	Arg	Asp	Thr	Val	Leu	Gln	Asn
		260					265						270		
Met	Val	Ala	Ala	Gly	Tyr	Ile	Asp	Lys	Asn	Gln	Glu	Thr	Glu	Ala	Ala
	275					280					285				
Glu	Val	Asp	Met	Thr	Ser	Gln	Leu	His	Asp	Lys	Tyr	Glu	Gly	Lys	Ile

290		295		300
Ser Asp Tyr Arg Tyr	Pro Ser Tyr Phe Asp	Ala Val Val Asn Glu Ala		
305	310	315		320
Val Ser Lys Tyr Asn	Leu Thr Glu Glu Glu	Ile Val Asn Asn Gly Tyr		
	325	330		335
Arg Ile Tyr Thr Glu	Leu Asp Gln Asn Tyr	Gln Ala Asn Met Gln Ile		
	340	345		350
Val Tyr Glu Asn Ile	Ser Leu Phe Pro Arg	Ala Glu Asp Gly Thr Phe		
	355	360		365
Ala Gln Ser Gly Ser	Val Ala Leu Glu Pro	Lys Thr Gly Gly Val Arg		
	370	375		380
Gly Val Val Gly Gln	Val Ala Asp Asn Asp	Lys Thr Gly Phe Arg Asn		
385	390	395		400
Phe Asn Tyr Ala Thr	Gln Ser Lys Arg Ser	Pro Gly Ser Thr Ile Lys		
	405	410		415
Pro Leu Val Val Tyr	Thr Pro Ala Val Glu	Ala Gly Trp Ala Leu Asn		
	420	425		430
Lys Gln Leu Asp Asn	His Thr Met Gln Tyr	Asp Ser Tyr Lys Val Asp		
	435	440		445
Asn Tyr Ala Gly Ile	Lys Thr Ser Arg Glu	Val Pro Met Tyr Gln Ala		
	450	455		460
Leu Ala Glu Ser Leu	Asn Leu Pro Ala Val	Ala Thr Val Asn Asp Leu		
465	470	475		480
Gly Val Asp Lys Ala	Phe Glu Ala Gly Glu	Lys Phe Gly Leu Asn Met		
	485	490		495
Glu Lys Val Asp Arg	Val Leu Gly Val Ala	Leu Gly Ser Gly Val Glu		
	500	505		510
Thr Asn Pro Leu Gln	Met Ala Gln Ala Tyr	Ala Ala Phe Ala Asn Glu		
	515	520		525
Gly Leu Met Pro Glu	Ala His Phe Ile Ser	Arg Ile Glu Asn Ala Ser		
	530	535		540
Gly Gln Val Ile Ala	Asn His Lys Asn Ser	Gln Lys Arg Val Ile Asp		
545	550	555		560
Lys Ser Val Ala Asp	Lys Met Thr Ser Met	Met Met Leu Gly Thr Phe Thr		
	565	570		575
Asn Gly Thr Gly Ile	Ser Ser Ser Pro Ala	Asp Tyr Val Met Ala Gly		
	580	585		590
Lys Thr Gly Thr Thr	Glu Ala Val Phe Asn	Pro Glu Tyr Thr Ser Asp		
	595	600		605
Gln Trp Val Ile Gly	Tyr Thr Pro Asp Val	Val Ile Ser His Trp Leu		
	610	615		620
Gly Phe Pro Thr Thr	Asp Glu Asn His Tyr	Leu Ala Gly Ser Thr Ser		
625	630	635		640
Asn Gly Ala Ala His	Val Phe Arg Asn Ile	Ala Asn Thr Ile Leu Pro		
	645	650		655
Tyr Thr Pro Gly Ser	Thr Phe Thr Val Glu	Asn Ala Tyr Lys Gln Asn		
	660	665		670
Gly Ile Ala Pro Ala	Asn Thr Lys Arg Gln	Val Gln Thr Asn Asp Asn		
	675	680		685
Ser Gln Thr Asp Asp	Asn Leu Ser Asp Ile	Arg Gly Arg Ala Gln Ser		
	690	695		700
Leu Val Asp Glu Ala	Ser Arg Ala Ile Ser	Asp Ala Lys Ile Lys Glu		
705	710	715		720
Lys Ala Arg Thr Leu	Lys Trp Tyr Ser Val			
	725	730		

(2) INFORMATION FOR SEQ ID NO:4708:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 151 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...151
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4708:

Arg	Gly	Arg	Ile	Val	Asn	Leu	Lys	Met	Asn	Lys	Lys	Glu	Arg	Leu	Glu
1				5					10					15	
Lys	Ile	Arg	Arg	Leu	Val	Thr	Asp	Tyr	Gln	Ile	Gly	Thr	Gln	Glu	Glu
			20					25					30		
Ile	Val	Glu	His	Leu	Lys	Glu	Ala	Gly	Ile	Thr	Ala	Thr	Gln	Ala	Thr
			35				40					45			
Val	Ser	Arg	Asp	Ile	Lys	Glu	Leu	Gly	Ile	Val	Lys	Ile	Pro	Leu	Arg
	50					55					60				
Asp	Asn	Thr	Tyr	Val	Tyr	Glu	Leu	Pro	Lys	Ser	Ile	Val	Lys	Ser	Leu
65					70					75					80
Gln	Leu	Ala	Glu	Asp	Asn	Ile	Glu	Ser	Ala	Glu	Leu	Met	Asp	Lys	Met
				85					90					95	
Ile	Asn	Leu	Gln	Val	Ile	Pro	Gly	Asn	Thr	Ala	Phe	Val	Lys	Ala	Gln
			100					105					110		
Leu	Ile	Asp	Thr	Phe	Ala	Asp	Lys	Ile	Phe	Ser	Cys	Leu	Thr	Asp	Asp
		115					120					125			
Ser	Ser	Ile	Leu	Val	Ile	Ala	Arg	Ser	Gly	Ser	Leu	Ala	Glu	Glu	Ile
	130					135					140				
Phe	Glu	Gln	Val	Lys	Asn	Trp									
145					150										

(2) INFORMATION FOR SEQ ID NO:4709:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 368 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...368

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4709:

Glu	Ile	Ser	Met	Thr	Ile	Thr	Gly	Ile	Ile	Ala	Glu	Phe	Asn	Pro	Phe
1				5					10					15	
His	Asn	Gly	His	Lys	Tyr	Leu	Leu	Asp	Gln	Ala	Glu	Gly	Leu	Lys	Ile
			20					25					30		
Val	Ala	Met	Ser	Gly	Asn	Phe	Met	Gln	Arg	Gly	Glu	Pro	Ala	Ile	Val
		35					40					45			
Asp	Lys	Trp	Thr	Arg	Thr	Gln	Met	Ala	Leu	Glu	Asn	Gly	Ala	Asp	Leu
	50					55					60				
Val	Val	Glu	Leu	Pro	Phe	Leu	Val	Ser	Val	Gln	Ala	Ala	Asp	Phe	Phe
65					70					75					80
Gly	Gln	Gly	Ala	Met	Asp	Ile	Leu	Asp	Arg	Leu	Gly	Ile	Asp	Ser	Leu
				85					90					95	
Val	Phe	Gly	Thr	Glu	Glu	Val	Arg	Asp	Tyr	Gln	Lys	Ile	Ala	Asp	Leu
			100					105					110		
Tyr	Thr	Glu	Lys	Gly	Ala	Glu	Met	Glu	Lys	Phe	Val	Glu	Asn	Leu	Pro
		115					120					125			
Asp	Ser	Leu	Ser	Tyr	Pro	Gln	Lys	Thr	Gln	Ala	Met	Trp	Lys	Glu	Phe
	130					135					140				
Ala	Gly	Leu	Asp	Phe	Ser	Gly	Asn	Thr	Pro	Asn	His	Val	Leu	Ala	Leu
145					150					155					160
Ala	Tyr	Ala	Lys	Ala	Val	Ala	Gly	Arg	Asn	Ile	Lys	Leu	His	Pro	Ile
				165					170					175	
Gln	Arg	Gln	Gly	Ala	Gly	Tyr	His	Ser	Val	Asn	Lys	Asp	Val	Asp	Phe
			180					185					190		
Ala	Ser	Ala	Thr	Ala	Leu	Arg	Gln	His	Gln	Lys	Asp	Gln	Asp	Phe	Leu
		195					200					205			
Glu	Arg	Phe	Met	Pro	Ser	Val	Ala	Leu	Phe	Glu	Gln	Ala	Ser	Lys	Val
	210					215					220				
Ile	Trp	Glu	Asp	Tyr	Phe	Pro	Leu	Leu	Arg	Tyr	Gln	Ile	Leu	Ser	Asn
225				230						235					240
Pro	Asp	Leu	Thr	Thr	Ile	Tyr	Gln	Val	Asn	Gln	Glu	Met	Ala	Val	Arg
				245					250					255	
Ile	Lys	Glu	Ala	Ile	Lys	Thr	Ala	Gln	Ser	Val	Glu	Glu	Leu	Val	Glu
			260					265					270		
Leu	Val	Thr	Thr	Lys	Arg	Tyr	Thr	Lys	Ala	Arg	Val	Arg	Arg	Leu	Leu
		275					280					285			
Thr	Tyr	Ile	Leu	Val	Gln	Ala	Arg	Glu	Asn	Val	Leu	Pro	Glu	Ala	Ile
	290					295						300			
His	Val	Leu	Gly	Phe	Thr	Glu	Lys	Gly	Arg	Gln	His	Leu	Lys	Ser	Leu
305				310						315					320
Lys	Gly	Gln	Val	Asn	Leu	Val	Ser	Arg	Ile	Gly	Lys	Glu	Pro	Trp	Asp
				325					330					335	
Ala	Met	Thr	Gln	Lys	Val	Asp	Gln	Ile	Tyr	Gln	Leu	Gly	Lys	Pro	Ser
			340					345					350		
Ile	Ala	Glu	Gln	Asn	Phe	Gly	Arg	Val	Pro	Ile	Arg	Ile	Glu	Thr	Asn
		355					360					365			

(2) INFORMATION FOR SEQ ID NO:4710:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 331 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4710:

```

Arg Ser Ser Met Glu Thr Ala Leu Ile Ser Val Ile Val Pro Val Tyr
1      5      10      15
Asn Val Ala Gln Tyr Leu Glu Lys Ser Ile Ala Ser Ile Gln Lys Gln
20      25      30
Thr Tyr Gln Asn Leu Glu Ile Ile Leu Val Asp Asp Gly Ala Thr Asp
35      40      45
Glu Ser Gly Arg Leu Cys Asp Ser Ile Ala Glu Gln Asp Asp Arg Val
50      55      60
Ser Val Leu His Lys Lys Asn Glu Gly Leu Ser Gln Ala Arg Asn Asp
65      70      75      80
Gly Met Lys Gln Ala His Gly Asp Tyr Leu Ile Phe Ile Asp Ser Asp
85      90      95
Asp Tyr Ile His Pro Glu Met Ile Gln Ser Leu Tyr Glu Gln Leu Val
100      105      110
Gln Glu Asp Ala Asp Val Ser Ser Cys Gly Val Met Asn Val Tyr Ala
115      120      125
Asn Asp Glu Ser Pro Gln Ser Ala Asn Gln Asp Asp Tyr Phe Val Cys
130      135      140
Asp Ser Gln Thr Phe Leu Lys Glu Tyr Leu Ile Gly Glu Lys Ile Pro
145      150      155      160
Gly Thr Ile Cys Asn Lys Leu Ile Lys Arg Gln Ile Ala Thr Asp Leu
165      170      175
Ser Phe Pro Lys Gly Leu Ile Tyr Glu Asp Ala Tyr Tyr His Phe Asp
180      185      190
Leu Ile Lys Leu Ala Lys Lys Tyr Val Val Asn Thr Lys Pro Tyr Tyr
195      200      205
Tyr Tyr Phe His Arg Gly Asp Ser Ile Thr Thr Lys Pro Tyr Ala Glu
210      215      220
Lys Asp Leu Ala Tyr Ile Asp Ile Tyr Gln Lys Phe Tyr Asn Glu Val
225      230      235      240
Val Lys Asn Tyr Pro Asp Leu Lys Glu Val Ala Phe Phe Arg Leu Ala
245      250      255
Tyr Ala His Phe Phe Ile Leu Asp Lys Met Leu Leu Asp Asp Gln Tyr
260      265      270
Lys Gln Phe Glu Ala Tyr Ser Gln Ile His Arg Phe Leu Lys Gly His
275      280      285
Ala Phe Ala Ile Ser Arg Asn Pro Ile Phe Arg Lys Gly Arg Arg Ile
290      295      300
Ser Ala Leu Ala Leu Phe Ile Asn Ile Ser Leu Tyr Arg Phe Leu Leu
305      310      315      320
Leu Lys Asn Ile Glu Lys Ser Lys Lys Leu His
325      330

```

(2) INFORMATION FOR SEQ ID NO:4711:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4711:

Ser	Thr	Ser	Ile	Val	Phe	Phe	Ser	Leu	Leu	Ile	Ile	Cys	Phe	Phe	Cys
1				5					10					15	
Phe	Trp	Leu	Phe	Ser	Trp	Leu	Val	Trp	Phe	Trp	Cys	Gly	Ser	Trp	Ile
		20						25					30		
Leu	Arg	Leu	Phe	Ser	Trp	Phe	Phe	Trp	Leu	Arg	Ser	Arg	Arg	Trp	Leu
		35					40					45			
Trp	Leu	Phe	Ser	Trp	Phe	Phe	Phe	Asn	Phe	Ile	Phe	Phe	Cys	Cys	Phe
	50					55				60					
Ser	Phe	Ser	Phe	Phe	Phe	Cys	Phe	Phe	Thr	Ile	Cys	Leu	Asp	Phe	Phe
65				70					75						80

(2) INFORMATION FOR SEQ ID NO:4712:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 405 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...405

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4712:

Asn	Arg	Ser	Ile	Gly	Gln	Gln	Gly	Gly	Pro	Met	Lys	Leu	Ser	Asn	Arg
1				5					10					15	
Val	Leu	Glu	Met	Glu	Glu	Ser	Val	Thr	Leu	Ala	Ala	Gly	Ala	Arg	Ala
		20						25					30		
Lys	Ala	Leu	Lys	Ala	Glu	Gly	Arg	Asp	Ile	Leu	Ser	Leu	Thr	Leu	Gly
		35					40					45			

Glu	Pro	Asp	Phe	Thr	Thr	Pro	Lys	Asn	Ile	Gln	Asp	Ala	Ala	Ile	Ala	50	55	60
Ser	Ile	Arg	Asp	Gly	Arg	Ala	Ser	Phe	Tyr	Thr	Val	Thr	Ser	Gly	Leu	65	70	75
Pro	Glu	Leu	Lys	Ala	Val	Val	Asn	Ser	Tyr	Phe	Glu	Arg	Phe	Tyr	Gly	85	90	95
Tyr	Ser	Val	Ala	Pro	Asn	Gln	Val	Thr	Val	Ala	Ala	Gly	Ala	Lys	Tyr	100	105	110
Ser	Leu	Tyr	Thr	Phe	Phe	Met	Ala	Val	Val	Asn	Pro	Gly	Asp	Glu	Val	115	120	125
Ile	Ile	Pro	Thr	Pro	Tyr	Trp	Val	Ser	Tyr	Gly	Asp	Gln	Val	Lys	Met	130	135	140
Ala	Glu	Gly	Val	Pro	Val	Phe	Val	Ser	Ala	Lys	Glu	Asp	Asn	His	Phe	145	150	155
Lys	Val	Thr	Val	Glu	Gln	Leu	Glu	Ala	Ala	Arg	Thr	Asp	Lys	Thr	Lys	165	170	175
Val	Leu	Val	Leu	Asn	Ser	Pro	Ser	Asn	Pro	Thr	Gly	Met	Ile	Tyr	Thr	180	185	190
Arg	Glu	Glu	Leu	Leu	Ala	Ile	Gly	Asn	Trp	Ala	Val	Glu	Asn	Asp	Ile	195	200	205
Leu	Ile	Leu	Ala	Asp	Asp	Ile	Tyr	Gly	Arg	Leu	Val	Tyr	Asn	Gly	His	210	215	220
Glu	Phe	Thr	Pro	Ile	Ser	Ser	Leu	Ser	Glu	Ala	Ile	Arg	Lys	Gln	Thr	225	230	235
Val	Val	Ile	Asn	Gly	Val	Ser	Lys	Thr	Tyr	Ala	Met	Thr	Gly	Trp	Arg	245	250	255
Ile	Gly	Tyr	Ala	Val	Gly	Glu	Ala	Asp	Ile	Ile	Ala	Ala	Met	Ser	Lys	260	265	270
Ile	Ala	Gly	Gln	Thr	Thr	Ser	Asn	Pro	Ser	Ala	Val	Ala	Gln	Tyr	Ala	275	280	285
Ala	Val	Glu	Ala	Leu	Ser	Gly	Glu	Gln	Asp	Thr	Val	Glu	Ser	Met	Arg	290	295	300
Gln	Ala	Phe	Glu	Lys	Arg	Leu	Asn	Thr	Ile	Tyr	Pro	Leu	Leu	Ala	Glu	305	310	315
Val	Pro	Gly	Phe	Glu	Val	Val	Lys	Pro	Gln	Gly	Ala	Phe	Tyr	Leu	Phe	325	330	335
Pro	Asn	Val	Lys	Lys	Ala	Met	Glu	Met	Lys	Gly	Tyr	Thr	Asp	Val	Thr	340	345	350
Asp	Phe	Thr	Thr	Ala	Ile	Leu	Glu	Glu	Ala	Glu	Val	Ala	Leu	Val	Thr	355	360	365
Gly	Ala	Gly	Phe	Gly	Ala	Pro	Glu	Asn	Val	Arg	Leu	Ser	Tyr	Ala	Thr	370	375	380
Asp	Leu	Asp	Thr	Leu	Lys	Glu	Ala	Val	Glu	Arg	Leu	Lys	Ala	Phe	Met	385	390	395
Gly	Ser	Glu	Asn	Asp												405		

(2) INFORMATION FOR SEQ ID NO:4713:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4713:

Phe	Ile	Gly	Ile	Arg	Ser	Leu	Ser	Glu	Ile	Gly	Asn	Pro	Gly	Trp	Thr
1				5					10					15	
Pro	His	Pro	Asn	Ser	Ala	Leu	Pro	Pro	Arg	Ile	Ser	Asn	Val	Asp	Ala
			20					25					30		
Ser	Pro	Lys	Ala	Ile	Ser	Glu	Arg	Thr	Ser	Tyr	Leu	Gln	Val	Arg	Leu
		35					40					45			
Glu	Phe	Leu	Arg	Tyr	Pro	Gln	Val	Ile	Gln	Ala	Leu	Phe	Asn	Val	Pro
	50					55				60					
Trp	Phe	Gly	Pro	Pro	Val	Arg	Leu	Thr	Ala	Pro	Ser	Thr	Cys	Ser	Trp
65					70				75					80	
Val	Gly	His	Met	Val	Ser	Gly	Leu	Arg	His	Asp	Thr	Lys	Ala	Pro	Tyr
				85				90					95		
Ser	Asp	Ser	Val	Ser	Leu	Arg	Leu	Arg	Leu	Phe	Asn	Leu	Thr	Ser	His
			100				105					110			
His	Asn	Val	Thr	Arg	Arg	Phe	Ile	Leu	Gln	Lys	Ala	Arg	Ser	His	Pro
		115				120						125			
Leu	Thr	Gly	Ser	Asn	Leu	Leu									
	130					135									

(2) INFORMATION FOR SEQ ID NO:4714:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 71 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...71

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4714:

Gly	Glu	Gly	Met	Lys	Leu	Asn	Glu	Val	Lys	Glu	Phe	Val	Lys	Glu	Leu
1				5				10						15	
Arg	Gly	Leu	Ser	Gln	Glu	Glu	Leu	Ala	Lys	Arg	Glu	Asn	Glu	Leu	Lys
			20					25					30		
Lys	Glu	Leu	Phe	Glu	Leu	Arg	Phe	Gln	Ala	Ala	Thr	Gly	Gln	Leu	Glu
		35				40					45				
Gln	Thr	Ala	Arg	Leu	Lys	Glu	Val	Lys	Lys	Gln	Ile	Ala	Arg	Ile	Lys
	50					55				60					

Thr Val Gln Ser Glu Ala Lys
65 70

(2) INFORMATION FOR SEQ ID NO:4715:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...77

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4715:

Phe	Phe	Val	Leu	Tyr	Pro	Asn	Met	Asn	Arg	Asp	Val	Ala	Asn	Lys	Leu
1			5					10					15		
Asn	Asn	Ile	Phe	Gly	Lys	Met	Arg	Asn	Ser	Asn	Ile	Thr	Arg	Thr	Phe
		20				25					30				
Arg	Asn	Asn	Gln	Tyr	Leu	Lys	Arg	Lys	Lys	Leu	Lys	Glu	Phe	Ile	Lys
		35				40					45				
Pro	Cys	Tyr	Asn	Arg	Tyr	Ser	Tyr	Asn	Phe	Ile	Tyr	Asn	Lys	Arg	Ile
	50				55			60							
Glu	Met	Thr	Glu	Leu	Glu	Arg	Lys	Asn	Arg	Lys	Ile	Ser			
65				70				75							

(2) INFORMATION FOR SEQ ID NO:4716:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4716:

Phe	Ile	Leu	Ile	Tyr	Phe	Lys	Gly	Val	Leu	Met	Lys	Leu	Arg	Ile	Phe
1			5					10					15		

Ala	Glu	Asp	Lys	Pro	Ala	Lys	Lys	Val	Phe	Glu	Tyr	Gln	Leu	Glu	Leu
			20					25					30		
Ala	Asp	Arg	Thr	Ile	Leu	Leu	Ser	Thr	Ala	Leu	Leu	Ser	Gly	Ala	Ile
		35					40					45			
Ala	Leu	Ala	Gly	Ile	Phe	Ser	Ala	Leu	Lys	Glu	Lys				
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:4717:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4717:

Asn	Ile	Leu	Ile	Ile	Phe	Met	Asn	Phe	Gln	Leu	Ala	Lys	Tyr	Ser	Leu
1				5					10					15	
Leu	Lys	Lys	Phe	Leu	Glu	Asn	Ile	Gly	Phe	Thr	Thr	Leu	Glu	Glu	Tyr
			20					25					30		
Gly	Ala	Ile	Phe	Lys	Tyr	Leu	Ile	Glu	Asn	Val	Lys	Thr	Asp	Arg	Gln
		35				40					45				
Ile	Ile	Cys	Ser	Pro	His	Cys	His	Asp	Asp	Leu	Gly	Met	Ala	Val	Ala
	50					55				60					
Asn	Ser	Leu	Ala	Ala	Val	Lys	Asn	Gly	Ala	Gly	Arg	Val	Glu	Gly	Thr
65				70				75					80		
Ile	Asn	Gly	Ile	Arg	Glu	Arg	Ala	Glu	Asn	Ala	Ala	Leu	Glu	Glu	Ile
			85					90					95		
Ala	Val	Ala	Leu	Asn	Ile	Arg	Gln	Asp	Tyr	Tyr	Gln	Val	Glu	Thr	Ser
		100					105						110		
Ile	Val	Leu	Asn	Glu	Thr	Ile	Asn	Thr	Ser	Glu	Met	Val	Ser	Arg	Phe
	115					120						125			
Ser	Gly	Ile	Pro	Val	Pro	Lys	Asn	Lys	Ala	Val	Val	Gly	Gly	Asn	Thr
	130					135					140				
Phe	Ser	His	Glu	Ser	Gly	Ile	His	Gln	Asp	Gly	Val	Leu	Lys	Asn	Pro
145				150				155						160	
Leu	Thr	Tyr	Glu	Ile	Ile	Thr	Pro	Glu	Leu	Val	Gly	Val	Lys	Ile	Pro
			165					170					175		
Leu	Gly	Glu	Leu	Ser	Gly	Arg	His	Ala	Phe	Val	Glu	Lys	Leu	Arg	Glu
		180				185						190			
Leu	Ala	Leu	Asp	Phe	Thr	Glu	Glu	Asp	Ile	Lys	Pro	Leu	Phe	Ala	Lys
	195					200						205			
Phe	Lys	Ala	Leu	Ala	Asp	Lys	Lys								
	210					215									

(2) INFORMATION FOR SEQ ID NO:4718:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...73
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4718:

```

Lys Tyr Leu Ile Leu Glu Ile Lys Ser Leu Ser Phe Leu Ser Lys Ile
1          5          10          15
Val Asn Gly Leu Ile Gln Asn Ile Glu Glu Asn Leu Glu Asp Asp Ile
          20          25          30
Glu Arg Ile Leu Lys Tyr Leu Tyr Ile Cys Leu Phe Asn Glu Ile Phe
          35          40          45
Ile Ile Lys Asn Lys Val Asn Phe Phe Asp Asp Val Glu Phe Asn Gln
          50          55          60
Thr Leu Ser Glu Phe Leu Asp Lys Leu
65          70

```

(2) INFORMATION FOR SEQ ID NO:4719:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 258 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...258
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4719:

```

Leu Asp Leu Ile Phe Phe Leu Met Tyr Ile Lys Arg Gln Glu Glu Tyr
1          5          10          15
Lys Phe Met Ile Arg Ile Glu Asn Leu Ser Val Ser Tyr Lys Glu Thr
          20          25          30
Leu Ala Leu Lys Asp Ile Ser Leu Val Leu His Gly Pro Thr Ile Thr
          35          40          45
Gly Ile Ile Gly Pro Asn Gly Ala Gly Lys Ser Thr Leu Leu Lys Gly

```

50		55		60											
Met	Leu	Gly	Ile	Ile	Pro	His	Gln	Gly	Gln	Ala	Phe	Leu	Asp	Asp	Lys
65					70					75					80
Glu	Val	Lys	Lys	Ser	Leu	His	Arg	Ile	Ala	Tyr	Val	Glu	Gln	Lys	Ile
				85					90					95	
Asn	Ile	Asp	Tyr	Asn	Phe	Pro	Ile	Lys	Val	Lys	Glu	Cys	Val	Ser	Leu
		100						105					110		
Gly	Leu	Phe	Pro	Ser	Ile	Pro	Leu	Phe	Arg	Ser	Leu	Lys	Ala	Lys	His
	115						120					125			
Trp	Lys	Lys	Val	Gln	Glu	Ala	Leu	Glu	Ile	Val	Gly	Leu	Ala	Asp	Tyr
130						135					140				
Ala	Glu	Arg	Gln	Ile	Ser	Gln	Leu	Ser	Gly	Gly	Gln	Phe	Gln	Arg	Val
145					150					155					160
Leu	Ile	Ala	Arg	Cys	Leu	Val	Gln	Glu	Ala	Asp	Tyr	Ile	Leu	Leu	Asp
				165					170					175	
Glu	Pro	Phe	Ala	Gly	Ile	Asp	Ser	Val	Ser	Glu	Glu	Ile	Ile	Met	Asn
		180						185					190		
Thr	Leu	Arg	Asp	Leu	Lys	Lys	Ala	Gly	Lys	Thr	Val	Leu	Ile	Val	His
	195						200					205			
His	Asp	Leu	Ser	Lys	Ile	Pro	His	Tyr	Phe	Asp	Gln	Val	Leu	Leu	Val
210					215					220					
Asn	Arg	Glu	Val	Ile	Ala	Phe	Gly	Pro	Thr	Lys	Glu	Thr	Phe	Thr	Glu
225					230					235					240
Thr	Asn	Leu	Lys	Glu	Ala	Tyr	Gly	Asn	Gln	Leu	Phe	Phe	Asn	Gly	Gly
			245					250						255	
Asp	Leu														

(2) INFORMATION FOR SEQ ID NO:4720:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4720:

Pro	Cys	Leu	Ile	Lys	Arg	Arg	Lys	Gln	Met	Glu	Leu	Val	Leu	Pro	Asn
1				5				10						15	
Asn	Tyr	Val	Val	Ile	Asp	Glu	Glu	Glu	Met	Met	Tyr	Leu	Asp	Gly	Gly
		20						25					30		
Gly	Val	Gly	Cys	Asn	Trp	Trp	Asn	Ser	Arg	Gly	Ser	Phe	Ala	Thr	Val
	35					40						45			
Leu	Asp	Val	Gly	Leu	Ala	Ile	Tyr	Ser	Gly	Gly	Ala	Thr	Ile	Tyr	Ser
50					55				60						
Ala	Tyr	Ala	Ile	Lys	Lys	Ala	Ile	Ser	Ala	Asn	Arg	Gly	Ala	Ile	Thr

65					70					75					80
Arg	Thr	Leu	Arg	Ser	Leu	Ile	Ile	Lys	His	Val	Gly	Ser	Ala	Ala	Gly
				85					90					95	
His	Leu	Val	Asn	Thr	Ala	Leu	Asn	Val	Ala	Leu	Thr	Val	Thr	Gly	Phe
			100					105					110		
Ser	Leu	Gly	Gly	Ala	Ile	Ala	Tyr	Gly	Ala	Asp	Trp	Ala	Asp	Gly	Ser
		115					120					125			
Leu	Asp	Gly	Tyr	Ile	Phe	Ala									
	130					135									

(2) INFORMATION FOR SEQ ID NO:4721:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 225 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4721:

Met	Lys	Leu	Ile	Val	Ser	Val	Met	Pro	Arg	Ser	Leu	Glu	Glu	Ala	Gln
1				5				10						15	
Ala	Leu	Asp	Ala	Thr	Arg	Tyr	Leu	Asp	Ala	Asp	Ile	Ile	Glu	Trp	Arg
			20					25					30		
Ala	Asp	Tyr	Leu	Pro	Lys	Glu	Ala	Ile	Leu	Gln	Val	Ala	Pro	Ala	Ile
		35				40					45				
Phe	Glu	Lys	Phe	Ala	Gly	Arg	Glu	Leu	Val	Phe	Thr	Leu	Arg	Thr	Arg
	50				55					60					
Ser	Glu	Gly	Gly	Glu	Ile	Asp	Leu	Ser	Pro	Glu	Glu	Tyr	Ile	His	Leu
65				70						75				80	
Ile	Lys	Glu	Val	Ala	Gln	Phe	Tyr	Gln	Pro	Asp	Tyr	Ile	Asp	Phe	Glu
			85					90					95		
Tyr	Tyr	Ser	Tyr	Lys	Asp	Val	Phe	Glu	Glu	Met	Leu	Tyr	Phe	Pro	Asn
		100					105						110		
Leu	Val	Leu	Ser	Tyr	His	Asn	Phe	Gln	Glu	Thr	Pro	Glu	Asn	Met	Met
	115					120						125			
Glu	Ile	Leu	Ser	Glu	Leu	Thr	Ile	Leu	Asn	Pro	Lys	Leu	Val	Lys	Val
	130					135				140					
Ala	Val	Met	Ala	His	Thr	Glu	Gln	Asp	Val	Leu	Asp	Leu	Met	Asn	Tyr
145				150						155				160	
Thr	Arg	Gly	Phe	Lys	Thr	Leu	Asn	Pro	Glu	Gln	Glu	Tyr	Val	Thr	Ile
			165					170					175		
Ser	Met	Gly	Lys	Val	Gly	Lys	Val	Ser	Arg	Ile	Thr	Ala	Asp	Val	Thr
		180						185					190		

Gly Ser Ser Trp Ser Phe Ala Ser Leu Asp Glu Val Ser Ala Pro Gly

	195		200		205
Gln	Ile	Ser	Leu	Ala	Ser
	210		215		220
Ala					
225					

(2) INFORMATION FOR SEQ ID NO:4722:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 224 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4722:

Thr	His	Ser	Leu	Asp	Ser	Val	Leu	Phe	Val	Ser	Leu	Ser	Leu	Arg	Leu
1			5					10						15	
Glu	Met	Leu	Cys	Ser	Ala	His	Lys	Ser	Val	Leu	Leu	Leu	Arg	Ala	Ser
		20					25						30		
Val	His	Gly	Gln	Leu	Arg	Ile	Met	Phe	Pro	Met	Val	Ala	Leu	Leu	Lys
	35					40					45				
Glu	Phe	Arg	Ala	Ala	Lys	Ala	Val	Phe	Asp	Glu	Glu	Lys	Ala	Asn	Leu
50					55					60					
Leu	Ala	Glu	Gly	Val	Ala	Val	Ala	Asp	Asn	Ile	Gln	Val	Gly	Ile	Met
65				70					75					80	
Ile	Glu	Ile	Pro	Ala	Ala	Ala	Met	Leu	Ala	Asp	Gln	Phe	Ala	Lys	Glu
			85						90					95	
Val	Asp	Phe	Phe	Ser	Ile	Gly	Thr	Asn	Asp	Leu	Ile	Gln	Tyr	Thr	Met
		100						105					110		
Ala	Ala	Asp	Arg	Met	Asn	Glu	Gln	Val	Ser	Tyr	Leu	Tyr	Gln	Pro	Tyr
		115					120					125			
Asn	Pro	Ser	Ile	Leu	Arg	Leu	Ile	Asn	Asn	Val	Ile	Lys	Ala	Ala	His
130						135					140				
Ala	Glu	Gly	Lys	Trp	Ala	Gly	Met	Cys	Gly	Glu	Met	Ala	Gly	Asp	Gln
145				150						155					160
Gln	Ala	Val	Pro	Leu	Leu	Val	Gly	Met	Gly	Leu	Asp	Glu	Phe	Ser	Met
			165						170					175	
Ser	Ala	Thr	Ser	Val	Leu	Arg	Thr	Arg	Ser	Leu	Met	Lys	Lys	Leu	Asp
		180						185					190		
Thr	Ala	Lys	Met	Glu	Glu	Tyr	Ala	Asn	Arg	Ala	Leu	Thr	Glu	Cys	Ser
	195					200					205				
Thr	Met	Glu	Glu	Val	Leu	Glu	Leu	Gln	Lys	Glu	Tyr	Val	Asn	Phe	Asp
210						215					220				

(2) INFORMATION FOR SEQ ID NO:4723:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 285 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4723:

Cys	Tyr	Leu	Ile	Arg	Lys	Cys	Phe	Phe	Cys	Arg	Lys	Tyr	Asn	Met	Ile
1				5					10					15	
Arg	Cys	Lys	Lys	Glu	Ile	Arg	Ser	Leu	Tyr	Met	Ala	Glu	Gln	Asp	Leu
		20					25						30		
Ala	Met	Gln	Val	Leu	Gln	Gln	Val	Val	Lys	Leu	Pro	Val	Val	Lys	Val
		35					40					45			
Asp	Ser	Ser	Lys	Phe	Leu	Val	Asp	Lys	Phe	Ser	Lys	Glu	Leu	Gly	Pro
	50					55					60				
Gln	Asp	Ile	Pro	Thr	Leu	Leu	Glu	Gln	Gly	Pro	Thr	Ser	Leu	Leu	Ser
65					70					75					80
Gln	Glu	Ile	Leu	Asp	Arg	Val	Ala	Asn	Ala	Cys	Ile	Arg	Asp	Asn	Val
				85					90					95	
Leu	Leu	Ala	Ser	Gly	Thr	Ser	Val	Leu	Ala	Gly	Leu	Pro	Gly	Gly	Leu
			100						105				110		
Ala	Met	Ala	Ile	Thr	Ile	Pro	Ala	Asp	Val	Ala	Gln	Phe	Tyr	Ala	Phe
		115					120					125			
Ser	Leu	Lys	Leu	Ala	Gln	Glu	Leu	Gly	Tyr	Ile	Tyr	Gly	Tyr	Glu	Asp
	130					135					140				
Leu	Trp	Val	Ser	Arg	Glu	Glu	Leu	Ser	Glu	Asp	Ala	Gln	Asn	Thr	Leu
145					150					155					160
Leu	Leu	Tyr	Leu	Gly	Val	Met	Leu	Gly	Val	Asn	Gly	Thr	Ala	Ala	Leu
				165					170					175	
Leu	Arg	Ala	Gly	Ile	Thr	Ile	Ala	Lys	Gln	Val	Met	Lys	Thr	Val	
		180					185					190			
Pro	Asn	Lys	Ala	Leu	Thr	Lys	Thr	Leu	Trp	Tyr	Pro	Ile	Leu	Lys	Lys
		195					200					205			
Val	Leu	Lys	Ile	Phe	Gly	Val	Asn	Leu	Thr	Lys	Gly	Gly	Leu	Ala	Lys
	210					215					220				
Gly	Met	Gly	Lys	Phe	Ile	Pro	Ile	Leu	Gly	Gly	Ile	Ile	Ser	Gly	Gly
225					230					235					240
Leu	Thr	Phe	Ala	Thr	Met	Lys	Pro	Met	Gly	Glu	Ser	Leu	Gln	Lys	Glu
				245					250					255	
Leu	Ser	Lys	Leu	Val	Asn	Tyr	Ser	Glu	Val	Gln	Tyr	Gln	Glu	Asp	Val
		260					265					270			
Glu	Thr	Ile	Arg	Lys	Glu	Ala	Glu	Ile	Ile	Glu	Gly	Glu			
		275					280					285			

(2) INFORMATION FOR SEQ ID NO:4724:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...64

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4724:

Val	Asn	Leu	Ile	Leu	Lys	Ile	Lys	Glu	Gln	Thr	Arg	Lys	Leu	Ala	Ala
1				5					10					15	
Gly	Cys	Ser	Lys	His	Cys	Phe	Glu	Val	Val	Asp	Glu	Thr	Asp	Glu	Val
			20					25					30		
Ser	Asn	His	Thr	Tyr	Gly	Lys	Ala	Met	Leu	Thr	Trp	Leu	Glu	Glu	Ile
		35				40						45			
Phe	Glu	Glu	Tyr	Lys	Ile	Lys	Phe	Tyr	Pro	Thr	Asp	Pro	Ser	Ile	Ser
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:4725:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 819 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...819

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4725:

Phe	Phe	Ile	Met	Lys	Thr	Ile	Gly	Asn	Arg	Tyr	Val	Val	Val	Asp	Leu
1				5					10					15	
Glu	Ala	Thr	Ser	Thr	Gly	Ser	Lys	Ala	Lys	Ile	Ile	Gln	Val	Gly	Ile
			20					25					30		
Val	Val	Ile	Glu	Asp	Gly	Glu	Ile	Val	Asp	His	Tyr	Thr	Thr	Asp	Val
		35				40						45			
Asn	Pro	His	Glu	Pro	Leu	Asp	Ala	His	Ile	Lys	Glu	Leu	Thr	Gly	Leu
	50					55					60				
Thr	Asp	Gln	Arg	Leu	Ala	Gln	Ala	Pro	Asp	Phe	Ser	Gln	Val	Ala	Arg

65					70					75					80
Lys	Ile	Phe	Asp	Leu	Val	Glu	Asp	Gly	Ile	Phe	Val	Ala	His	Asn	Val
				85					90					95	
Gln	Phe	Asp	Ala	Asn	Leu	Leu	Ala	Glu	Asn	Leu	Phe	Phe	Glu	Gly	Tyr
			100					105					110		
Glu	Leu	Arg	Asn	Pro	Arg	Val	Asp	Thr	Val	Glu	Leu	Ala	Gln	Val	Phe
		115					120					125			
Phe	Pro	Glu	Leu	Glu	Lys	Tyr	Ser	Leu	Pro	Ile	Leu	Cys	Arg	Glu	Leu
	130					135					140				
Gly	Ile	Pro	Leu	Lys	His	Ala	His	Thr	Ala	Leu	Ser	Asp	Ala	Gln	Ala
145					150					155					160
Thr	Ala	Glu	Leu	Leu	Leu	Phe	Leu	Arg	Glu	Lys	Met	Thr	Gln	Leu	Pro
			165					170						175	
Lys	Gly	Leu	Leu	Glu	Arg	Leu	Leu	Glu	Met	Ala	Asp	Ala	Leu	Leu	Tyr
		180						185					190		
Glu	Ser	Tyr	Leu	Val	Ile	Glu	Glu	Thr	Tyr	Arg	Asn	Gln	Ser	Ile	Leu
		195					200					205			
Ser	Ser	Pro	Asp	Leu	Val	Gln	Val	Gln	Gly	Leu	Tyr	Phe	Lys	Lys	Thr
	210					215					220				
Ala	Ala	Ser	Leu	Glu	Leu	Arg	Lys	Leu	Ser	Gln	Asp	Phe	Ser	Lys	Asn
225					230					235					240
Ile	Ser	Leu	Leu	Asn	Leu	Glu	Val	Arg	Glu	Glu	Gln	Glu	Ser	Phe	Ala
			245						250					255	
Lys	Glu	Val	Gly	Leu	Leu	Leu	Lys	Asp	Glu	Pro	Val	Phe	Leu	Ile	Gln
		260						265					270		
Ala	Pro	Thr	Gly	Ile	Gly	Lys	Thr	Tyr	Gly	Tyr	Leu	Leu	Pro	Ala	Leu
		275					280					285			
Ser	Gln	Ser	Lys	Glu	Arg	Gln	Ile	Val	Leu	Ser	Val	Pro	Thr	Lys	Ile
	290					295					300				
Leu	Gln	Asn	Gln	Ile	Met	Glu	Glu	Glu	Gly	Lys	Arg	Leu	Lys	Glu	Val
305				310					315						320
Phe	His	Thr	Asp	Ile	His	Ser	Leu	Lys	Gly	Pro	Gln	Asn	Tyr	Leu	Lys
			325						330					335	
Leu	Asp	Ala	Phe	Tyr	His	Ser	Leu	Gln	Glu	Asn	Asp	Glu	Asn	Arg	Leu
		340						345				350			
Phe	Arg	Arg	Phe	Lys	Met	Gln	Val	Leu	Val	Trp	Leu	Thr	Glu	Thr	Glu
	355					360						365			
Thr	Gly	Asp	Leu	Asp	Glu	Ile	Gly	Gln	Leu	Tyr	Arg	Tyr	Gln	His	Phe
	370					375					380				
Leu	Ala	Asp	Leu	Arg	His	Asp	Gly	Asn	Leu	Ser	Ser	Gln	Ser	Leu	Phe
385					390				395						400
Val	Thr	Glu	Asp	Phe	Trp	Lys	Arg	Ser	Gln	Glu	Arg	Ala	Glu	Thr	Cys
			405						410					415	
Lys	Leu	Leu	Val	Thr	Asn	His	Ala	Tyr	Leu	Val	Thr	Arg	Leu	Glu	Asp
			420					425					430		
Asn	Pro	Glu	Phe	Val	Ser	Asp	Arg	Leu	Leu	Ile	Ile	Asp	Glu	Val	Gln
	435						440					445			
Lys	Ile	Leu	Leu	Ala	Leu	Glu	Asn	Leu	Leu	Gln	Glu	Thr	Tyr	Asp	Ile
	450					455				460					
Gln	Ser	Ile	Ile	Asp	Leu	Ile	Asp	Lys	Ala	Leu	Val	Gly	Glu	Glu	Asn
465					470				475						480
Arg	Val	Gln	Gln	Arg	Ile	Leu	Glu	Ser	Ile	Arg	Phe	Glu	Cys	Leu	Tyr
			485						490					495	
Leu	Ile	Glu	Gln	Phe	Gln	Ser	Gly	Lys	Ser	Arg	Lys	Asn	Ile	Leu	Asp
		500					505					510			
Ser	Leu	Asp	Asn	Leu	His	Gln	Tyr	Phe	Ser	Glu	Leu	Glu	Val	Glu	Gly
		515					520					525			

Phe	Asp	Glu	Leu	Val	Arg	Tyr	Phe	Thr	Ala	Glu	Gly	Asp	Tyr	Trp	Leu	530	535	540
Glu	Val	Thr	Glu	Thr	Ser	Gln	Lys	Lys	Ile	Gln	Ile	Ser	Ser	Thr	Lys	545	550	555
Ser	Gly	Arg	Thr	Leu	Leu	Ser	Ser	Leu	Leu	Pro	Glu	Ser	Cys	Gln	Val	565	570	575
Leu	Gly	Val	Ser	Ala	Thr	Leu	Glu	Ile	Ser	Gln	Arg	Val	Ser	Leu	Ala	580	585	590
Asp	Leu	Leu	Gly	Tyr	Pro	Glu	Ala	Lys	Phe	Val	Lys	Ile	Glu	Ser	Arg	595	600	605
Gly	Lys	Gln	Glu	Gln	Glu	Val	Val	Met	Val	Lys	Asp	Phe	Pro	Leu	Val	610	615	620
Thr	Glu	Thr	Ser	Leu	Glu	Val	Tyr	Ala	Arg	Glu	Val	Ala	Ala	Leu	Leu	625	630	635
Val	Glu	Ile	Gln	Ala	Phe	Gln	Gln	Pro	Ile	Leu	Val	Leu	Phe	Thr	Ala	645	650	655
Lys	Asp	Met	Leu	Leu	Ala	Val	Ser	Asp	Leu	Leu	Thr	Val	Ser	His	Leu	660	665	670
Ala	Gln	Tyr	Lys	Asn	Gly	Asp	Val	His	Gln	Leu	Lys	Lys	Arg	Phe	Glu	675	680	685
Lys	Gly	Glu	Gln	Gln	Ile	Leu	Leu	Gly	Ala	Ala	Ser	Phe	Trp	Glu	Gly	690	695	700
Val	Asp	Phe	Ser	Ser	His	Pro	Phe	Val	Ile	Gln	Val	Val	Pro	Arg	Leu	705	710	715
Pro	Phe	Gln	Asn	Pro	Gln	Glu	Pro	Leu	Thr	Lys	Lys	Ile	Asn	Gln	Glu	725	730	735
Leu	Asn	Gln	Glu	Gly	Lys	Asn	Ala	Phe	Tyr	Asp	Tyr	Gln	Leu	Pro	Met	740	745	750
Ala	Ile	Ile	Arg	Leu	Lys	Gln	Ala	Leu	Gly	Arg	Ser	Met	Arg	Arg	Glu	755	760	765
Tyr	Gln	Arg	Ser	Leu	Thr	Leu	Ile	Leu	Asp	Arg	Arg	Ile	Val	Gly	Lys	770	775	780
Arg	Tyr	Gly	Lys	Gln	Ile	Val	Ala	Ser	Leu	Ala	Glu	Glu	Ala	Thr	Val	785	790	795
Lys	Thr	Ile	Ser	Arg	Ser	Glu	Val	Asp	Glu	Ala	Ile	Asp	Arg	Phe	Phe	805	810	815
Asn	Glu	Leu																

(2) INFORMATION FOR SEQ ID NO:4726:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 215 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...215

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4726:

```
Arg Ile Val Phe Asn Gly Cys Arg Gly Arg Gly Arg Arg Phe Arg Ile
1      5      10      15
Gly Tyr Leu Lys Gly Lys Arg Met Ile Lys Lys Val Thr Ile Glu Lys
20      25      30
Ile Lys Ser Pro Glu Arg Phe Leu Glu Val Pro Leu Leu Thr Lys Glu
35      40      45
Glu Val Gly Gln Ala Ile Asp Lys Val Ile Arg Gln Leu Glu Leu Asn
50      55      60
Leu Asp Tyr Phe Lys Glu Asp Phe Pro Thr Pro Ala Thr Phe Asp Asn
65      70      75      80
Val Tyr Pro Ile Met Asp Asn Thr Glu Trp Thr Asn Gly Phe Trp Thr
85      90      95
Gly Glu Leu Trp Leu Ala Tyr Glu Tyr Ser Gln Gln Asp Ala Phe Lys
100      105      110
Asn Ile Ala His Lys Asn Val Leu Ser Phe Leu Asp Arg Val Asn Lys
115      120      125
Arg Val Glu Leu Asp His His Asp Leu Gly Phe Leu Tyr Thr Pro Ser
130      135      140
Cys Met Ala Glu Tyr Lys Ile Asn Gly Asp Gly Glu Ala Arg Glu Ala
145      150      155      160
Thr Leu Lys Ala Ala Asp Lys Leu Ile Glu Arg Tyr Gln Glu Lys Gly
165      170      175
Gly Phe Ile Gln Ala Trp Gly Asp Leu Gly Lys Lys Glu His Tyr Arg
180      185      190
Leu Ile Ile Asp Cys Leu Leu Asn Ile Gln Leu Leu Phe Phe Ala Tyr
195      200      205
Gln Glu Thr Gly Asp Gln Lys
210      215
```

(2) INFORMATION FOR SEQ ID NO:4727:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 81 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...81

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4727:

```
Lys Thr Ile Ile Lys Ser Asn Ile Tyr Asp Thr Asn Gln Lys Gly Asp
1      5      10      15
Gln Met Asn Arg Val Lys Glu Phe Arg Lys Glu Leu Gly Ile Ser Gln
20      25      30
```

Leu	Glu	Leu	Ala	Lys	Asp	Ile	Gly	Val	Ser	Arg	Gln	Thr	Ile	Asn	Met
		35					40					45			
Ile	Glu	Asn	Asp	Lys	Tyr	Asn	Pro	Thr	Leu	Glu	Leu	Cys	Leu	Asn	Leu
	50					55				60					
Ala	Arg	Ser	Leu	Gln	Thr	Asp	Leu	Asn	Ser	Leu	Phe	Trp	Lys	Glu	Asp
65					70					75					80
Phe															

(2) INFORMATION FOR SEQ ID NO:4728:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 751 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...751

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4728:

Ser	Gly	Ile	Ile	Leu	Phe	Arg	Lys	Asn	Ile	Leu	Glu	Lys	Ser	Met	His
1				5					10					15	
Met	Ile	Ala	Leu	Glu	Glu	Lys	Ile	Thr	Ile	Leu	Pro	Thr	Leu	Phe	Val
		20						25					30		
Glu	Lys	Arg	Asp	Gly	Arg	Arg	Val	Val	Phe	Asp	Val	Asp	Lys	Ile	Asp
		35					40					45			
Lys	Ala	Leu	His	Lys	Ala	Ala	Asp	Lys	Val	Met	Asp	Val	Thr	Pro	Leu
	50				55					60					
Val	Glu	Lys	Arg	Leu	Asn	Asp	Leu	Thr	Glu	Arg	Ile	Ile	Thr	Glu	Ile
65					70				75						80
His	Ser	Arg	Phe	Pro	Gln	Gly	Ile	Lys	Ile	Tyr	Glu	Ile	Gln	Asn	Ile
			85					90					95		
Val	Glu	His	Glu	Leu	Leu	Glu	Ala	Lys	Glu	Tyr	Ala	Leu	Ala	Glu	Glu
		100						105					110		
Tyr	Ile	Thr	Tyr	Arg	Thr	Gln	Arg	Asp	Phe	Glu	Arg	Ser	Lys	Ala	Thr
		115					120					125			
Asp	Ile	Asn	Phe	Ser	Ile	His	Lys	Leu	Leu	Asn	Lys	Asp	Gln	Thr	Val
	130					135				140					
Val	Asn	Glu	Asn	Ala	Asn	Lys	Asp	Ser	Asp	Val	Phe	Asn	Thr	Gln	Arg
145				150					155						160
Asp	Leu	Thr	Ala	Gly	Ile	Val	Gly	Lys	Ser	Ile	Gly	Leu	Gln	Met	Leu
			165					170					175		
Pro	Lys	His	Val	Ala	Asn	Ala	His	Gln	Lys	Gly	Asp	Ile	His	Tyr	His
		180					185					190			
Asp	Leu	Asp	Tyr	Ser	Pro	Tyr	Thr	Pro	Met	Thr	Asn	Cys	Cys	Leu	Ile
	195					200				205					
Asp	Phe	Lys	Gly	Met	Leu	Glu	Asn	Gly	Phe	Lys	Ile	Gly	Asn	Ala	Glu
210						215					220				

Val	Glu	Ser	Pro	Lys	Ser	Ile	Gln	Thr	Ala	Thr	Ala	Gln	Ile	Ser	Gln
225					230					235					240
Ile	Ile	Ala	Asn	Val	Ala	Ser	Ser	Gln	Tyr	Gly	Gly	Cys	Ser	Ala	Asp
			245						250					255	
Arg	Ile	Asp	Glu	Ile	Leu	Ala	Pro	Tyr	Ala	Glu	Lys	Asn	Tyr	Gln	Lys
		260						265					270		
His	Leu	Lys	Asp	Ala	Glu	Glu	Trp	Val	Leu	Pro	Glu	Lys	Arg	Glu	Asp
	275						280					285			
Tyr	Ala	Trp	Lys	Lys	Thr	Gln	Lys	Asp	Ile	Tyr	Asp	Ala	Met	Gln	Ser
	290					295					300				
Leu	Glu	Tyr	Glu	Ile	Asn	Thr	Leu	Phe	Thr	Ser	Asn	Gly	Gln	Thr	Pro
305					310					315					320
Phe	Thr	Ser	Leu	Gly	Phe	Gly	Leu	Gly	Thr	Ser	Arg	Phe	Glu	Arg	Glu
			325						330					335	
Ile	Gln	Lys	Ala	Ile	Leu	Asn	Ile	Arg	Ile	Lys	Gly	Leu	Gly	Ser	Glu
			340					345					350		
His	Arg	Thr	Ala	Ile	Phe	Pro	Lys	Leu	Ile	Phe	Thr	Leu	Lys	Arg	Gly
		355					360					365			
Leu	Asn	Leu	Glu	Glu	Gly	Thr	Pro	Asn	Tyr	Asp	Ile	Lys	Gln	Leu	Ala
	370					375					380				
Leu	Glu	Cys	Ala	Thr	Lys	Arg	Met	Tyr	Pro	Asp	Val	Leu	Ser	Tyr	Asp
385					390					395					400
Lys	Ile	Val	Asp	Leu	Thr	Gly	Ser	Phe	Lys	Val	Pro	Met	Gly	Cys	Arg
				405					410					415	
Ser	Phe	Leu	Gln	Gly	Trp	Lys	Asp	Glu	Asn	Gly	Val	Glu	Val	Asn	Ser
			420					425					430		
Gly	Arg	Met	Asn	Leu	Gly	Val	Val	Thr	Val	Asn	Leu	Pro	Arg	Ile	Ala
		435					440					445			
Leu	Glu	Ser	Glu	Gly	Asp	Met	Asn	Lys	Phe	Trp	Glu	Ile	Phe	Asn	Glu
	450					455					460				
Arg	Met	Asn	Ile	Ala	Glu	Asp	Ala	Leu	Val	Tyr	Arg	Val	Glu	Arg	Thr
465					470					475					480
Lys	Glu	Ala	Thr	Pro	Ala	Asn	Ala	Pro	Ile	Leu	Tyr	Gln	Tyr	Gly	Ala
				485				490						495	
Phe	Gly	His	Arg	Leu	Gly	Lys	Glu	Glu	Ser	Val	Asp	Gln	Leu	Phe	Lys
		500					505					510			
Asn	Arg	Arg	Ala	Thr	Val	Ser	Leu	Gly	Tyr	Ile	Gly	Leu	Tyr	Glu	Val
	515					520						525			
Ala	Thr	Val	Phe	Phe	Gly	Asn	Ser	Trp	Glu	Ser	Asn	Pro	Asp	Ala	Lys
	530					535					540				
Glu	Phe	Thr	Leu	Asp	Ile	Ile	His	Asp	Met	Lys	Arg	Arg	Val	Glu	Glu
545					550					555					560
Trp	Ser	Asp	Gln	Tyr	Gly	Tyr	His	Phe	Ser	Ile	Tyr	Ser	Thr	Pro	Ser
			565					570						575	
Glu	Ser	Leu	Thr	Asp	Arg	Phe	Cys	Arg	Leu	Asp	Ile	Asp	Lys	Phe	Gly
		580						585				590			
Ser	Ile	Pro	Asp	Ile	Thr	Asp	Lys	Glu	Tyr	Tyr	Thr	Asn	Ser	Phe	His
	595					600						605			
Tyr	Asp	Val	Arg	Lys	Asn	Pro	Thr	Pro	Phe	Glu	Lys	Leu	Asp	Phe	Glu
	610				615					620					
Lys	Val	Tyr	Pro	Glu	Ala	Gly	Ala	Ser	Gly	Gly	Phe	Ile	His	Tyr	Cys
625					630					635					640
Glu	Tyr	Pro	Val	Leu	Gln	Gln	Asn	Pro	Lys	Ala	Leu	Glu	Ala	Val	Trp
			645					650						655	
Asp	Tyr	Ala	Tyr	Asp	Arg	Val	Gly	Tyr	Leu	Gly	Thr	Asn	Thr	Pro	Ile
		660						665					670		

Asp	Arg	Cys	Tyr	Lys	Cys	Asp	Phe	Glu	Gly	Asp	Phe	Glu	Pro	Thr	Glu
		675					680					685			
Arg	Gly	Phe	Ala	Cys	Pro	Asn	Cys	Gly	Asn	Ser	Asp	Pro	Lys	Thr	Val
	690					695					700				
Asp	Val	Val	Lys	Arg	Thr	Cys	Gly	Tyr	Leu	Gly	Asn	Pro	Gln	Ala	Arg
705					710					715					720
Pro	Met	Val	Asn	Gly	Arg	His	Lys	Glu	Ile	Ala	Ala	Arg	Val	Lys	His
			725						730					735	
Met	Asn	Gly	Ser	Thr	Ile	Lys	Ile	Ala	Gly	His	Gln	Val	Thr	Asn	
		740						745					750		

(2) INFORMATION FOR SEQ ID NO:4729:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 61 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...61

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4729:

Glu	Ser	Ser	Phe	Ser	Ser	Phe	Tyr	Tyr	Ser	Thr	Phe	Leu	Asn	Leu	Gly
1				5				10						15	
Leu	Leu	Asp	Ser	Met	Leu	Leu	Ser	Ile	Tyr	Ser	Glu	Lys	Lys	Ala	Phe
		20					25					30			
Leu	Gln	Lys	Lys	Ala	Asn	Ser	Leu	Phe	Glu	Ile	Phe	Ser	Ser	Leu	Leu
		35				40					45				
Asp	Ser	Pro	Val	Tyr	Leu	Cys	Tyr	Asn	Glu	Arg	Arg	Ile			
50						55					60				

(2) INFORMATION FOR SEQ ID NO:4730:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 139 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...139

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4730:

Gln	Gln	Ile	Ile	Lys	Met	Leu	Phe	Leu	Ser	His	Lys	Lys	Ala	Val	Ser
1				5					10					15	
Ile	Lys	Glu	Arg	Gly	Gly	Leu	Ile	Leu	Leu	His	Cys	Cys	Ser	Arg	Cys
			20					25					30		
Asp	Phe	Phe	Glu	Arg	Lys	Asn	Lys	Met	Lys	Thr	Lys	Lys	His	Arg	Leu
		35				40						45			
Leu	Ala	Leu	Ala	Leu	Ile	Ser	Ser	Phe	Thr	Leu	Leu	Gly	Ala	Ala	Ser
	50					55					60				
Ala	Ala	Val	Gln	Tyr	Pro	Asp	Gly	Gly	Val	Trp	Thr	Tyr	Gly	Glu	Gly
65					70				75					80	
Ser	Gly	Gly	Gly	Trp	Ala	Phe	Ser	Asn	Tyr	Tyr	His	Gly	Lys	Lys	Tyr
				85				90						95	
His	Tyr	Ser	Ser	Leu	Val	Ser	Arg	Trp	Asn	Ser	His	Ser	Asp	Lys	Gly
		100						105					110		
Glu	Ala	Pro	Ala	Gly	Lys	Thr	Ser	Tyr	Ala	Trp	Ile	Trp	Thr	Lys	Trp
		115					120					125			
Gly	Glu	Gln	Val	Ala	Phe	Tyr	Cys	Asp	Tyr	Asp					
	130						135								

(2) INFORMATION FOR SEQ ID NO:4731:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 439 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...439

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4731:

Glu	Glu	Ile	Met	Ser	Met	Phe	Leu	Asp	Thr	Ala	Lys	Ile	Lys	Val	Lys
1				5					10					15	
Ala	Gly	Asn	Gly	Gly	Asp	Gly	Met	Val	Ala	Phe	Arg	Arg	Glu	Lys	Tyr
			20					25					30		
Val	Pro	Asn	Gly	Gly	Pro	Trp	Gly	Gly	Asp	Gly	Gly	Arg	Gly	Gly	Asn
			35				40						45		
Val	Val	Phe	Val	Val	Asp	Glu	Gly	Leu	Arg	Thr	Leu	Met	Asp	Phe	Arg
	50					55					60				
Tyr	Asn	Arg	His	Phe	Lys	Ala	Asp	Ser	Gly	Glu	Lys	Gly	Met	Thr	Lys
65					70				75					80	
Gly	Met	His	Gly	Arg	Gly	Ala	Glu	Asp	Leu	Arg	Val	Arg	Val	Ser	Gln
				85				90						95	

Gly	Thr	Thr	Val	Arg	Asp	Ala	Glu	Thr	Gly	Lys	Val	Leu	Thr	Asp	Leu
			100					105					110		
Ile	Lys	His	Gly	Gln	Glu	Phe	Ile	Val	Ala	His	Gly	Gly	Arg	Gly	Gly
		115					120					125			
Arg	Gly	Asn	Ile	Arg	Phe	Ala	Thr	Pro	Lys	Asn	Pro	Ala	Pro	Glu	Ile
	130					135					140				
Ser	Glu	Asn	Gly	Glu	Pro	Gly	Gln	Glu	Arg	Glu	Leu	Gln	Leu	Glu	Leu
145					150					155					160
Lys	Ile	Leu	Ala	Asp	Val	Gly	Leu	Val	Gly	Phe	Pro	Ser	Val	Gly	Lys
				165					170					175	
Ser	Thr	Leu	Leu	Ser	Val	Ile	Thr	Ser	Ala	Lys	Pro	Lys	Ile	Gly	Ala
		180					185						190		
Tyr	His	Phe	Thr	Thr	Ile	Val	Pro	Asn	Leu	Gly	Met	Val	Arg	Thr	Gln
		195				200						205			
Ser	Gly	Glu	Ser	Phe	Ala	Val	Ala	Asp	Leu	Pro	Gly	Leu	Ile	Glu	Gly
	210					215					220				
Ala	Ser	Gln	Gly	Val	Gly	Leu	Gly	Thr	Gln	Phe	Leu	Arg	His	Ile	Glu
225					230					235					240
Arg	Thr	Arg	Val	Ile	Leu	His	Ile	Ile	Asp	Met	Ser	Ala	Ser	Glu	Gly
				245					250					255	
Arg	Asp	Pro	Tyr	Glu	Asp	Tyr	Leu	Ala	Ile	Asn	Lys	Glu	Leu	Glu	Ser
		260					265					270			
Tyr	Asn	Leu	Arg	Leu	Met	Glu	Arg	Pro	Gln	Ile	Ile	Val	Ala	Asn	Lys
	275					280						285			
Met	Asp	Met	Pro	Glu	Ser	Gln	Glu	Asn	Leu	Glu	Glu	Phe	Lys	Lys	Lys
	290					295					300				
Leu	Ala	Glu	Asn	Tyr	Asp	Glu	Phe	Glu	Glu	Leu	Pro	Ala	Ile	Phe	Pro
305					310					315					320
Ile	Ser	Gly	Leu	Thr	Lys	Gln	Gly	Leu	Ala	Thr	Leu	Leu	Asp	Ala	Thr
				325					330					335	
Ala	Glu	Leu	Leu	Asp	Lys	Thr	Pro	Glu	Phe	Leu	Leu	Tyr	Asp	Glu	Ser
			340					345					350		
Asp	Met	Glu	Glu	Glu	Ala	Tyr	Tyr	Gly	Phe	Asp	Glu	Glu	Glu	Lys	Ala
		355				360						365			
Phe	Glu	Ile	Ser	Arg	Asp	Asp	Asp	Ala	Thr	Trp	Val	Leu	Ser	Gly	Glu
	370					375					380				
Lys	Leu	Met	Lys	Leu	Phe	Asn	Met	Thr	Asn	Phe	Asp	Arg	Asp	Glu	Ser
385					390					395					400
Val	Met	Lys	Phe	Ala	Arg	Gln	Leu	Arg	Gly	Met	Gly	Val	Asp	Glu	Ala
				405					410					415	
Leu	Arg	Ala	Arg	Gly	Ala	Lys	Asp	Gly	Asp	Leu	Val	Arg	Ile	Gly	Lys
		420					425						430		
Phe	Glu	Phe	Glu	Phe	Val	Asp									
			435												

(2) INFORMATION FOR SEQ ID NO:4732:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...74

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4732:

```
Pro Thr Ser Phe Ser Phe His Thr Leu Gln Lys Ser Leu Gln Thr Ala
1          5          10          15
Ser Thr Ser Pro Trp Pro Leu Tyr Met Leu Leu Thr Ser Ser Val Leu
          20          25          30
Ser Ala Thr Ser Lys Gln Cys Phe Glu Leu Thr Ser Ser Val Leu Ser
          35          40          45
Ala Thr Ser Lys Gln Cys Phe Glu Gln Pro Ala Ala Ser Phe Leu Val
          50          55          60
Cys Ser Leu Ile Phe Ile Glu Tyr Gln Ile
65          70
```

(2) INFORMATION FOR SEQ ID NO:4733:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4733:

```
His Leu Ile Ile Cys Val Phe Ser Lys Trp Ile Ser Arg Val Glu Asp
1          5          10          15
Phe Ser His Ile Ile Leu Phe Glu Asn Leu Cys Lys Leu Arg Gln Leu
          20          25          30
Pro Ser Ala Thr Ser Lys Gln Tyr Phe Glu Leu Thr Ser Ser Val Leu
          35          40          45
Ser Ala Thr Ser Lys Gln Tyr Phe Glu Leu Thr Ser Ser Val Leu Ser
          50          55          60
Ala Thr Ser Lys Gln Tyr Phe Glu Leu Thr Ser Ser Val Leu Ser Ala
65          70          75          80
Thr Ser Lys Gln Tyr Phe Glu Leu Thr Ser Ser Val Leu Ser Ala Thr
          85          90          95
Ser Lys Gln Tyr Phe Glu Leu Thr Ser Ser Val Leu Ser Ala Thr Ser
          100          105          110
Lys Gln Tyr Phe Glu Leu Thr Ser Ser Val Leu Ser Ala Thr Ser Lys
          115          120          125
Gln Tyr Phe Glu Leu Thr Ser Ser Val Leu Ser Thr Thr Ser Lys Gln
130          135          140
```

Cys	Phe	Glu	Gln	Pro	Val	Ala	Ser	Phe	Leu	Val	Cys	Ala	Leu	Ile	Phe
145					150					155					160
Ile	Glu	Tyr	Lys	Gly	Lys	Tyr	Ser	Glu	Leu	Lys					
				165						170					

(2) INFORMATION FOR SEQ ID NO:4734:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...90
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4734:

Ser	Thr	Ile	Met	Ile	Phe	Leu	Ile	Arg	Met	Ile	Tyr	Asn	Ala	Val	Asp
1				5					10					15	
Ile	Tyr	Ser	Leu	Ile	Leu	Ile	Ala	Phe	Ala	Val	Met	Ser	Trp	Phe	Pro
			20					25					30		
Gly	Ala	Tyr	Glu	Ser	Ser	Leu	Gly	Arg	Trp	Ile	Val	Ala	Leu	Val	Lys
		35					40					45			
Pro	Val	Leu	Ala	Pro	Leu	Gln	Arg	Leu	Pro	Leu	Gln	Ile	Ala	Gly	Leu
		50				55					60				
Asp	Leu	Ser	Val	Trp	Val	Ala	Ile	Val	Leu	Val	Arg	Phe	Leu	Gly	Glu
65					70					75					80
Asn	Leu	Val	Arg	Phe	Leu	Ala	Met	Ile	Gly						
				85					90						

(2) INFORMATION FOR SEQ ID NO:4735:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...93
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4735:

```

Ile Glu Val Ile Arg Met Arg Leu Asp Lys Tyr Leu Lys Val Ser Arg
1      5      10      15
Ile Ile Lys Arg Arg Thr Val Ala Lys Glu Val Ala Asp Lys Gly Arg
20      25      30
Ile Lys Val Asn Gly Ile Leu Ala Lys Ser Ser Thr Asp Leu Lys Val
35      40      45
Asn Asp Gln Val Glu Ile Arg Phe Gly Asn Lys Leu Leu Leu Val Lys
50      55      60
Val Leu Glu Met Lys Asp Ser Thr Lys Lys Glu Asp Ala Ala Gly Met
65      70      75      80
Tyr Glu Ile Ile Ser Glu Thr Arg Val Glu Glu Asn Val
85      90

```

(2) INFORMATION FOR SEQ ID NO:4736:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 185 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...185
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4736:

```

Arg Leu Ser Phe Thr Ser Ala Leu Phe Leu Leu Lys Met Arg Lys Phe
1      5      10      15
Arg Tyr Asn Ser Gln Thr Arg Ser Arg Phe Lys Glu Arg Gly Gly Phe
20      25      30
Val Met Arg Phe Lys Asn Thr Ser Asp His Ile Glu Ala Tyr Ile Lys
35      40      45
Ala Ile Leu Asp Gln Ser Gly Ile Val Glu Leu Gln Arg Ser Gln Leu
50      55      60
Ala Asp Thr Phe Gln Val Val Pro Ser Gln Ile Asn Tyr Val Ile Lys
65      70      75      80
Thr Arg Phe Thr Glu Ser Arg Gly Tyr Leu Val Glu Ser Lys Arg Gly
85      90      95
Gly Gly Gly Tyr Ile Arg Ile Gly Arg Ile Glu Phe Ser Ser His His
100      105      110
Glu Met Leu Arg Glu Leu Leu Tyr Ser Ile Gly Glu Arg Val Ser Gln
115      120      125
Glu Ile Tyr Glu Asp Ile Leu Gln Leu Leu Val Glu Gln Glu Leu Met
130      135      140
Thr Lys Gln Glu Met Asn Leu Leu Glu Ser Val Ala Leu Asp Arg Val
145      150      155      160
Leu Gly Glu Glu Ala Pro Val Val Arg Ala Asn Met Leu Arg Gln Ile
165      170      175
Ile Gln Glu Val Asp Arg Lys Gly Lys

```

(2) INFORMATION FOR SEQ ID NO:4737:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4737:

```

Leu Lys Ser Phe Ser Lys Asn His Leu Phe Leu Ile Phe Asn Pro Ile
1      5      10      15
Cys Cys Met Ile Arg Glu Lys Lys Gly Asp Arg Asp Met Ala Phe Thr
      20      25      30
Asn Thr His Met Arg Ser Ala Ser Phe Gly Ile Val Thr Ser Leu Pro
      35      40      45
Asp Asp Ile Ile Asp Ser Phe Trp Tyr Ile Ile Asp His Phe Leu Lys
      50      55      60
Asn Val Phe Glu Leu Glu Glu Glu Leu Glu Phe Gln Leu Leu Asn Asn
65      70      75      80
Gln Gly Lys Ile Thr Phe His Phe Ser Ser Gln His Leu Pro Thr Ala
      85      90      95
Ile Asp Phe Asp Phe Asn His Pro Phe Asp Pro Arg Tyr Pro Pro Arg
      100     105     110
Val Leu Val Leu Asp Met Asp Gly Arg Glu Thr Ile Leu Leu Pro Glu
      115     120     125
Glu Asn Asp Leu Phe
      130

```

(2) INFORMATION FOR SEQ ID NO:4738:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 144 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4738:

Val	Ile	Ser	Met	Leu	Ile	Gly	Ile	Pro	Lys	Glu	Ile	Lys	Asn	Asn	Glu
1				5					10					15	
Asn	Arg	Val	Ala	Leu	Thr	Pro	Ala	Gly	Val	His	Ser	Leu	Val	Ser	Arg
			20					25					30		
Gly	His	Arg	Val	Leu	Ile	Glu	Thr	Asn	Ala	Gly	Leu	Gly	Ser	Gly	Phe
			35					40					45		
Thr	Asp	Ala	Asp	Tyr	Gln	Lys	Gln	Gly	Ala	Glu	Ile	Val	Ala	Thr	Ala
			50				55					60			
Gly	Glu	Ala	Trp	Ala	Ala	Glu	Leu	Val	Val	Lys	Val	Lys	Glu	Pro	Leu
65					70					75					80
Ser	Ser	Glu	Tyr	Gly	Tyr	Phe	Arg	Asp	Asp	Leu	Leu	Leu	Phe	Thr	Tyr
					85				90					95	
Leu	His	Met	Ala	Ala	Ala	Pro	Glu	Leu	Ala	Asp	Ala	Met	Leu	Ala	Ala
			100					105					110		
Lys	Thr	Thr	Gly	Ile	Ala	Tyr	Glu	Thr	Val	Arg	Asp	Asn	Gln	Gly	Gln
			115				120					125			
Leu	Pro	Leu	Leu	Val	Pro	Met	Ser	Glu	Val	Ala	Asp	Arg	Met	Ala	Val
			130				135					140			

(2) INFORMATION FOR SEQ ID NO:4739:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4739:

Lys	Tyr	Ser	Ile	Tyr	Lys	Leu	Lys	Cys	Asp	Arg	Asn	Glu	Asn	Lys	Gly
1				5				10						15	
Asp	Val	Gly	Lys	Lys	Ala	Glu	Asn	Leu	Ile	Gln	Gly	Gln	Phe	Glu	Gly
			20					25					30		
Ser	Lys	Ala	Met	Glu	Lys	Cys	Tyr	Thr	Asp	Val	Thr	Glu	Phe	Ala	Ile
			35				40					45			
Pro	Ala	Ser	Thr	Gln	Lys	Leu	Tyr	Leu	Ser	Pro	Val	Leu	Asp	Gly	Phe
			50				55				60				
Asn	Ser	Glu	Ile	Ile	Ala	Tyr	Asn	Leu	Ser	Thr	Ser	Pro	Asn	Leu	Glu
65					70					75					80
Gln	Val	Lys	Ser	Met	Leu	Glu	Gln	Ala	Phe	Thr	Glu	Lys	His	Tyr	Glu
				85					90					95	
Asn	Thr	Ile	Leu	His	Ser	Asp	Gln	Gly	Trp	Gln	Tyr	Arg	His	Asp	Ser
			100					105					110		

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Tyr His Arg Phe Leu Glu Ser Lys Gly Ile Gln Ala Ser Met Ser Arg
    115                120                125
Lys Gly Asn Ser Pro Asp Asn Gly Met Met Glu Ser Phe Phe Gly Ile
    130                135                140
Leu Lys Ser Glu Met Phe Tyr Gly Phe Glu Lys Ser Phe Gln Ser Leu
    145                150                155                160
Lys Gln Leu Glu Gln Ala Ile Ile Asp Tyr Ile Asp Tyr Tyr Asn Asn
                165                170                175
Lys Arg Ile Lys Val Lys Leu Lys Gly Leu Ile Pro Val Gln Tyr Arg
    180                185                190
Thr Lys Ser Phe Gly
    195

```

(2) INFORMATION FOR SEQ ID NO:4740:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 136 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4740:

```

Lys Tyr Ser Ile Tyr Lys Leu Lys Cys Asp Arg Asn Glu Asn Lys Gly
1      5      10      15
Asp Val Gly Lys Lys Ala Glu Asn Leu Ile Gln Gly Gln Phe Glu Gly
    20      25      30
Ser Lys Thr Met Glu Lys Cys Tyr Thr Asp Val Thr Glu Phe Ala Ile
    35      40      45
Pro Ala Ser Thr Gln Lys Leu Tyr Leu Ser Pro Val Leu Asp Gly Phe
    50      55      60
Asn Ser Glu Ile Ile Ala Tyr Asn Leu Ser Thr Ser Pro Asn Leu Glu
    65      70      75      80
Gln Val Gln Thr Met Leu Glu Gln Ala Phe Thr Glu Lys Tyr Tyr Glu
    85      90      95
Asn Thr Ile Leu His Ser Asp Gln Gly Trp Gln Tyr Arg His Asp Ser
    100     105     110
Tyr His Arg Phe Leu Arg Val Arg Glu Phe Lys His Leu Cys His Ala
    115     120     125
Arg Glu Thr Ala Lys Thr Thr Val
    130     135

```

(2) INFORMATION FOR SEQ ID NO:4741:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 197 amino acids
 - (B) TYPE: amino acid

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...197
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4741:

Lys	Tyr	Ser	Ile	Tyr	Lys	Leu	Lys	Cys	Asp	Arg	Asn	Glu	Asn	Lys	Gly
1				5					10					15	
Asp	Val	Gly	Lys	Lys	Ala	Glu	Asn	Leu	Ile	Gln	Gly	Gln	Phe	Glu	Gly
			20					25					30		
Ser	Lys	Thr	Met	Glu	Gln	Cys	Tyr	Ile	Asp	Val	Thr	Glu	Phe	Ala	Ile
		35					40					45			
Pro	Ala	Ser	Thr	Gln	Lys	Leu	Tyr	Leu	Ser	Pro	Val	Leu	Asp	Gly	Phe
	50					55					60				
Asn	Ser	Glu	Ile	Ile	Ala	Tyr	Asn	Leu	Ser	Thr	Ser	Pro	Asn	Leu	Glu
65					70					75					80
Gln	Val	Gln	Thr	Met	Leu	Glu	Gln	Ala	Phe	Lys	Glu	Lys	His	Tyr	Glu
				85					90					95	
Asn	Thr	Ile	Leu	His	Ser	Asp	Gln	Gly	Trp	Gln	Tyr	Arg	His	Asp	Ser
			100					105					110		
Tyr	His	Arg	Phe	Leu	Glu	Ser	Lys	Gly	Ile	Gln	Ala	Ser	Met	Ser	Arg
		115					120					125			
Lys	Gly	Asn	Ser	Pro	Asp	Asn	Gly	Met	Met	Glu	Ser	Phe	Phe	Gly	Ile
	130					135					140				
Leu	Lys	Ser	Glu	Met	Phe	Tyr	Gly	Tyr	Glu	Lys	Ser	Phe	Gln	Ser	Leu
145					150					155					160
Lys	Gln	Leu	Glu	Gln	Ala	Ile	Val	Asp	Tyr	Ile	Asp	Tyr	Tyr	Asn	Asn
				165				170						175	
Lys	Arg	Ile	Lys	Val	Lys	Leu	Lys	Gly	Leu	Ser	Pro	Val	Gln	Tyr	Arg
			180					185					190		
Thr	Lys	Ser	Phe	Gly											
			195												

(2) INFORMATION FOR SEQ ID NO:4742:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 366 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...366

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4742:

Thr	Ser	Ser	Ile	Pro	Met	Ile	Trp	Ser	Gln	Trp	Pro	Asn	Lys	Leu	Phe
1				5					10					15	
Leu	Lys	Gln	His	Leu	Ala	Ile	Ser	Ser	Ser	Gly	Ala	Glu	Asp	Thr	Leu
			20					25					30		
Thr	Leu	Arg	Glu	Asn	Ile	Arg	Ala	Phe	Asn	His	Lys	Leu	Ile	Val	Pro
		35					40					45			
His	Thr	Leu	Cys	Asp	Val	Glu	Asn	Pro	Ser	Thr	Glu	Ile	Glu	Phe	Ala
	50					55					60				
Gly	Glu	Lys	Leu	Ser	Ser	Pro	Ile	Ile	Met	Ala	Pro	Val	Ala	Ala	His
65					70					75					80
Lys	Leu	Ala	Asn	Glu	Gln	Gly	Glu	Val	Ala	Thr	Ala	Arg	Gly	Val	His
			85						90					95	
Glu	Phe	Gly	Ser	Leu	Tyr	Thr	Thr	Ser	Ser	Tyr	Ser	Thr	Val	Asp	Leu
			100					105					110		
Pro	Glu	Ile	Ser	Glu	Ala	Leu	Gln	Gly	Thr	Pro	His	Trp	Phe	Gln	Phe
		115					120					125			
Tyr	Phe	Ser	Lys	Asp	Asp	Gly	Ile	Asn	Arg	His	Ile	Met	Asp	Arg	Val
	130					135					140				
Lys	Ala	Glu	Gly	Tyr	Lys	Ala	Ile	Val	Leu	Thr	Ala	Asp	Ala	Thr	Val
145					150					155					160
Gly	Gly	Asn	Arg	Glu	Val	Asp	Lys	Arg	Asn	Gly	Phe	Val	Phe	Pro	Val
			165						170					175	
Gly	Met	Pro	Ile	Val	Glu	Glu	Tyr	Leu	Pro	Glu	Gly	Ala	Gly	Lys	Ser
			180					185					190		
Met	Asp	Phe	Val	Tyr	Lys	Ser	Ala	Lys	Gln	Arg	Leu	Ser	Pro	Arg	Asp
	195						200					205			
Val	Glu	Phe	Ile	Ala	Glu	Tyr	Ser	Gly	Leu	Pro	Val	Tyr	Val	Lys	Gly
	210					215					220				
Pro	Gln	Cys	Arg	Glu	Asp	Val	Glu	Arg	Ser	Leu	Ala	Ala	Gly	Ala	Ser
225					230					235					240
Gly	Ile	Trp	Val	Thr	Asn	His	Gly	Gly	Arg	Gln	Ile	Asp	Gly	Gly	Pro
			245						250					255	
Ala	Ala	Phe	Asp	Ser	Leu	Gln	Glu	Val	Ala	Glu	Ala	Val	Asp	Arg	Arg
		260						265					270		
Val	Pro	Ile	Val	Leu	Asn	Ser	Gly	Val	Arg	Arg	Gly	Gln	His	Val	Phe
	275						280					285			
Lys	Ala	Leu	Ala	Ser	Gly	Ala	Asp	Leu	Val	Ala	Ile	Gly	Arg	Pro	Val
	290					295					300				
Ile	Tyr	Gly	Leu	Ala	Leu	Gly	Gly	Ser	Val	Gly	Val	Arg	Gln	Val	Phe
305					310					315					320
Glu	His	Leu	Asn	Ala	Glu	Leu	Lys	Thr	Val	Met	Gln	Leu	Ser	Gly	Ala
			325						330					335	
Gln	Thr	Ile	Glu	Asp	Val	Lys	His	Phe	Lys	Leu	Arg	His	Asn	Pro	Tyr
		340						345					350		
Asn	Pro	Thr	Phe	Pro	Val	Asp	Pro	Arg	Asp	Leu	Lys	Leu	Tyr		
		355					360					365			

(2) INFORMATION FOR SEQ ID NO:4743:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 75 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4743:

Val	Leu	Ser	Ile	Val	Leu	Ala	Ile	Ser	Pro	Pro	Arg	Ala	Ser	Thr	Ser
1				5					10					15	
Arg	Thr	Thr	Ile	Pro	Leu	Ala	Glu	Pro	Pro	Ile	Glu	Gly	Leu	Gln	Gly
			20					25					30		
Met	Lys	Ala	Ser	Ile	Ser	Ile	Leu	Met	Val	Ala	Ser	Arg	Thr	Leu	Gln
		35				40					45				
Pro	Ile	Arg	Leu	Ala	Ala	Lys	Glu	Ala	Ser	Thr	Pro	Ala	Cys	Pro	Ala
	50					55					60				
Pro	Ile	Thr	Ile	Ile	Ser	Tyr	Ser	Ser	Val	Lys					
65				70					75						

(2) INFORMATION FOR SEQ ID NO:4744:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 136 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...136

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4744:

Tyr	Thr	Val	Phe	Met	Thr	Asp	Leu	Ser	Lys	Gln	Leu	Leu	Glu	Lys	Ala
1				5					10					15	
His	Gly	Gly	Leu	Lys	Ile	Asn	Pro	Asp	Glu	Gln	Arg	Arg	Tyr	Leu	Gly
			20					25					30		
Thr	Phe	Glu	Glu	Arg	Val	Leu	Gly	Tyr	Val	Asp	Ile	Asp	Thr	Ala	Asn
		35				40					45				
Ser	Pro	Gln	Leu	Glu	Lys	Gly	Phe	Leu	Phe	Ile	Leu	Glu	Asn	Leu	Gln
	50					55					60				
Glu	Lys	Ala	Glu	Pro	Leu	Phe	Val	Lys	Ile	Ser	Pro	Thr	Ile	Glu	Phe
65					70					75				80	
Asp	Lys	Gln	Val	Phe	Tyr	Leu	Lys	Glu	Ala	Lys	Glu	Thr	Asp	Ser	Gln

				85					90					95		
Ala	Thr	Ile	Val	Ser	Glu	Glu	His	Ile	Thr	Ser	Pro	Phe	Gly	Leu	Val	
			100					105					110			
Ile	His	Ser	Asn	Ala	Pro	Val	Gln	Val	Glu	Glu	Ile	Arg	Pro	Ser	Thr	
		115					120					125				
Cys	Phe	Ser	Lys	Thr	Leu	Gly	Ser									
	130					135										

(2) INFORMATION FOR SEQ ID NO:4745:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 257 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4745:

Val	Lys	Ser	Met	Pro	Arg	Ser	Leu	Cys	Trp	Lys	Asp	Glu	Tyr	Thr	Glu	
1				5				10						15		
Tyr	Met	His	Glu	Ile	Cys	Pro	Gly	Arg	Leu	Thr	Pro	Glu	Val	Thr	Arg	
			20					25					30			
Leu	Leu	Asn	Glu	Lys	Phe	Gly	Thr	Asn	Tyr	Asn	Lys	Ser	Gln	Ile	Gly	
		35				40						45				
Gly	Val	Arg	Lys	Arg	Leu	Gly	Leu	Ala	Val	Gly	Lys	Val	Tyr	Gln	Gly	
	50					55					60					
Arg	Leu	Leu	Thr	Lys	Glu	Gln	His	Asp	Tyr	Leu	Val	Leu	Ile	Gln	Lys	
65				70				75						80		
Asn	Lys	Ile	Ser	Arg	Asn	Val	Ala	Asn	Glu	Met	Asn	Gln	Lys	Phe	Gly	
			85					90						95		
Leu	Ser	Leu	Thr	Glu	Lys	Gln	Ile	Lys	Ser	Tyr	Arg	Arg	Asn	Asn	Asn	
		100						105					110			
Leu	His	Ser	Gly	Leu	Thr	Gly	Arg	Phe	Glu	Lys	Gly	Gln	Thr	Pro	His	
	115					120						125				
Asn	Lys	Gly	Lys	Lys	Tyr	Pro	Asn	Met	Pro	Lys	Asn	Gly	Gly	Gln	Phe	
	130					135					140					
Lys	Lys	Gly	Asn	Arg	Pro	Pro	Asn	Tyr	Val	Pro	Val	Gly	Thr	Ile	Asn	
145				150				155						160		
Tyr	Thr	Thr	Asn	Gly	Tyr	Pro	Lys	Glu	Lys	Ile	Gly	Glu	Pro	Asn	Gln	
			165					170						175		
Trp	Val	Leu	Lys	His	Arg	Lys	Val	Trp	Glu	Asp	His	His	Gly	Leu	Ile	
		180						185					190			
Pro	Lys	Gly	Tyr	Ser	Ile	Val	Phe	Leu	Asp	Gly	Asp	Lys	Thr	Asn	Tyr	
	195					200						205				
Asp	Ile	Ser	Asn	Leu	Ala	Cys	Leu	Ser	Lys	Asn	Glu	Ile	Ala	Arg	Met	
	210					215					220					
Asn	Gln	Asn	His	Leu	Phe	Thr	Ser	Asn	Ala	Asp	Leu	Thr	Lys	Ser	Gly	

225		230		235		240									
Ile	Gly	Leu	Thr	Lys	Leu	Thr	Asn	Lys	Ile	Arg	Glu	Val	Glu	Lys	Asn
		245							250					255	
Gly															

(2) INFORMATION FOR SEQ ID NO:4746:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...64
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4746:

Lys	Phe	Pro	Ile	Leu	Gly	Ser	Lys	Gln	Thr	Pro	Phe	Ile	Thr	Thr	Ser
1				5				10					15		
Ala	Phe	Lys	Leu	Leu	Leu	Ser	Ala	Lys	Glu	Ser	Ser	Ser	Leu	Lys	Lys
			20				25					30			
Ala	Thr	Arg	Arg	Ala	Lys	Asn	Val	Leu	Glu	Lys	Ser	Leu	Ile	Ala	Ser
		35				40					45				
Ala	Ser	Val	Gly	Glu	Thr	Asn	Ile	Thr	Phe	Leu	Ile	Leu	Ala	Val	Leu
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:4747:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 892 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...892
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4747:

Leu	Phe	Pro	Met	Val	Phe	Phe	Asp	Ser	Phe	Leu	Tyr	Asn	Gly	Cys	Met
1				5				10					15		

Asp	Lys	Lys	Lys	Leu	Leu	Leu	Ile	Asp	Gly	Ser	Ser	Val	Ala	Phe	Arg
			20					25					30		
Ala	Phe	Phe	Ala	Leu	Tyr	Gln	Gln	Leu	Asp	Arg	Phe	Lys	Asn	Ala	Ala
		35					40					45			
Gly	Leu	His	Thr	Asn	Ala	Ile	Tyr	Gly	Phe	Gln	Leu	Met	Leu	Ser	His
	50					55					60				
Leu	Leu	Glu	Arg	Val	Glu	Pro	Ser	His	Ile	Leu	Val	Ala	Phe	Asp	Ala
					70					75					80
Gly	Lys	Thr	Thr	Phe	Arg	Thr	Glu	Met	Tyr	Ala	Asp	Tyr	Lys	Gly	Gly
				85					90					95	
Arg	Ala	Lys	Thr	Pro	Asp	Glu	Phe	Arg	Glu	Gln	Phe	Pro	Phe	Ile	Arg
			100					105					110		
Glu	Leu	Leu	Asp	His	Met	Gly	Ile	Arg	His	Tyr	Glu	Leu	Ala	Gln	Tyr
		115					120					125			
Glu	Ala	Asp	Asp	Ile	Ile	Gly	Thr	Leu	Asp	Lys	Leu	Ala	Glu	Gln	Asp
	130					135					140				
Gly	Phe	Asp	Ile	Thr	Ile	Val	Ser	Gly	Asp	Lys	Asp	Leu	Ile	Gln	Leu
	145				150					155					160
Thr	Asp	Glu	His	Thr	Val	Val	Glu	Ile	Ser	Lys	Lys	Gly	Val	Ala	Glu
			165						170					175	
Phe	Glu	Ala	Phe	Thr	Pro	Asp	Tyr	Leu	Met	Glu	Glu	Met	Gly	Leu	Thr
			180					185					190		
Pro	Ala	Gln	Phe	Ile	Asp	Leu	Lys	Ala	Leu	Met	Gly	Asp	Lys	Ser	Asp
		195					200					205			
Asn	Ile	Pro	Gly	Val	Thr	Lys	Val	Gly	Glu	Lys	Thr	Gly	Ile	Lys	Leu
	210					215					220				
Leu	Leu	Glu	His	Gly	Ser	Leu	Glu	Gly	Ile	Tyr	Glu	Asn	Ile	Asp	Gly
	225				230					235					240
Met	Lys	Thr	Ser	Lys	Met	Lys	Glu	Asn	Leu	Ile	Asn	Asp	Lys	Glu	Gln
				245					250					255	
Ala	Phe	Leu	Ser	Lys	Thr	Leu	Ala	Thr	Ile	Asp	Thr	Lys	Ala	Pro	Ile
			260					265					270		
Ala	Ile	Gly	Leu	Glu	Asp	Leu	Val	Tyr	Ser	Gly	Pro	Asp	Val	Glu	Asn
		275					280					285			
Leu	Gly	Lys	Phe	Tyr	Asp	Glu	Met	Gly	Phe	Lys	Gln	Leu	Lys	Gln	Ala
	290					295					300				
Leu	Asn	Val	Ser	Ser	Ala	Asp	Val	Ala	Lys	Gly	Leu	Asp	Phe	Thr	Ile
	305				310					315					320
Val	Asp	Gln	Ile	Ser	Gln	Asp	Met	Leu	Ser	Glu	Glu	Ser	Ile	Phe	His
				325					330					335	
Phe	Glu	Leu	Phe	Gly	Glu	Asn	Tyr	His	Thr	Asp	Asn	Leu	Val	Gly	Phe
			340					345					350		
Ala	Trp	Ser	Cys	Gly	Asp	Lys	Leu	Tyr	Ala	Thr	Asp	Lys	Leu	Glu	Leu
		355					360					365			
Leu	Gln	Asp	Pro	Ile	Phe	Lys	Asp	Phe	Leu	Glu	Lys	Thr	Ser	Leu	Arg
	370					375						380			
Val	Tyr	Asp	Phe	Lys	Lys	Val	Lys	Val	Leu	Leu	Gln	Arg	Phe	Gly	Val
	385				390					395					400
Asp	Leu	Gln	Ala	Pro	Ala	Phe	Asp	Ile	Arg	Leu	Ala	Lys	Tyr	Leu	Leu
				405					410					415	
Ser	Thr	Val	Glu	Asp	Asn	Glu	Ile	Ala	Thr	Ile	Ala	Ser	Leu	Tyr	Gly
			420					425					430		
Gln	Thr	Tyr	Leu	Val	Asp	Asp	Glu	Thr	Phe	Tyr	Gly	Lys	Gly	Val	Lys
		435					440					445			
Lys	Ala	Ile	Pro	Glu	Arg	Glu	Lys	Phe	Leu	Glu	His	Leu	Ala	Cys	Lys
	450					455					460				
Leu	Ala	Val	Leu	Val	Glu	Thr	Glu	Pro	Ile	Leu	Leu	Glu	Lys	Leu	Ser

465					470					475				480
Glu	Asn	Gly	Gln	Leu	Glu	Leu	Leu	Tyr	Asp	Met	Glu	Gln	Pro	Leu
				485					490					495
Phe	Val	Leu	Ala	Lys	Met	Glu	Ile	Ala	Gly	Ile	Val	Val	Lys	Lys
			500					505					510	
Thr	Leu	Leu	Glu	Met	Gln	Ala	Glu	Asn	Glu	Leu	Val	Ile	Glu	Lys
			515				520					525		
Thr	Gln	Glu	Ile	Tyr	Glu	Leu	Ala	Gly	Glu	Glu	Phe	Asn	Val	Asn
			530			535					540			
Pro	Lys	Gln	Leu	Gly	Val	Leu	Leu	Phe	Glu	Lys	Leu	Gly	Leu	Pro
545					550					555				560
Glu	Tyr	Thr	Lys	Lys	Thr	Lys	Thr	Gly	Tyr	Ser	Thr	Ala	Val	Asp
			565					570						575
Leu	Glu	Arg	Leu	Ala	Pro	Ile	Ala	Pro	Ile	Val	Lys	Lys	Ile	Leu
			580				585						590	
Tyr	Arg	Gln	Ile	Ala	Lys	Ile	Gln	Ser	Thr	Tyr	Val	Ile	Gly	Leu
		595				600					605			
Asp	Trp	Ile	Leu	Ala	Asp	Gly	Lys	Ile	His	Thr	Arg	Tyr	Met	Gln
	610				615						620			
Leu	Thr	Gln	Thr	Gly	Arg	Leu	Ser	Ser	Val	Asp	Pro	Asn	Leu	Gln
625				630						635				640
Ile	Pro	Ala	Arg	Leu	Glu	Gln	Gly	Arg	Leu	Ile	Arg	Lys	Ala	Phe
			645					650						655
Pro	Glu	Trp	Glu	Asp	Ser	Val	Leu	Leu	Ser	Ser	Asp	Tyr	Ser	Gln
			660				665						670	
Glu	Leu	Arg	Val	Leu	Ala	His	Ile	Ser	Lys	Asp	Glu	His	Leu	Ile
		675				680						685		
Ala	Phe	Gln	Glu	Gly	Ala	Asp	Ile	His	Thr	Ser	Thr	Ala	Met	Arg
	690				695						700			
Phe	Gly	Ile	Glu	Arg	Pro	Asp	Asn	Val	Thr	Ala	Asn	Asp	Arg	Arg
705				710					715					720
Ala	Lys	Ala	Val	Asn	Phe	Gly	Val	Val	Tyr	Gly	Ile	Ser	Asp	Phe
			725				730						735	
Leu	Ser	Asn	Asn	Leu	Gly	Ile	Ser	Arg	Lys	Glu	Ala	Lys	Ala	Tyr
		740					745					750		
Asp	Thr	Tyr	Phe	Glu	Arg	Phe	Pro	Gly	Ile	Lys	Asn	Tyr	Met	Asp
	755					760					765			
Val	Val	Arg	Glu	Ala	Arg	Asp	Lys	Ser	Tyr	Val	Glu	Thr	Leu	Phe
	770				775					780				
Arg	Arg	Arg	Glu	Leu	Pro	Asp	Ile	Asn	Ser	Arg	Asn	Phe	Asn	Ile
785				790					795					800
Gly	Phe	Ala	Glu	Arg	Thr	Ala	Ile	Asn	Ser	Pro	Ile	Gln	Gly	Ser
			805					810					815	
Ala	Asp	Ile	Leu	Lys	Ile	Ala	Met	Ile	Gln	Leu	Asp	Lys	Ala	Leu
		820				825						830		
Ala	Gly	Gly	Tyr	Gln	Thr	Lys	Met	Leu	Leu	Gln	Val	His	Asp	Glu
	835				840						845			
Val	Leu	Glu	Val	Pro	Lys	Ser	Glu	Leu	Val	Glu	Met	Lys	Lys	Leu
	850				855				860					
Lys	Gln	Thr	Met	Glu	Glu	Ala	Ile	Gln	Leu	Ser	Val	Pro	Leu	Ile
865				870				875						880
Asp	Glu	Asn	Glu	Gly	Ala	Thr	Trp	Tyr	Glu	Ala	Lys			
			885					890						

(2) INFORMATION FOR SEQ ID NO:4748:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...91

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4748:

Met	Thr	Pro	Ile	Thr	Lys	Pro	Thr	Pro	Thr	Thr	Cys	Met	Ala	Ile	Ser
1				5					10					15	
Leu	Glu	Ile	Pro	Lys	Arg	Leu	Gln	Ala	Thr	Gly	Ile	Arg	Arg	Arg	Glu
			20					25					30		
Pro	Pro	Ala	Ile	Pro	Glu	Ala	Pro	Gln	Ala	Glu	Ile	Ala	Ala	Thr	Thr
		35					40					45			
Leu	Arg	Thr	Lys	Ala	Val	Ala	Lys	Ser	Thr	Gly	Ile	Pro	Arg	Val	Leu
	50					55					60				
Thr	Ala	Ala	Arg	Val	Lys	Arg	Leu	Met	Val	Ile	Ala	Thr	Pro	Ala	Ile
65					70					75					80
Leu	Ile	Val	Glu	Pro	Ser	Gly	Ile	Glu	Thr	Glu					
				85						90					

(2) INFORMATION FOR SEQ ID NO:4749:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 389 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...389

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4749:

Met	Lys	Pro	Ile	Asp	Arg	Phe	Ser	Tyr	Leu	Lys	Asn	Asn	Arg	Val	Ser
1				5					10					15	
Gln	Asp	Thr	Ser	Ser	Leu	Val	Gln	Cys	Tyr	Leu	Pro	Ile	Ile	Gly	Gln
			20					25					30		
Glu	Ala	Leu	Ser	Leu	Tyr	Leu	Tyr	Thr	Ile	Ser	Phe	Trp	Asp	Asn	Gly
		35					40					45			
Arg	Lys	Glu	Tyr	Leu	Phe	Ser	Ser	Ile	Leu	Asn	His	Leu	Asn	Phe	Gly

50		55		60											
Met	Asp	Arg	Leu	Ile	Lys	Ser	Leu	Lys	Ile	Leu	Ser	Ala	Phe	Asn	Leu
65					70					75					80
Leu	Thr	Leu	Tyr	Gln	Lys	Gly	Asp	Val	Tyr	Gln	Leu	Ala	Leu	His	Ala
				85					90						95
Pro	Leu	Ser	Ser	Gln	Asp	Phe	Leu	Gly	His	Pro	Val	Tyr	Arg	Arg	Leu
				100				105						110	
Leu	Glu	Lys	Lys	Ile	Gly	Asp	Val	Ala	Val	Glu	Asp	Leu	Lys	Val	Glu
				115			120					125			
Ser	Ala	Asp	Gly	Glu	Glu	Ile	Pro	Val	Ser	Leu	Asn	Gln	Val	Phe	Pro
				130			135					140			
Glu	Leu	Ala	Glu	Leu	Gly	Ser	Gln	Glu	Tyr	Leu	Gly	Leu	Lys	Lys	Lys
145					150					155					160
Val	Ala	Asn	Asp	Phe	Asp	Leu	Asp	His	Phe	Arg	Gln	Leu	Met	Ala	Arg
				165					170						175
Asp	Gly	Leu	Arg	Phe	Ala	Asp	Glu	Gln	Ser	Asp	Val	Leu	Asn	Leu	Phe
				180				185						190	
Ala	Ile	Ala	Glu	Glu	Lys	Lys	Trp	Thr	Trp	Phe	Glu	Thr	Tyr	Gln	Leu
				195			200							205	
Ala	Lys	Ser	Thr	Ala	Val	Ser	Gln	Val	Ile	Ser	Thr	Lys	Arg	Met	Arg
				210			215					220			
Glu	Lys	Ile	Ala	Gln	Lys	Pro	Val	Ser	Ser	Asp	Phe	Ser	Leu	Lys	Glu
225					230					235					240
Ala	Ile	Ile	Ile	Lys	Glu	Ala	Lys	Ser	Lys	Thr	Ala	Leu	Gln	Phe	Leu
				245					250						255
Ala	Glu	Ile	Lys	Gln	Thr	Arg	Lys	Gly	Thr	Ile	Thr	Gln	Thr	Glu	Arg
				260				265						270	
Glu	Leu	Leu	Gln	Gln	Met	Ala	Gly	Leu	Gly	Leu	Leu	Asp	Glu	Val	Ile
				275			280					285			
Asn	Ile	Ile	Leu	Leu	Leu	Thr	Phe	Asn	Lys	Val	Asp	Ser	Ala	Asn	Ile
				290			295				300				
Asn	Glu	Lys	Tyr	Ala	Met	Lys	Val	Ala	Asn	Asp	Tyr	Ala	Tyr	Gln	Lys
305					310					315					320
Ile	His	Ser	Ala	Glu	Glu	Ala	Val	Leu	Arg	Ile	Arg	Glu	Arg	Gly	Gln
				325					330					335	
Lys	Ala	Lys	Thr	Gln	Lys	Gln	Asn	Gln	Thr	Ala	Pro	Ala	Lys	Thr	Asn
				340				345						350	
Ile	Pro	Lys	Trp	Ser	Asn	Pro	Glu	Tyr	Lys	Asn	Thr	Ser	Ser	Ala	Glu
				355			360					365			
Glu	Leu	Glu	Glu	Met	Glu	Arg	Gln	Thr	Leu	Glu	Leu	Leu	Ala	Lys	Leu
				370			375				380				
Asp	Asn	Gly	Gly	Asp											
385															

(2) INFORMATION FOR SEQ ID NO:4750:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4750:

```
Glu Asp Thr Ile Met Lys Lys Thr Val Tyr Lys Lys Leu Gly Ile Ser
1          5          10          15
Ile Ile Ala Ser Thr Leu Leu Ala Ser Gln Leu Ser Thr Val Ser Ala
          20          25          30
Leu Ser Val Ile Ser Ser Thr Gly Glu Glu Tyr Glu Val Ser Glu Thr
          35          40          45
Leu Glu Lys Gly Pro Gly Ser Asn Asp Ser Ser Leu Ser Glu Ile Ser
          50          55          60
Pro Thr Tyr Gly Ser Tyr Tyr Gln Lys Gln Ser Glu Val Leu Ser Val
65          70          75          80
Met Met Ile
```

(2) INFORMATION FOR SEQ ID NO:4751:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 109 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...109

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4751:

```
Leu Ser Thr Met Met Met Ala Leu Ile Arg Pro Lys Ser Lys Arg Phe
1          5          10          15
Ile Met Asp His Lys Ala Tyr Met Tyr Val Leu Glu Cys Arg Asp Gly
          20          25          30
Ser Tyr Tyr Ile Gly Tyr Thr Thr Asp Met Arg Arg Arg Leu Ala Ile
          35          40          45
His Asn Ser Gly Lys Gly Ala Lys Tyr Thr Arg Ala Arg Leu Pro Val
          50          55          60
Lys Leu Ile Tyr Ala Gln Gly Phe Ala Ser Lys Glu Glu Ala Met Ser
65          70          75          80
Ala Glu Ala Leu Leu Lys Arg Lys Lys Arg Pro Gln Lys Glu Glu Phe
          85          90          95
Leu Ser Glu Asn Gln Asp Arg Asn Leu Leu Arg Leu Phe
          100          105
```

(2) INFORMATION FOR SEQ ID NO:4752:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 331 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...331
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4752:

Ile	Lys	Thr	Met	Thr	Ser	Thr	Lys	Gln	His	Lys	Lys	Val	Ile	Leu	Val
1			5					10					15		
Gly	Asp	Gly	Ala	Val	Gly	Ser	Ser	Tyr	Ala	Phe	Ala	Leu	Val	Asn	Gln
		20					25					30			
Gly	Ile	Ala	Gln	Glu	Leu	Gly	Ile	Ile	Glu	Ile	Pro	Gln	Leu	His	Glu
	35					40					45				
Lys	Ala	Val	Gly	Asp	Ala	Leu	Asp	Leu	Ser	His	Ala	Leu	Ala	Phe	Thr
	50				55					60					
Ser	Pro	Lys	Lys	Ile	Tyr	Ala	Ala	Gln	Tyr	Ser	Asp	Cys	Ala	Asp	Ala
65				70					75					80	
Asp	Leu	Val	Val	Ile	Thr	Ala	Gly	Ala	Pro	Gln	Lys	Pro	Gly	Glu	Thr
		85					90						95		
Arg	Leu	Asp	Leu	Val	Gly	Lys	Asn	Leu	Ala	Ile	Asn	Lys	Ser	Ile	Val
	100						105					110			
Thr	Gln	Val	Val	Glu	Ser	Gly	Phe	Lys	Gly	Ile	Phe	Leu	Val	Ala	Ala
	115					120						125			
Asn	Pro	Val	Asp	Val	Leu	Thr	Tyr	Ser	Thr	Trp	Lys	Phe	Ser	Gly	Phe
	130				135					140					
Pro	Lys	Glu	Arg	Val	Ile	Gly	Ser	Gly	Thr	Ser	Leu	Asp	Ser	Ala	Arg
145				150					155					160	
Phe	Arg	Gln	Ala	Leu	Ala	Glu	Lys	Leu	Asp	Val	Asp	Ala	Arg	Ser	Val
		165					170						175		
His	Ala	Tyr	Ile	Met	Gly	Glu	His	Gly	Asp	Ser	Glu	Phe	Ala	Val	Trp
	180						185					190			
Ser	His	Ala	Asn	Ile	Ala	Gly	Val	Asn	Leu	Glu	Glu	Phe	Leu	Lys	Asp
	195				200							205			
Thr	Gln	Asn	Val	Gln	Glu	Ala	Glu	Leu	Ile	Glu	Leu	Phe	Glu	Gly	Val
	210				215						220				
Arg	Asp	Ala	Ala	Tyr	Thr	Ile	Ile	Asn	Lys	Lys	Gly	Ala	Thr	Tyr	Tyr
225				230					235					240	
Gly	Ile	Ala	Val	Ala	Leu	Ala	Arg	Ile	Thr	Lys	Ala	Ile	Leu	Asp	Asp
		245					250						255		
Glu	Asn	Ala	Val	Leu	Pro	Leu	Ser	Val	Phe	Gln	Glu	Gly	Gln	Tyr	Gly
	260				265							270			
Val	Glu	Asn	Val	Phe	Ile	Gly	Gln	Pro	Ala	Val	Val	Gly	Ala	His	Gly
	275				280							285			
Ile	Val	Arg	Pro	Val	Asn	Ile	Pro	Leu	Asn	Asp	Ala	Glu	Thr	Gln	Lys
	290				295						300				

Met	Gln	Ala	Ser	Ala	Lys	Glu	Leu	Gln	Ala	Ile	Ile	Asp	Glu	Ala	Trp
305					310					315					320
Lys	Asn	Pro	Glu	Phe	Gln	Glu	Ala	Ser	Lys	Asn					
				325					330						

(2) INFORMATION FOR SEQ ID NO:4753:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...74

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4753:

Tyr	Glu	Thr	Ile	Ala	Lys	Thr	Phe	Ile	Glu	Ile	Asn	Phe	Thr	Phe	Pro
1				5				10					15		
Ile	Asp	Leu	Phe	Ser	Ser	Tyr	Phe	Asn	Leu	Leu	Tyr	Asn	Ser	Pro	Cys
		20						25				30			
Cys	Gly	Trp	Ile	Leu	Phe	Ser	Leu	Leu	Ile	Leu	Phe	Glu	Thr	Leu	Phe
		35					40				45				
Lys	Pro	Arg	Gln	Leu	His	Leu	Ala	Val	Gly	Met	Val	Thr	Asp	Phe	Val
	50				55					60					
Ser	Ser	Ile	His	Asn	Leu	Lys	Thr	Val	Phe						
65					70										

(2) INFORMATION FOR SEQ ID NO:4754:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4754:

Tyr Glu Thr Ile Ala Lys Thr Phe Ile Glu Ile Asn Phe Thr Phe Pro

1				5				10					15			
Ile	Asp	Leu	Phe	Ser	Ser	Tyr	Phe	Asn	Pro	Leu	Tyr	Ile	Met	Val	Ser	
			20					25					30			
Asn	Leu	His	Gln	Asn	Asp	Lys	Ile	Asn	Gln	Leu	Ile	Ser	Asp	Tyr	Lys	
		35					40					45				
Gln	Asn	Met	Lys	Ala	Phe	Tyr	Ile	Thr	Ile	Glu	Lys	Phe	Ile	Arg	Asp	
	50					55					60					
Asp	Glu	Ser	Leu	Lys	Cys	Tyr	Phe	Thr	Lys	Val	Ile	Ser	Ser	Arg	Ser	
65					70					75					80	
Lys	Val	Thr	Ser	Leu	Asp	Gln	Ile	Glu	Ala	Asp	Lys	Thr	Ile	Gln	Arg	
				85					90					95		
Lys	Tyr	Ser	Ser	Glu	Leu	Lys	Lys	Phe	Ile	Gly	Phe	Tyr	Asn	Glu	Ile	
			100					105					110			
Ile	Cys	Glu	Glu	Asn	Ser	Phe	Leu	His	Val	Arg	Lys	Arg	Trp	Ser	Ser	
		115					120					125				
Trp	Phe	Arg														
		130														

(2) INFORMATION FOR SEQ ID NO:4755:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4755:

Pro	Met	Thr	Ile	Glu	Leu	Leu	Thr	Pro	Phe	Thr	Lys	Val	Glu	Leu	Glu	
1				5				10					15			
Pro	Glu	Ile	Lys	Glu	Lys	Lys	Arg	Lys	Gln	Val	Gly	Ile	Leu	Gly	Gly	
			20					25				30				
Asn	Phe	Asn	Pro	Val	His	Asn	Ala	His	Leu	Ile	Val	Ala	Asp	Gln	Val	
		35					40					45				
Arg	Gln	Gln	Leu	Gly	Leu	Asp	Gln	Val	Leu	Leu	Met	Pro	Glu	Tyr	Gln	
	50					55				60						
Pro	Pro	His	Val	Asp	Lys	Lys	Glu	Thr	Ile	Pro	Glu	His	His	Arg	Leu	
65					70				75						80	
Lys	Met	Leu	Glu	Leu	Ala	Ile	Glu	Gly	Ile	Asp	Gly	Leu	Val	Ile	Glu	
				85				90						95		
Thr	Ile	Glu	Leu	Glu	Arg	Lys	Gly	Ile	Ser	Tyr	Thr	Tyr	Asp	Thr	Met	
			100				105						110			
Lys	Ile	Leu	Thr	Glu	Lys	Asn	Pro	Asp	Thr	Asp	Tyr	Tyr	Phe	Ile	Ile	
		115					120					125				
Gly	Ala	Asp	Met	Val	Asp	Tyr	Leu	Pro	Lys	Trp	Tyr	Arg	Ile	Asp	Glu	
	130					135					140					
Leu	Val	Asp	Met	Val	Gln	Phe	Val	Gly	Val	Gln	Arg	Pro	Arg	Tyr	Lys	

145		150		155		160									
Val	Gly	Thr	Ser	Tyr	Pro	Val	Ile	Trp	Val	Asp	Val	Pro	Leu	Met	Asp
		165		170		175									
Ile	Ser	Ser	Ser	Met	Val	Arg	Ala	Phe	Leu	Ala	Gln	Gly	Arg	Lys	Pro
		180		185		190									
Asn	Phe	Leu	Leu	Pro	Gln	Pro	Val	Leu	Asp	Tyr	Ile	Glu	Lys	Glu	Gly
		195		200		205									
Leu	Tyr														
	210														

(2) INFORMATION FOR SEQ ID NO:4756:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 196 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4756:

Leu	Met	Thr	Met	Lys	Ala	Met	Lys	Thr	Met	Met	Arg	Ile	Thr	Asp	Asn
1				5				10						15	
Gln	His	Lys	Ile	Ile	Lys	Glu	Lys	Phe	Val	Glu	Glu	Tyr	Pro	Lys	Leu
		20						25					30		
Ser	Asn	Leu	Leu	Leu	Asp	Arg	Thr	Leu	Glu	Ser	Leu	Ser	Gln	Asp	Glu
		35					40						45		
Arg	Ile	Phe	Ile	Phe	Pro	Asn	Asp	Leu	Thr	His	Thr	Pro	Asp	Leu	Asp
		50				55					60				
Lys	Lys	Gln	Lys	Ile	Leu	Glu	Thr	Ile	Asn	Gln	Glu	Ile	Lys	Thr	Gly
65				70					75					80	
Asn	Val	Ile	Gly	Phe	Leu	Gly	Tyr	Gly	Gln	Glu	Arg	Leu	Thr	Ile	Ser
			85					90						95	
Ser	Arg	Phe	Ser	Asp	Glu	Ser	Asn	Asp	His	Phe	Leu	His	Tyr	Leu	Leu
		100					105						110		
Asn	Lys	Val	Leu	His	Ile	Asn	Leu	Thr	Ser	Leu	Asp	Val	Ala	Leu	Ser
		115					120					125			
Arg	Glu	Glu	Arg	Leu	Tyr	Gln	Leu	Leu	Met	Tyr	Leu	Phe	Pro	Lys	Tyr
		130				135					140				
Leu	Gln	Ala	Ala	Ile	Arg	Lys	Gly	Leu	Tyr	Lys	Glu	Tyr	His	Arg	Phe
145				150					155					160	
Ser	His	Asn	Asp	Ser	His	Val	Lys	Gly	Val	Ile	Asp	Val	Arg	Asn	His
		165					170						175		
Pro	Gln	Glu	Lys	Ser	Ser	Phe	His	Gly	Lys	Tyr	Cys	Leu	His	Asn	Glu
		180					185						190		
Arg	Val	His	Leu												
	195														

(2) INFORMATION FOR SEQ ID NO:4757:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 121 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4757:

Arg	Met	Thr	Ile	Lys	Leu	Val	Ala	Thr	Asp	Met	Asp	Gly	Thr	Phe	Leu
1				5					10					15	
Tyr	Gly	Asn	Gly	Arg	Phe	Asp	Met	Asp	Arg	Leu	Lys	Ser	Leu	Leu	Ala
			20					25					30		
Ser	Tyr	Lys	Glu	Lys	Gly	Ile	Tyr	Phe	Ala	Val	Ala	Ser	Gly	Arg	Gly
		35				40						45			
Phe	Leu	Ser	Leu	Glu	Lys	Leu	Phe	Ala	Gly	Val	Arg	Asp	Asp	Ile	Ile
	50					55					60				
Phe	Ile	Ala	Glu	Asn	Gly	Ser	Leu	Val	Lys	Tyr	Gln	Gly	Gln	Asp	Leu
65					70					75				80	
Tyr	Glu	Ala	Thr	Met	Ser	Arg	Asp	Phe	Tyr	Leu	Ala	Thr	Phe	Glu	Lys
			85					90						95	
Leu	Lys	Thr	Ser	Pro	Tyr	Val	Asp	Ile	Asn	Lys	Leu	Leu	Leu	Thr	Gly
			100				105						110		
Lys	Lys	Val	His	Met	Ser	Arg	Tyr	Gly							
		115					120								

(2) INFORMATION FOR SEQ ID NO:4758:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...68

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4758:

```

Arg Arg Thr Ile Leu Ala Gly Ile Pro Thr Thr Val Thr Ser Leu Gly
1      5      10      15
Thr Ser Ala Thr Thr Ala Ala Ala Pro Thr Leu Ala Phe Ser Pro
      20      25      30
Ile Ser Thr Gly Pro Ile Thr Trp Ala Trp Ala Asp Met Arg Ala Pro
      35      40      45
Phe Arg Thr Val Gly Trp Arg Leu Pro Gln Ser Phe Pro Val Pro Pro
      50      55      60
Arg Val Thr Pro
65

```

(2) INFORMATION FOR SEQ ID NO:4759:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...72

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4759:

```

Thr Arg Ala Ile Gln Ile Gly Ser Arg Leu Leu Val Phe Arg Gln Leu
1      5      10      15
Glu Arg Lys Lys Cys Tyr Phe Leu Gln Leu Tyr Leu Thr Glu Arg Leu
      20      25      30
Arg Arg His Thr Ser Arg Lys Ile Cys Leu Ile Met Pro Val Glu Ser
      35      40      45
Val Thr Thr Pro Lys Asp Asn Lys Thr Ile Ile Pro Tyr Leu Thr Gln
      50      55      60
Lys Cys Lys Lys Lys Ser His Thr
65      70

```

(2) INFORMATION FOR SEQ ID NO:4760:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 834 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...834

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4760:

Lys	Phe	Pro	Phe	Cys	Gly	Ile	Ile	Asp	Lys	Val	Arg	Lys	Ser	Met	Gln
1				5					10					15	
Asn	Gln	Leu	Asn	Glu	Leu	Lys	Arg	Lys	Met	Leu	Glu	Phe	Phe	Gln	Gln
			20					25					30		
Lys	Gln	Lys	Asn	Lys	Lys	Ser	Ala	Arg	Pro	Gly	Lys	Lys	Gly	Ser	Ser
		35					40					45			
Thr	Lys	Lys	Ser	Lys	Thr	Leu	Asp	Lys	Ser	Val	Ile	Phe	Pro	Ala	Ile
	50					55					60				
Leu	Leu	Ser	Ile	Lys	Ala	Leu	Phe	Asn	Leu	Leu	Phe	Val	Leu	Gly	Phe
65					70					75					80
Leu	Gly	Gly	Met	Leu	Gly	Ala	Gly	Ile	Ala	Leu	Gly	Tyr	Gly	Val	Ala
				85					90					95	
Leu	Phe	Asp	Lys	Val	Arg	Val	Pro	Gln	Thr	Glu	Glu	Leu	Val	Asn	Gln
			100					105					110		
Val	Lys	Asp	Ile	Ser	Ser	Ile	Ser	Glu	Ile	Thr	Tyr	Ser	Asp	Gly	Thr
		115					120					125			
Val	Ile	Ala	Ser	Ile	Glu	Ser	Asp	Leu	Leu	Arg	Thr	Ser	Ile	Ser	Ser
	130					135					140				
Glu	Gln	Ile	Ser	Glu	Asn	Leu	Lys	Lys	Ala	Ile	Ile	Ala	Thr	Glu	Asp
145					150					155					160
Glu	His	Phe	Lys	Glu	His	Lys	Gly	Val	Val	Pro	Lys	Ala	Val	Ile	Arg
				165					170					175	
Ala	Thr	Leu	Gly	Lys	Phe	Val	Gly	Leu	Gly	Ser	Ser	Ser	Gly	Gly	Ser
			180					185					190		
Thr	Leu	Thr	Gln	Gln	Leu	Ile	Lys	Gln	Gln	Val	Val	Gly	Asp	Ala	Pro
		195					200					205			
Thr	Leu	Ala	Arg	Lys	Ala	Ala	Glu	Ile	Val	Asp	Ala	Leu	Ala	Leu	Glu
	210					215					220				
Arg	Ala	Met	Asn	Lys	Asp	Glu	Ile	Leu	Thr	Thr	Tyr	Leu	Asn	Val	Ala
225					230					235					240
Pro	Phe	Gly	Arg	Asn	Asn	Lys	Gly	Gln	Asn	Ile	Ala	Gly	Ala	Arg	Gln
				245					250					255	
Ala	Ala	Glu	Gly	Ile	Phe	Gly	Val	Asp	Ala	Ser	Gln	Leu	Thr	Val	Pro
		260						265					270		
Gln	Ala	Ala	Phe	Leu	Ala	Gly	Leu	Pro	Gln	Ser	Pro	Ile	Thr	Tyr	Ser
		275					280					285			
Pro	Tyr	Glu	Asn	Thr	Gly	Glu	Leu	Lys	Ser	Asp	Glu	Asp	Leu	Glu	Ile
	290					295					300				
Gly	Leu	Arg	Arg	Ala	Lys	Ala	Val	Leu	Tyr	Ser	Met	Tyr	Arg	Thr	Gly
305					310					315					320
Ala	Leu	Ser	Lys	Asp	Glu	Tyr	Ser	Gln	Tyr	Lys	Asp	Tyr	Asp	Leu	Lys
				325					330					335	
Gln	Asp	Phe	Leu	Pro	Ser	Gly	Thr	Val	Thr	Gly	Ile	Ser	Arg	Asp	Tyr
		340						345					350		
Leu	Tyr	Phe	Thr	Thr	Leu	Ala	Glu	Ala	Gln	Glu	Arg	Met	Tyr	Asp	Tyr
		355					360					365			
Leu	Ala	Gln	Arg	Asp	Asn	Val	Ser	Ala	Lys	Glu	Leu	Lys	Asn	Glu	Ala
	370					375					380				
Thr	Gln	Lys	Phe	Tyr	Arg	Asp	Leu	Ala	Ala	Lys	Glu	Ile	Glu	Asn	Gly
385					390					395					400
Gly	Tyr	Lys	Ile	Thr	Thr	Thr	Ile	Asp	Gln	Lys	Ile	His	Ser	Ala	Met

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...69
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4761:

```

Tyr Lys Ile Lys Lys Lys Lys Lys Lys Lys Asn Lys Lys Lys Lys Lys
1      5      10      15
Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Glu Lys
      20      25      30
Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
      35      40      45
Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Asn Phe Ile Thr Ser Gln Lys
      50      55      60
Gln Arg Ile Met Trp
65

```

(2) INFORMATION FOR SEQ ID NO:4762:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 192 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...192
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4762:

```

Met Ser Gln Ile Glu Arg Ile Lys Gln Ala Ile Met Ala Asp Ser Gln
1      5      10      15
Asn Ala Ser Tyr Thr Glu Arg Gly Ile Glu Pro Leu Phe Ala Ala Pro
      20      25      30
Lys Thr Ala Arg Ile Asn Ile Ile Gly Gln Ala Pro Gly Leu Lys Thr
      35      40      45

```

Gln	Glu	Ala	Gly	Leu	Tyr	Trp	Lys	Asp	Lys	Ser	Gly	Asp	Arg	Leu	Arg
50						55					60				
Asp	Trp	Leu	Gly	Val	Asp	Glu	Asp	Thr	Phe	Tyr	Asn	Ser	Gly	Tyr	Phe
65					70					75					80
Ala	Val	Leu	Pro	Met	Asp	Phe	Tyr	Phe	Pro	Gly	His	Gly	Lys	Ser	Gly
				85					90					95	
Asp	Leu	Pro	Pro	Arg	Thr	Gly	Phe	Ala	Glu	Lys	Trp	His	Pro	Gln	Val
			100					105					110		
Leu	Gln	Glu	Leu	Pro	Asp	Ile	Gln	Leu	Thr	Leu	Leu	Ile	Gly	Gln	Tyr
		115					120					125			
Ala	Gln	Ala	Tyr	Tyr	Leu	Gln	Glu	Lys	Ile	Ser	Gly	Lys	Val	Thr	Glu
	130					135					140				
Arg	Val	Lys	His	Tyr	Lys	Asp	Tyr	Leu	Pro	Ala	Tyr	Phe	Pro	Leu	Val
145					150					155					160
His	Pro	Ser	Pro	Arg	Asn	Gln	Ile	Trp	Met	Ala	Lys	Asn	Pro	Trp	Phe
				165					170					175	
Glu	Ala	Glu	Val	Val	Pro	Asp	Leu	Lys	Lys	Arg	Ile	Lys	Thr	Ile	Leu
			180					185						190	

(2) INFORMATION FOR SEQ ID NO:4763:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 217 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...217

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4763:

Ala	Tyr	Gln	Ile	Gly	Glu	Thr	Met	Thr	Ser	Ile	Thr	Ala	Ile	Phe	Phe
1				5					10					15	
Asp	Leu	Asp	Gly	Thr	Leu	Val	Asp	Ser	Ser	Ile	Gly	Ile	His	Asn	Ala
			20					25					30		
Phe	Thr	Tyr	Thr	Phe	Lys	Glu	Leu	Gly	Val	Pro	Ser	Pro	Asp	Ala	Lys
		35				40						45			
Thr	Ile	Arg	Gly	Phe	Met	Gly	Pro	Pro	Leu	Glu	Ser	Ser	Phe	Ala	Thr
	50				55						60				
Cys	Leu	Ser	Lys	Asp	Gln	Ile	Ser	Glu	Ala	Val	Gln	Ile	Tyr	Arg	Ser
65				70					75					80	
Tyr	Tyr	Lys	Ala	Lys	Gly	Ile	Tyr	Glu	Ala	Gln	Leu	Phe	Pro	Gln	Ile
			85					90						95	
Ile	Asp	Leu	Leu	Glu	Glu	Leu	Ser	Ser	Ser	Tyr	Pro	Leu	Tyr	Ile	Thr
			100					105					110		
Thr	Thr	Lys	Asp	Thr	Ser	Thr	Ala	Gln	Asp	Met	Ala	Lys	Asn	Leu	Glu
		115				120						125			
Ile	His	His	Phe	Phe	Asp	Gly	Ile	Tyr	Gly	Ser	Ser	Pro	Glu	Ala	Pro
	130					135					140				

His	Lys	Ala	Asp	Val	Ile	His	Gln	Ala	Leu	Gln	Thr	His	Gln	Leu	Ala
145					150				155						160
Pro	Glu	Gln	Ala	Ile	Ile	Ile	Gly	Asp	Thr	Lys	Phe	Asp	Met	Leu	Gly
				165					170						175
Ala	Arg	Glu	Thr	Gly	Ile	Gln	Lys	Leu	Ala	Ile	Thr	Trp	Gly	Phe	Gly
			180					185					190		
Glu	Gln	Ala	Asp	Leu	Leu	Asn	Tyr	Gln	Pro	Asp	Tyr	Ile	Ala	His	Lys
		195					200					205			
Pro	Leu	Glu	Val	Leu	Ala	Tyr	Phe	Gln							
	210					215									

(2) INFORMATION FOR SEQ ID NO:4764:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4764:

Ser	His	Gln	Ile	Lys	Lys	Asp	Ser	Lys	Glu	Asn	Pro	Met	Lys	Phe	Asn
1				5					10					15	
Pro	Asn	Gln	Arg	Tyr	Thr	Arg	Trp	Ser	Ile	Arg	Arg	Leu	Ser	Val	Gly
			20					25				30			
Val	Ala	Ser	Val	Val	Val	Ala	Ser	Gly	Phe	Phe	Val	Leu	Val	Gly	Gln
		35					40					45			
Pro	Ser	Ser	Val	Arg	Ala	Asp	Val	Val	Asn	Pro	Thr	Pro	Gly	Gln	Val
	50					55					60				
Leu	Pro	Glu	Glu	Thr	Ser	Gly	Thr	Lys	Glu	Gly	Asp	Leu	Ser	Glu	Lys
65				70					75					80	
Pro	Gly	Asp	Thr	Val	Leu	Thr	Gln	Ala	Lys	Pro	Glu	Gly	Val	Thr	Gly
			85					90					95		
Asn	Thr	Asn	Ser	Leu	Pro	Thr	Pro	Thr	Glu	Arg	Thr	Glu	Val	Ser	Glu
			100					105					110		
Glu	Thr	Asn	Ser	Ser	Ser	Leu	Asp	Thr	Leu	Phe	Glu	Lys	Asp	Glu	Glu
		115					120					125			
Ala	Gln	Lys	Asn	Pro	Glu	Leu	Thr	Asp	Val	Leu	Lys	Glu	Thr	Val	Asp
	130					135					140				
Thr	Ala	Asp	Val	Asp	Gly	Thr	Gln	Ala	Ser	Pro	Ala	Glu	Thr	Thr	Pro
145				150					155						160
Glu	Gln	Val	Lys	Gly	Gly	Val	Lys	Glu	Asn	Thr	Lys	Asp	Ser	Ile	Asp
			165					170						175	
Val	Pro	Ala	Ala	Tyr	Leu	Glu	Lys	Ala	Glu	Gly	Lys	Gly	Pro	Phe	Thr
		180						185					190		
Ala	Gly	Val	Asn	Gln	Val	Ile	Pro	Tyr	Glu	Leu	Phe	Ala	Gly	Asp	Gly
		195					200					205			

Met	Leu	Thr	Arg	Leu	Leu	Leu	Lys	Ala	Ser	Asp	Asn	Ala	Pro	Trp	Ser
210						215					220				
Asp	Asn	Gly	Thr	Ala	Lys	Asn	Pro	Ala	Leu	Pro	Pro	Leu	Glu	Gly	Leu
225					230					235					240
Thr	Lys	Gly	Lys	Tyr	Phe	Tyr	Glu	Val	Asp	Leu	Asn	Gly	Asn	Thr	Val
				245					250					255	
Gly	Lys	Gln	Gly	Gln	Ala	Leu	Ile	Asp	Gln	Leu	Arg	Ala	Asn	Gly	Thr
			260					265					270		
Gln	Thr	Tyr	Lys	Ala	Thr	Val	Lys	Val	Tyr	Gly	Asn	Lys	Asp	Gly	Lys
		275					280					285			
Ala	Asp	Leu	Thr	Asn	Leu	Val	Ala	Thr	Lys	Asn	Val	Asp	Ile	Asn	Ile
	290					295					300				
Asn	Gly	Leu	Val	Ala	Lys	Glu	Asn	Cys	Arg	Lys	Ser	Arg	Cys	Arg	Gln
305					310					315					320
Arg															

(2) INFORMATION FOR SEQ ID NO:4765:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 216 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...216

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4765:

Gly	Asp	Gln	Ile	Met	Asn	Leu	Leu	Ile	Met	Gly	Leu	Pro	Gly	Ala	Gly
1				5					10					15	
Lys	Gly	Thr	Gln	Ala	Ala	Lys	Ile	Val	Glu	Gln	Phe	His	Val	Ala	His
			20					25					30		
Ile	Ser	Thr	Gly	Asp	Met	Phe	Arg	Ala	Ala	Met	Ala	Asn	Gln	Thr	Glu
		35				40						45			
Met	Gly	Val	Leu	Ala	Lys	Ser	Tyr	Ile	Asp	Lys	Gly	Glu	Leu	Val	Pro
	50				55					60					
Asp	Glu	Val	Thr	Asn	Gly	Ile	Val	Lys	Glu	Arg	Leu	Ser	Gln	Asp	Asp
65				70					75					80	
Ile	Lys	Glu	Thr	Gly	Phe	Leu	Leu	Asp	Gly	Tyr	Pro	Arg	Thr	Ile	Glu
			85					90					95		
Gln	Ala	His	Ala	Leu	Asp	Lys	Thr	Leu	Ala	Glu	Leu	Gly	Ile	Glu	Leu
		100					105					110			
Glu	Gly	Val	Ile	Asn	Ile	Glu	Val	Asn	Pro	Asp	Ser	Leu	Leu	Glu	Arg
		115				120				125					
Leu	Ser	Gly	Arg	Ile	Ile	His	Arg	Val	Thr	Gly	Glu	Thr	Phe	His	Lys
	130				135					140					
Val	Phe	Asn	Pro	Pro	Val	Asp	Tyr	Lys	Glu	Glu	Asp	Tyr	Tyr	Gln	Arg
145					150					155					160

Glu	Asp	Asp	Lys	Pro	Glu	Thr	Val	Lys	Arg	Arg	Leu	Asp	Val	Asn	Ile
				165					170					175	
Ala	Gln	Gly	Glu	Pro	Ile	Ile	Ala	His	Tyr	Arg	Ala	Lys	Gly	Leu	Val
			180					185					190		
His	Asp	Ile	Glu	Gly	Asn	Gln	Asp	Ile	Asn	Asp	Val	Phe	Ser	Asp	Ile
		195					200					205			
Glu	Lys	Val	Leu	Thr	Asn	Leu	Lys								
	210					215									

(2) INFORMATION FOR SEQ ID NO:4766:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 663 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...663

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4766:

Asn	Val	Gln	Ile	Glu	Leu	Glu	Val	Ser	Lys	Leu	Arg	Met	Leu	Leu	Thr
1				5					10					15	
Lys	Arg	Glu	Glu	Gln	Leu	Leu	Lys	Ala	Phe	Leu	His	Val	Gly	Lys	Leu
			20					25					30		
Ser	Met	Gln	Asp	Met	Thr	Glu	Ile	Leu	Gln	Val	Ser	Ser	Arg	Thr	Ile
		35					40					45			
Tyr	Arg	Thr	Leu	Ser	Asp	Leu	Thr	Asp	Ser	Met	Glu	Gln	Tyr	Gly	Ile
		50				55					60				
Glu	Ile	Thr	Lys	His	Gly	Lys	Tyr	Tyr	Ile	Leu	Thr	Gly	Glu	Leu	Asp
65					70					75				80	
Asp	Leu	Pro	Thr	Glu	Leu	Glu	Val	Leu	Val	Glu	Tyr	Ser	Pro	Gln	Glu
				85					90					95	
Arg	Gln	Glu	Leu	Ile	Thr	Tyr	Arg	Leu	Leu	Thr	Glu	Ser	Gly	Phe	Val
			100					105					110		
Thr	Asn	Glu	Ala	Leu	Gln	Glu	Cys	Thr	Lys	Val	Ser	Asn	Val	Thr	Ile
		115					120					125			
Ile	Gln	Asp	Ile	Ser	Asp	Ile	Asp	Lys	Arg	Leu	Leu	Asp	Phe	Asp	Leu
	130					135					140				
Lys	Ile	Glu	Arg	Gln	Lys	Gly	Tyr	Arg	Ile	Ser	Gly	Asp	Ser	Val	Gly
145					150					155					160
Lys	Arg	Arg	Phe	Leu	Ala	Ile	Leu	Leu	Thr	Asn	Cys	Ile	Ser	Val	Ala
				165					170					175	
Asp	Phe	Ser	Thr	Gly	Asn	Phe	Gly	Ser	Phe	Asp	Ile	Leu	Glu	Ala	Asp
			180					185					190		
Arg	Thr	Arg	Leu	Ala	Ser	Gln	Ile	Val	Asn	Lys	Gln	Leu	Ser	Gly	Phe
		195					200					205			
Pro	Asp	Met	Asp	Ala	Arg	Met	Lys	Met	Phe	Phe	Ala	Ile	Leu	Leu	Ser
	210					215					220				

Leu	Ile	Gly	Gln	Glu	Gln	Asn	Ile	Glu	Asn	Ser	Pro	Asn	Thr	Ser	Lys
225					230				235						240
Gln	Ala	Leu	Glu	Ile	Ser	Gln	Lys	Ile	Phe	Gln	Ala	Tyr	Ser	Lys	Gln
			245						250					255	
Thr	Ala	Gln	Phe	Tyr	Ser	Ile	Gln	Glu	Ile	Ile	Tyr	Phe	Ala	Ser	Ile
		260						265					270		
Leu	Asp	Glu	Leu	Ile	Ile	Lys	Arg	Gln	Asp	Asn	Pro	Leu	Phe	Thr	Glu
	275						280					285			
Lys	Phe	Asp	Gly	Glu	Phe	Phe	Tyr	Asn	Ile	Ser	Asn	Leu	Ile	Asp	Thr
	290					295					300				
Val	Ser	Met	Tyr	Thr	Lys	Ile	Asp	Phe	Phe	Lys	Asp	Lys	Val	Leu	Phe
305					310					315					320
Asn	Phe	Leu	Phe	His	His	Ile	Arg	Leu	Ser	Leu	Gly	Val	Pro	Ile	Leu
				325					330					335	
Phe	Gln	Ser	Glu	Asn	Leu	Pro	Glu	Ser	Val	Gln	Ile	Leu	Val	Glu	Arg
			340					345					350		
Asn	Lys	Phe	Leu	Tyr	Thr	Val	Ile	Ser	Leu	Leu	Val	Asn	Asp	Ile	Phe
		355					360					365			
Pro	Lys	Tyr	Leu	His	Thr	Asp	Tyr	Glu	Tyr	Gly	Met	Ile	Ala	Leu	His
	370					375					380				
Phe	Ile	Ser	Ser	Leu	Gly	Arg	Ser	Pro	Glu	Ile	Tyr	Pro	Val	Arg	Val
385					390					395					400
Leu	Leu	Leu	Thr	Asp	Glu	Arg	Arg	Val	Thr	Arg	Asp	Leu	Leu	Val	Ser
				405					410					415	
Lys	Ile	Lys	Ser	Val	Ala	Pro	Phe	Val	Glu	Leu	Ile	Asp	Ile	Gln	Ser
			420					425					430		
Leu	Val	Asp	Tyr	His	Ser	Ile	Asp	Leu	Ser	Gln	Tyr	Asp	Tyr	Ile	Leu
	435						440					445			
Ser	Thr	Lys	Pro	Leu	Thr	Asn	Gln	Glu	Ile	Asp	Val	Ile	Ser	Ser	Phe
	450					455					460				
Pro	Thr	Val	Lys	Glu	Leu	Leu	Glu	Leu	Gln	Glu	Arg	Leu	Gln	Tyr	Val
465					470					475					480
Gln	Ala	His	Arg	Thr	Ile	Val	Ala	Arg	Asp	Ala	Ile	Ala	Pro	Glu	Lys
				485					490					495	
Ser	Tyr	Asp	Leu	Gln	Asp	Tyr	Leu	Ile	Ser	Ser	Ser	Gln	Leu	Leu	Ser
		500						505					510		
Gln	Phe	Glu	Leu	Val	Gln	Leu	Glu	Asn	Asn	Gln	Ser	Phe	Glu	His	Thr
	515						520					525			
Val	Glu	Gln	Ile	Ile	Gln	Tyr	Gln	Lys	Asn	Val	Ser	Asp	Arg	Asp	Tyr
	530					535					540				
Leu	Thr	Arg	Lys	Leu	Leu	Ser	His	Phe	Gln	Asn	Ser	Pro	Met	Ala	Ile
545					550					555					560
Pro	Asn	Thr	Gly	Leu	Val	Leu	Leu	His	Ser	Gln	Ser	Ser	Lys	Val	Thr
				565					570					575	
Thr	Asn	Ser	Phe	Thr	Met	Phe	Glu	Leu	Lys	Leu	Pro	Ile	Ser	Ala	Leu
			580					585					590		
Ser	Met	Lys	Arg	Glu	Glu	Glu	Glu	Val	Lys	Arg	Cys	Leu	Leu	Met	Leu
		595					600					605			
Met	Ser	Lys	Glu	Ala	Ser	Glu	Glu	Ala	Arg	Asp	Leu	Met	Thr	Ala	Ile
	610					615					620				
Ser	Gln	Ser	Ile	Ile	Glu	Asn	His	Leu	Tyr	Thr	Glu	Ile	Tyr	Lys	Thr
625					630					635					640
Gly	Asn	Gln	Ser	Ile	Ile	Tyr	Gln	Met	Leu	Asn	Thr	Ile	Phe	Asn	Glu
				645					650					655	
Lys	Ile	Lys	Lys	Leu	Glu	Asn									

(2) INFORMATION FOR SEQ ID NO:4767:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4767:

```

Ser Arg Gln Ile Pro Tyr Phe Gln Lys Val Tyr His Phe Tyr Phe Asn
1          5          10          15
Phe Leu Asp Glu Lys Lys Asp Ile Phe Met Lys Lys Leu His Arg Ala
          20          25          30
Phe Asn Val Phe Ser Cys Phe Gln Thr Arg Lys Lys Gly Ala Thr Glu
          35          40          45
Pro Asn Ser Leu Ser His Phe Lys Ala Cys Glu Lys Arg Pro Leu Gly
          50          55          60
Ser
65

```

(2) INFORMATION FOR SEQ ID NO:4768:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4768:

```

Ile Phe Lys Met Lys Lys Met Met Thr Phe Leu Lys Lys Ala Lys Val
1          5          10          15
Lys Ala Phe Thr Leu Val Glu Met Leu Val Val Leu Leu Ile Ile Ser
          20          25          30

```

Val	Leu	Phe	Leu	Leu	Phe	Val	Pro	Asn	Leu	Thr	Lys	Gln	Lys	Glu	Ala
		35					40					45			
Val	Asn	Asp	Lys	Gly	Lys	Ala	Ala	Val	Val	Lys	Val	Val	Glu	Ser	Gln
	50					55					60				
Ala	Glu	Leu	Tyr	Ser	Leu	Glu	Lys	Asn	Glu	Asp	Ala	Ser	Leu	Ser	Lys
65					70					75					80
Leu	Gln	Ala	Asp	Gly	Arg	Ile	Thr	Glu	Glu	Gln	Ala	Lys	Ala	Tyr	Lys
				85					90					95	
Glu	Tyr	His	Asp	Lys	Asn	Gly	Val	Ala	Asn	Arg	Lys	Val	Asn	Asp	
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:4769:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 270 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...270

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4769:

Glu	Phe	Lys	Met	Lys	Gln	Leu	Thr	Val	Glu	Asp	Ala	Lys	Gln	Ile	Glu
1				5					10					15	
Leu	Glu	Ile	Leu	Asp	Tyr	Ile	Asp	Thr	Leu	Cys	Lys	Lys	His	Asn	Ile
			20					25					30		
Asn	Tyr	Ile	Ile	Asn	Tyr	Gly	Thr	Leu	Ile	Gly	Ala	Val	Arg	His	Glu
		35				40						45			
Gly	Phe	Ile	Pro	Trp	Asp	Asp	Asp	Ile	Asp	Leu	Ser	Met	Pro	Arg	Glu
	50				55						60				
Asp	Tyr	Gln	Arg	Phe	Ile	Asn	Ile	Phe	Gln	Lys	Glu	Lys	Ser	Lys	Tyr
65				70						75					80
Lys	Leu	Leu	Ser	Leu	Glu	Thr	Asp	Lys	Asn	Tyr	Phe	Asn	Asn	Phe	Ile
				85					90					95	
Lys	Ile	Thr	Asp	Ser	Thr	Thr	Lys	Ile	Ile	Asp	Thr	Arg	Asn	Thr	Lys
			100					105					110		
Thr	Tyr	Glu	Ser	Gly	Ile	Phe	Ile	Asp	Ile	Phe	Pro	Ile	Asp	Arg	Phe
		115					120					125			
Asp	Asp	Pro	Lys	Val	Ile	Asp	Thr	Cys	Tyr	Lys	Leu	Glu	Ser	Phe	Lys
	130					135					140				
Leu	Leu	Ser	Phe	Ser	Lys	His	Lys	Asn	Ile	Val	Tyr	Lys	Asp	Ser	Leu
145					150					155					160
Leu	Lys	Asp	Trp	Ile	Arg	Thr	Ala	Phe	Trp	Leu	Leu	Leu	Arg	Pro	Val
			165						170					175	
Ser	Pro	Arg	Tyr	Phe	Ala	Asn	Lys	Ile	Glu	Lys	Glu	Ile	Gln	Lys	Tyr
			180					185					190		
Ser	Arg	Glu	Asn	Gly	Gln	Tyr	Met	Ala	Phe	Ile	Pro	Ser	Lys	Phe	Lys
		195					200					205			

Glu	Lys	Glu	Val	Phe	Pro	Ser	Gly	Thr	Phe	Asp	Lys	Thr	Ile	Asp	Leu
210						215				220					
Pro	Phe	Glu	Asn	Leu	Ser	Leu	Pro	Ala	Pro	Glu	Lys	Phe	Asp	Thr	Ile
225				230						235					240
Leu	Thr	Gln	Phe	Tyr	Gly	Asp	Tyr	Met	Thr	Leu	Pro	Pro	Glu	Glu	Lys
			245						250					255	
Arg	Phe	Tyr	Ser	His	Glu	Phe	His	Ala	Tyr	Lys	Leu	Glu	Asp		
		260						265					270		

(2) INFORMATION FOR SEQ ID NO:4770:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 63 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4770:

Leu	Ile	Lys	Ile	Met	Glu	Asn	Ile	Asp	Met	Phe	Lys	Ser	Asn	His	Glu
1				5				10						15	
Arg	Arg	Met	Arg	Tyr	Ser	Ile	Arg	Lys	Phe	Ser	Val	Gly	Val	Ala	Ser
			20					25						30	
Val	Ala	Val	Ala	Ser	Leu	Phe	Met	Gly	Ser	Val	Val	His	Ala	Thr	Glu
		35					40					45			
Lys	Glu	Gly	Ser	Thr	Gln	Ala	Ala	Asn	Val	Ile	Lys	Leu	Val	Ile	
50						55					60				

(2) INFORMATION FOR SEQ ID NO:4771:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1529 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1529

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4771:

Gly	Ile	Lys	Met	Lys	Lys	Ser	Thr	Val	Leu	Ser	Leu	Thr	Thr	Ala	Ala
1			5						10					15	
Val	Ile	Leu	Ala	Tyr	Ala	Pro	Asn	Glu	Val	Val	Leu	Ala	Asp	Thr	
		20					25				30				
Ser	Ser	Ser	Glu	Asp	Ala	Leu	Ser	Ile	Ser	Asp	Lys	Glu	Lys	Val	Val
		35					40				45				
Val	Asp	Lys	Glu	Thr	Glu	Asn	Lys	Glu	Lys	His	Lys	Asp	Ile	His	Ser
	50					55					60				
Ala	Met	Glu	Thr	Ser	Gln	Asp	Phe	Lys	Glu	Lys	Lys	Ile	Ala	Val	Ile
65					70				75						80
Lys	Glu	Lys	Glu	Val	Val	Ser	Lys	Thr	Pro	Val	Ile	Asp	Thr	Lys	Thr
				85					90					95	
Ser	Asn	Glu	Glu	Asn	Ser	Asn	Lys	Ser	Gln	Gly	Asp	His	Thr	Asp	Ser
			100					105					110		
Phe	Val	Asn	Lys	Asn	Thr	Glu	Asn	Pro	Lys	Lys	Glu	Asp	Lys	Val	Val
		115					120					125			
Tyr	Ile	Ala	Glu	Phe	Lys	Asp	Lys	Glu	Ser	Gly	Glu	Lys	Ala	Ile	Lys
	130					135					140				
Glu	Leu	Ser	Ser	Leu	Lys	Asn	Thr	Lys	Val	Leu	Tyr	Thr	Tyr	Asp	Arg
145					150					155					160
Ile	Phe	Asn	Gly	Ser	Ala	Ile	Glu	Thr	Ile	Pro	Asp	Asn	Leu	Asp	Lys
				165					170					175	
Ile	Lys	Gln	Ile	Glu	Gly	Ile	Ser	Ser	Val	Glu	Arg	Ala	Gln	Lys	Val
		180						185					190		
Gln	Pro	Met	Met	Asn	His	Ala	Arg	Lys	Glu	Ile	Gly	Val	Glu	Glu	Ala
		195					200						205		
Ile	Asp	Tyr	Leu	Lys	Ser	Ile	Asn	Ala	Pro	Phe	Gly	Lys	Asn	Phe	Asp
	210					215					220				
Gly	Arg	Gly	Met	Val	Ile	Ser	Asn	Ile	Asp	Thr	Gly	Thr	Asp	Tyr	Arg
225					230					235					240
His	Lys	Ala	Met	Arg	Ile	Asp	Asp	Asp	Ala	Lys	Ala	Ser	Met	Arg	Phe
			245						250					255	
Lys	Lys	Glu	Asp	Leu	Lys	Gly	Thr	Asp	Lys	Asn	Phe	Trp	Leu	Ser	Asp
		260						265					270		
Lys	Ile	Pro	His	Ala	Phe	Asn	Tyr	Tyr	Asn	Gly	Gly	Lys	Ile	Thr	Val
		275					280					285			
Glu	Lys	Tyr	Asp	Asp	Gly	Arg	Asp	Tyr	Phe	Asp	Pro	His	Gly	Met	His
	290					295					300				
Ile	Ala	Gly	Ile	Leu	Ala	Gly	Asn	Asp	Thr	Glu	Gln	Asp	Ile	Lys	Asn
305					310					315					320
Phe	Asn	Gly	Ile	Asp	Gly	Ile	Ala	Pro	Asn	Ala	Gln	Ile	Phe	Ser	Tyr
			325						330					335	
Lys	Met	Tyr	Ser	Asp	Ala	Gly	Ser	Gly	Phe	Ala	Gly	Asp	Glu	Thr	Met
		340						345					350		
Phe	His	Ala	Ile	Glu	Asp	Ser	Ile	Lys	His	Asn	Val	Asp	Val	Val	Ser
		355					360						365		
Val	Ser	Ser	Gly	Phe	Thr	Gly	Thr	Gly	Leu	Val	Gly	Glu	Lys	Tyr	Trp
	370					375					380				
Gln	Ala	Ile	Arg	Ala	Leu	Arg	Lys	Ala	Gly	Ile	Pro	Met	Val	Val	Ala
385					390					395					400
Thr	Gly	Asn	Tyr	Ala	Thr	Ser	Ala	Ser	Ser	Ser	Ser	Trp	Asp	Leu	Val
				405					410					415	
Ala	Asn	Asn	His	Leu	Lys	Met	Thr	Asp	Thr	Gly	Asn	Val	Thr	Arg	Thr
			420					425					430		
Ala	Ala	His	Glu	Asp	Ala	Ile	Ala	Val	Ala	Ser	Ala	Lys	Asn	Gln	Thr

Lys	Asn	Lys	Asn	Lys	Phe	Val	Glu	Ser	Phe	Ile	His	Phe	Glu	Ser	Val
			900					905					910		
Glu	Glu	Met	Glu	Ala	Leu	Ser	Ser	Asn	Gly	Lys	Lys	Thr	Asp	Phe	Gln
		915					920					925			
Pro	Ser	Leu	Ser	Met	Pro	Leu	Met	Gly	Phe	Ala	Gly	Asn	Trp	Asn	His
		930				935					940				
Glu	Pro	Ile	Leu	Asp	Lys	Trp	Ala	Trp	Glu	Glu	Gly	Ser	Lys	Ser	Lys
945					950					955					960
Thr	Met	Glu	Gly	Tyr	Asp	Asp	Asp	Gly	Lys	Pro	Lys	Ile	Pro	Gly	Thr
				965					970					975	
Leu	Asn	Lys	Gly	Ile	Gly	Gly	Glu	His	Gly	Ile	Asp	Lys	Phe	Asn	Pro
			980					985					990		
Ala	Gly	Val	Ile	Gln	Asn	Arg	Lys	Asp	Lys	Asn	Arg	Thr	Ser	Leu	Asp
		995					1000					1005			
Gln	Asp	Pro	Asp	Leu	Phe	Ala	Phe	Asn	Asn	Gln	Gly	Val	His	Ala	Glu
	1010					1015					1020				
Ser	Thr	Ser	Gly	Ser	Lys	Ile	Ala	Asn	Ile	Tyr	Pro	Leu	Asp	Ser	Asn
1025					1030					1035					1040
Gly	Asn	Pro	Gln	Asp	Ala	Gln	Leu	Glu	Arg	Gly	Leu	Thr	Pro	Ser	Pro
				1045					1050					1055	
Leu	Val	Leu	Arg	Ser	Ala	Glu	Glu	Gly	Leu	Ile	Ser	Ile	Val	Asn	Thr
			1060					1065					1070		
Asn	Lys	Glu	Gly	Glu	Asn	Gln	Lys	Asp	Leu	Lys	Val	Val	Ser	Arg	Glu
		1075					1080					1085			
His	Phe	Ile	Arg	Gly	Ile	Leu	Asn	Ser	Lys	Gly	Asn	Asp	Ala	Lys	Gly
	1090					1095					1100				
Ile	Lys	Ser	Ser	Lys	Leu	Lys	Val	Trp	Gly	Asp	Leu	Lys	Trp	Asp	Gly
1105					1110					1115					1120
Leu	Ile	Tyr	Asn	Pro	Arg	Gly	Arg	Glu	Glu	Asn	Ala	Pro	Glu	Ser	Lys
			1125						1130					1135	
Asp	Asn	Gln	Asp	Pro	Ala	Thr	Lys	Ile	Arg	Gly	Gln	Phe	Glu	Pro	Ile
		1140						1145					1150		
Ala	Glu	Gly	Gln	Tyr	Phe	Tyr	Lys	Phe	Lys	Tyr	Arg	Leu	Thr	Lys	Asp
		1155					1160					1165			
Tyr	Pro	Trp	Gln	Val	Ser	Tyr	Ile	Pro	Val	Lys	Ile	Asp	Asn	Thr	Ala
	1170					1175					1180				
Pro	Lys	Ile	Val	Ser	Val	Asp	Phe	Ser	Asn	Pro	Glu	Lys	Ile	Lys	Leu
1185					1190					1195					1200
Ile	Thr	Lys	Asp	Thr	Tyr	His	Lys	Val	Lys	Asp	Gln	Tyr	Lys	Asn	Glu
			1205						1210					1215	
Thr	Leu	Phe	Ala	Arg	Asp	Gln	Lys	Glu	His	Pro	Glu	Lys	Phe	Asp	Glu
		1220						1225					1230		
Ile	Ala	Asn	Glu	Val	Trp	Tyr	Ala	Gly	Ala	Ala	Leu	Val	Asn	Glu	Asp
		1235					1240					1245			
Gly	Glu	Val	Glu	Lys	Asn	Leu	Glu	Val	Thr	Tyr	Ala	Gly	Glu	Gly	Gln
	1250					1255					1260				
Gly	Arg	Asn	Arg	Lys	Leu	Asp	Lys	Asp	Gly	Asn	Thr	Ile	Tyr	Glu	Ile
1265					1270					1275					1280
Ser	Gly	Ala	Gly	Asp	Leu	Arg	Gly	Lys	Ile	Ile	Glu	Val	Ile	Ala	Leu
			1285					1290					1295		
Asp	Gly	Ala	Ser	Asn	Phe	Thr	Lys	Ile	His	Arg	Ile	Lys	Phe	Ala	Asn
		1300						1305					1310		
Gln	Ala	Asp	Glu	Lys	Gly	Met	Ile	Ser	Tyr	Tyr	Leu	Val	Asp	Pro	Asp
		1315					1320					1325			
Gln	Asp	Ser	Ser	Lys	Tyr	Gln	Lys	Leu	Gly	Glu	Ile	Pro	Glu	Ser	Lys
	1330					1335					1340				
Phe	Lys	Asn	Leu	Lys	Asn	Val	Lys	Asp	Asp	Ser	Leu	Asn	Lys	Glu	Thr

1345		1350		1355		1360									
Ala	Glu	Val	Glu	Asn	Asn	Leu	Leu	Val	Asp	Asn	Gln	Ser	Ile	Glu	Gly
				1365					1370					1375	
Lys	Ser	Leu	Phe	Asn	Ile	His	Lys	Thr	Ile	Ser	Thr	Ile	Arg	Asp	Phe
				1380					1385					1390	
Glu	Asn	Lys	Asp	Leu	Lys	Lys	Leu	Ile	Lys	Lys	Lys	Tyr	Lys	Gln	Glu
				1395					1400					1405	
Asp	Asp	Phe	Val	Asn	Gly	Gly	Thr	Arg	Thr	Val	Glu	Arg	Asp	Tyr	Lys
				1410					1415					1420	
Tyr	Asp	Asp	Lys	Gly	Asn	Ile	Ile	Ala	Tyr	Asp	Asp	Gly	Thr	Asp	Leu
				1425					1430					1435	
Glu	Tyr	Glu	Thr	Glu	Lys	Leu	Asp	Glu	Ile	Lys	Ser	Lys	Ile	Tyr	Gly
				1445					1450					1455	
Val	Leu	Ser	Pro	Ser	Lys	Asp	Gly	His	Phe	Glu	Ile	Leu	Gly	Lys	Ile
				1460					1465					1470	
Ser	Asn	Val	Ser	Lys	Asn	Ala	Lys	Val	Tyr	Tyr	Gly	Asn	Asn	Tyr	Lys
				1475					1480					1485	
Ser	Ile	Glu	Ile	Lys	Ala	Thr	Lys	Tyr	Asp	Phe	His	Ser	Lys	Thr	Met
				1490					1495					1500	
Thr	Phe	Asp	Leu	Tyr	Ala	Asn	Ile	Asn	Asp	Ile	Val	Asp	Gly	Ile	Ser
				1505					1510					1515	
Phe	Cys	Arg	Arg	Tyr	Glu	Ile	Ile	Cys							1520
															1525

(2) INFORMATION FOR SEQ ID NO:4772:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 479 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...479

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4772:

Gly	Ile	Lys	Met	Ser	Ile	Leu	Glu	Val	Lys	Asn	Leu	Ser	His	Gly	Phe
1				5					10					15	
Gly	Asp	Arg	Ala	Ile	Phe	Glu	Asp	Val	Ser	Phe	Arg	Leu	Leu	Lys	Gly
			20					25					30		
Glu	His	Ile	Gly	Leu	Val	Gly	Ala	Asn	Gly	Glu	Gly	Lys	Ser	Thr	Phe
			35				40					45			
Met	Ser	Ile	Val	Thr	Gly	Lys	Met	Leu	Pro	Asp	Glu	Gly	Lys	Val	Glu
			50				55				60				
Trp	Ser	Lys	Tyr	Val	Thr	Ala	Gly	Tyr	Leu	Asp	Gln	His	Ser	Val	Leu
			65			70			75					80	
Ala	Glu	Arg	Gln	Ser	Val	Arg	Asp	Val	Leu	Arg	Thr	Ala	Phe	Asp	Glu
			85					90					95		
Leu	Phe	Lys	Ala	Glu	Ala	Arg	Ile	Asn	Asp	Leu	Tyr	Met	Glu	Met	Ala

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...428

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4773:

Gly	Ser	Lys	Met	Arg	Glu	Pro	Asp	Phe	Leu	Asn	His	Phe	Leu	Lys	Lys
1				5					10					15	
Gly	Tyr	Phe	Lys	Lys	His	Ala	Lys	Ala	Val	Leu	Ala	Leu	Ser	Gly	Gly
			20					25					30		
Leu	Asp	Ser	Met	Phe	Leu	Phe	Lys	Val	Leu	Ser	Thr	Tyr	Gln	Lys	Glu
			35				40					45			
Leu	Glu	Ile	Glu	Leu	Ile	Leu	Ala	His	Val	Asn	His	Lys	Gln	Arg	Ile
						55				60					
Glu	Ser	Asp	Trp	Glu	Glu	Lys	Glu	Leu	Arg	Lys	Leu	Ala	Ala	Glu	Ala
65						70				75				80	
Glu	Leu	Pro	Ile	Tyr	Ile	Ser	Asn	Phe	Ser	Gly	Glu	Phe	Ser	Glu	Ala
				85					90					95	
Arg	Ala	Arg	Asn	Phe	Arg	Tyr	Asp	Phe	Phe	Gln	Glu	Val	Met	Lys	Lys
			100					105					110		
Thr	Gly	Ala	Thr	Ala	Leu	Val	Thr	Ala	His	His	Ala	Asp	Asp	Gln	Val
			115				120					125			
Glu	Thr	Ile	Leu	Met	Arg	Leu	Ile	Arg	Gly	Thr	Arg	Leu	Arg	Tyr	Leu
			130				135				140				
Ser	Gly	Ile	Lys	Glu	Lys	Gln	Val	Val	Gly	Glu	Ile	Glu	Ile	Ile	Arg
145						150				155				160	
Pro	Phe	Leu	His	Phe	Gln	Lys	Lys	Asp	Phe	Pro	Ser	Ile	Phe	His	Phe
				165					170					175	
Glu	Asp	Thr	Ser	Asn	Gln	Glu	Asn	His	Tyr	Phe	Arg	Asn	Arg	Ile	Arg
			180					185					190		
Asn	Ser	Tyr	Leu	Pro	Glu	Leu	Glu	Lys	Glu	Asn	Pro	Arg	Phe	Arg	Asp
			195				200					205			
Ala	Ile	Leu	Gly	Ile	Gly	Asn	Glu	Ile	Leu	Asp	Tyr	Asp	Leu	Ala	Ile
			210			215					220				
Ala	Glu	Leu	Ser	Asn	Asn	Ile	Asn	Val	Glu	Asp	Leu	Gln	Gln	Leu	Phe
225					230					235				240	
Ser	Tyr	Ser	Glu	Ser	Thr	Gln	Arg	Val	Leu	Leu	Gln	Thr	Tyr	Leu	Asn
				245					250					255	
Arg	Phe	Pro	Asp	Leu	Asn	Leu	Thr	Lys	Ala	Gln	Phe	Ala	Glu	Val	Gln
			260					265					270		
Gln	Ile	Leu	Lys	Ser	Lys	Ser	Gln	Tyr	Arg	His	Pro	Ile	Lys	Asn	Gly
			275				280					285			
Tyr	Glu	Leu	Ile	Lys	Glu	Tyr	Gln	Gln	Phe	Gln	Ile	Cys	Lys	Ile	Ser
			290			295					300				
Pro	Gln	Ala	Asp	Glu	Lys	Glu	Asp	Glu	Leu	Val	Leu	His	Tyr	Gln	Asn
305					310					315				320	
Gln	Val	Ala	Tyr	Gln	Gly	Tyr	Leu	Phe	Ser	Phe	Gly	Leu	Pro	Leu	Glu
				325					330					335	
Gly	Glu	Ser	Ile	Gln	Gln	Ile	Pro	Val	Ser	Arg	Glu	Thr	Ser	Ile	His
			340					345				350			
Ile	Arg	His	Arg	Lys	Thr	Gly	Asp	Val	Leu	Ile	Gln	Asn	Gly	His	Arg
			355				360					365			

Lys	Lys	Leu	Arg	Arg	Leu	Phe	Ile	Asp	Leu	Lys	Ile	Pro	Met	Glu	Lys
370						375					380				
Arg	Asn	Ser	Ala	Leu	Ile	Ile	Glu	Gln	Phe	Gly	Glu	Ile	Val	Ser	Ile
385					390					395					400
Leu	Gly	Ile	Ala	Thr	Asn	Asn	Leu	Ser	Lys	Lys	Thr	Lys	Asn	Asp	Ile
				405					410					415	
Met	Asn	Thr	Val	Leu	Tyr	Ile	Glu	Lys	Ile	Asp	Arg				
			420					425							

(2) INFORMATION FOR SEQ ID NO:4774:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...128

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4774:

Tyr	Asn	Lys	Ile	Ile	Glu	Asn	Ala	Ile	Lys	Arg	Arg	Arg	Gly	Met	Ser
1			5					10					15		
Val	Met	Glu	His	Leu	Phe	Lys	Phe	Leu	Leu	Leu	Ala	Pro	Tyr	Phe	Tyr
			20				25				30				
Phe	Asp	Asn	Trp	Ile	Glu	Lys	Ala	Asn	Arg	Asn	Ser	Lys	Phe	Phe	Pro
			35				40				45				
Ile	Phe	Tyr	Tyr	Phe	Tyr	Trp	Ile	Tyr	Ile	Pro	Phe	Tyr	Ser	Leu	Phe
			50			55				60					
Ser	Leu	Ala	Trp	Thr	Val	Val	Ser	Val	Leu	Phe	Phe	Asn	Thr	Val	Leu
65				70				75						80	
Arg	Asn	Val	Thr	Asp	Ile	Lys	Leu	Trp	Gly	Ile	Trp	Phe	Leu	Phe	Ile
			85					90					95		
Leu	Leu	Ala	Ile	Gly	Met	Asn	Trp	Leu	Thr	Tyr	Ser	Cys	Phe	Lys	Glu
			100				105					110			
Met	Phe	Arg	Leu	Arg	Gln	Glu	Leu	Gly	Lys	Ser	Lys	Gly	Gly	Arg	His
			115				120					125			

(2) INFORMATION FOR SEQ ID NO:4775:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4775:

Thr	Gly	Lys	Ile	His	Lys	Ile	Gly	Glu	Leu	Thr	Arg	Cys	Val	Thr	Asn
1				5					10					15	
Gly	Leu	Asp	Gly	Ala	Arg	Ala	Arg	Thr	Trp	Tyr	His	Asp	His	Ile	Cys
			20					25					30		
Trp	Arg	Thr	Thr	Ala	Gln	Trp	Asn	Asn	His	Arg	Val	Asn	Ile	Ile	Asp
			35				40					45			
Thr	Pro	Gly	His	Val	Asp	Phe	Thr	Ile	Glu	Val	Gln	Arg	Ser	Leu	Arg
			50			55					60				
Val	Leu	Asp	Gly	Ala	Val	Thr	Val	Leu	Asp	Ser	Gln	Ser	Gly	Val	Glu
65					70				75						80
Pro	Gln	Thr	Glu	Thr	Val	Trp	Arg	Gln	Gln	Leu	Ser	Thr	Glu	Ser	Thr
				85					90					95	
Tyr	Arg	Ile	Cys	Gln	Gln	Asn	Gly	Gln	Asn	Arg	Cys				
			100					105							

(2) INFORMATION FOR SEQ ID NO:4776:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 221 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4776:

Gly	Gly	Lys	Ile	Val	Gly	Gln	Lys	Val	His	Pro	Ile	Gly	Met	Arg	Val
1				5					10					15	
Gly	Ile	Ile	Arg	Asp	Trp	Asp	Ala	Lys	Trp	Tyr	Ala	Glu	Lys	Glu	Tyr
			20					25					30		
Ala	Asp	Tyr	Leu	His	Glu	Asp	Leu	Ala	Ile	Arg	Lys	Phe	Val	Gln	Lys
			35				40					45			
Glu	Leu	Ala	Asp	Ala	Ala	Val	Ser	Thr	Ile	Glu	Ile	Glu	Arg	Ala	Val
			50			55					60				
Asn	Lys	Val	Asn	Val	Ser	Leu	His	Thr	Ala	Lys	Pro	Gly	Met	Val	Ile
65				70					75						80
Gly	Lys	Gly	Gly	Ala	Asn	Val	Asp	Ala	Leu	Arg	Ala	Lys	Leu	Asn	Lys
				85					90					95	
Leu	Thr	Gly	Lys	Gln	Val	His	Ile	Asn	Ile	Ile	Glu	Ile	Lys	Gln	Pro

		100					105				110				
Asp	Leu	Asp	Ala	His	Leu	Val	Gly	Glu	Gly	Ile	Ala	Arg	Gln	Leu	Glu
		115					120					125			
Gln	Arg	Val	Ala	Phe	Arg	Arg	Ala	Gln	Lys	Gln	Ala	Ile	Gln	Arg	Ala
		130					135					140			
Met	Arg	Ala	Gly	Ala	Lys	Gly	Ile	Lys	Thr	Gln	Val	Ser	Gly	Arg	Leu
					150						155				160
Asn	Gly	Ala	Asp	Ile	Ala	Arg	Ala	Glu	Gly	Tyr	Ser	Glu	Gly	Thr	Val
			165						170					175	
Pro	Leu	His	Thr	Leu	Arg	Ala	Asp	Ile	Asp	Tyr	Ala	Trp	Glu	Glu	Ala
			180					185					190		
Asp	Thr	Thr	Tyr	Gly	Lys	Leu	Gly	Val	Lys	Val	Trp	Ile	Tyr	Arg	Gly
		195					200					205			
Glu	Val	Leu	Pro	Ala	Arg	Lys	Asn	Thr	Lys	Gly	Gly	Lys			
		210				215					220				

(2) INFORMATION FOR SEQ ID NO:4777:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4777:

Glu	Ile	Lys	Ile	Lys	Leu	Val	Phe	Gly	Lys	Phe	Ser	Leu	Ile	Ala	Phe
1				5					10					15	
Lys	Ser	Leu	Asp	Ser	Val	Met	Val	Ser	Ser	Ala	Glu	Val	Ala	Ser	Ser
		20						25					30		
Arg	Met	Arg	Asn	Gly	Ala	Trp	Arg	Lys	Thr	Ala	Arg	Ala	Ile	Asp	Asn
		35					40					45			
Leu	Cys	Phe	Cys	Pro	Pro	Glu	Lys	Phe	Arg	Pro	Pro	Ala	Ser	Thr	Arg
	50					55				60					
Ala	Ser	Lys	Ser	Pro	Ser	Phe	Ser	Leu	Thr	Lys	Ser	Leu	Ala	Cys	Ala
65					70					75				80	
Ile	Ser	Lys	Ala	Cys	Gln	Ser	Ser	Trp	Ser	Asp	Thr	Ser			
			85					90							

(2) INFORMATION FOR SEQ ID NO:4778:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...89

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4778:

Ser	Ser	Lys	Ile	Val	Tyr	Thr	Gly	Thr	Ser	Pro	Cys	Pro	Leu	Ser	Glu
1				5					10					15	
Gln	Ile	Ile	Phe	Gln	Ser	Pro	Ser	Asn	Gly	Leu	Asn	Thr	Met	Gly	Thr
			20					25					30		
Ser	Gly	Leu	Glu	Pro	Pro	Thr	Ser	Arg	Leu	Ser	Gly	Val	Arg	Ser	Asn
			35				40					45			
His	Leu	Ser	Tyr	Ala	Pro	Lys	Ser	Lys	Thr	Trp	Tyr	Lys	Glu	Gln	Ser
	50					55					60				
Ser	Lys	Arg	Val	Thr	Arg	Ile	Glu	Leu	Ala	Thr	Thr	Ala	Trp	Lys	Ala
65					70				75						80
Val	Val	Leu	Pro	Leu	Asn	Tyr	Thr	Arg							
				85											

(2) INFORMATION FOR SEQ ID NO:4779:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 375 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...375

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4779:

Phe	Asn	Lys	Ile	Lys	Glu	Lys	Asn	Met	Val	Lys	Tyr	Gly	Val	Val	Gly
1				5					10					15	
Ala	Gly	Tyr	Phe	Gly	Ala	Glu	Leu	Ala	Arg	Tyr	Met	Gln	Lys	Asn	Asp
			20					25					30		
Gly	Ala	Glu	Ile	Thr	Leu	Leu	Tyr	Asp	Pro	Asp	Asn	Ala	Glu	Ala	Ile
			35				40					45			
Ala	Glu	Glu	Leu	Gly	Ala	Lys	Val	Ala	Ser	Ser	Leu	Asp	Glu	Leu	Val
	50					55					60				
Ser	Ser	Asp	Glu	Val	Asp	Cys	Val	Ile	Val	Ala	Thr	Pro	Asn	Asn	Leu
65					70				75						80
His	Lys	Ala	Pro	Val	Ile	Lys	Ala	Ala	Gln	His	Gly	Lys	Asn	Val	Phe
				85					90					95	

Cys	Glu	Lys	Pro	Ile	Ala	Leu	Ser	Tyr	Gln	Asp	Cys	Arg	Glu	Met	Val
			100					105					110		
Asp	Ala	Cys	Lys	Glu	Asn	Asn	Val	Thr	Phe	Met	Ala	Gly	His	Ile	Met
		115					120					125			
Asn	Phe	Asn	Gly	Val	His	His	Ala	Lys	Glu	Leu	Ile	Asn	Gln	Gly	
	130				135					140					
Val	Ile	Gly	Asp	Val	Leu	Tyr	Cys	His	Thr	Ala	Arg	Asn	Gly	Trp	Glu
145				150						155					160
Glu	Gln	Gln	Pro	Ser	Val	Ser	Trp	Lys	Lys	Ile	Arg	Glu	Lys	Ser	Gly
			165					170						175	
Gly	His	Leu	Tyr	His	His	Ile	His	Glu	Leu	Asp	Cys	Val	Gln	Phe	Leu
		180						185					190		
Met	Gly	Gly	Met	Pro	Glu	Thr	Val	Thr	Met	Thr	Gly	Gly	Asn	Val	Ala
	195						200					205			
His	Glu	Gly	Glu	His	Phe	Gly	Asp	Glu	Asp	Asp	Met	Ile	Phe	Val	Asn
	210					215					220				
Met	Glu	Phe	Ser	Asn	Lys	Arg	Phe	Ala	Leu	Leu	Glu	Trp	Gly	Ser	Ala
225					230					235					240
Tyr	Arg	Trp	Gly	Glu	His	Tyr	Val	Leu	Ile	Gln	Gly	Ser	Lys	Gly	Ala
			245						250					255	
Ile	Arg	Leu	Asp	Leu	Phe	Asn	Cys	Lys	Gly	Thr	Leu	Lys	Leu	Asp	Gly
		260						265					270		
Gln	Glu	Ser	Tyr	Phe	Leu	Ile	His	Glu	Ser	Gln	Glu	Glu	Asp	Asp	Asp
	275						280					285			
Arg	Thr	Arg	Ile	Tyr	His	Ser	Thr	Glu	Met	Asp	Gly	Ala	Ile	Ala	Tyr
	290					295					300				
Gly	Lys	Pro	Gly	Lys	Arg	Thr	Pro	Leu	Trp	Leu	Ser	Ser	Val	Ile	Asp
305					310					315					320
Lys	Glu	Met	Arg	Tyr	Leu	His	Glu	Ile	Met	Glu	Gly	Ala	Pro	Val	Ser
			325						330					335	
Glu	Glu	Phe	Ala	Lys	Leu	Leu	Thr	Gly	Glu	Ala	Ala	Leu	Glu	Ala	Ile
		340						345					350		
Ala	Thr	Ala	Asp	Ala	Cys	Thr	Gln	Ser	Met	Phe	Glu	Asp	Arg	Lys	Val
	355						360					365			
Lys	Leu	Ser	Glu	Ile	Val	Lys									
	370					375									

(2) INFORMATION FOR SEQ ID NO:4780:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 441 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...441
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4780:

Asp	Asn	Lys	Ile	Lys	Leu	Leu	Gln	Glu	Leu	Lys	Glu	Gln	Val	Glu	Val
1				5					10					15	
Gly	Thr	Ala	Ile	Asn	Ala	Ser	Asn	Ile	Glu	His	Ser	Lys	Ala	Arg	Gly
			20					25					30		
Asp	Leu	Gly	Ile	Ser	Tyr	Asp	Gln	Glu	Val	Leu	Arg	Leu	Ile	Asp	Lys
		35					40					45			
Phe	Asn	Glu	Leu	Gly	Ile	Phe	Val	Gly	Ser	Val	Val	Ile	Thr	Gln	Tyr
	50					55					60				
Thr	Gly	Gln	Pro	Ala	Ala	Asp	Ala	Phe	Arg	Asn	Gln	Leu	Glu	Lys	Asn
65					70					75					80
Gly	Ile	Asp	Ser	Tyr	Leu	His	Tyr	Pro	Ile	Lys	Gly	Tyr	Pro	Thr	Asp
				85					90					95	
Met	Asp	His	Ile	Ile	Ser	Ser	Lys	Gly	Met	Gly	Lys	Asn	Asp	Tyr	Ile
			100					105					110		
Lys	Thr	Ser	Arg	Asn	Leu	Ile	Val	Val	Thr	Ala	Pro	Gly	Pro	Gly	Ser
		115					120					125			
Gly	Lys	Leu	Ala	Thr	Cys	Met	Ser	Asn	Met	Tyr	His	Asp	Gln	Ile	Asn
	130					135					140				
Gly	Ile	Lys	Ser	Gly	Tyr	Ala	Lys	Phe	Glu	Thr	Phe	Pro	Val	Trp	Asn
145					150				155						160
Leu	Pro	Leu	His	His	Pro	Val	Asn	Leu	Ala	Tyr	Glu	Ala	Ala	Thr	Ala
				165					170					175	
Asp	Leu	Asp	Asp	Val	Asn	Met	Ile	Asp	Pro	Phe	His	Leu	Gln	Thr	Tyr
		180						185					190		
Gly	Glu	Thr	Thr	Val	Asn	Tyr	Asn	Arg	Asp	Ile	Glu	Ile	Phe	Pro	Val
		195					200					205			
Leu	Lys	Arg	Met	Leu	Glu	Arg	Ile	Leu	Gly	Lys	Ser	Pro	Tyr	Ala	Ser
	210					215					220				
Pro	Thr	Asp	Met	Gly	Val	Asn	Met	Val	Gly	Phe	Ala	Ile	Thr	Asp	Asp
225					230					235					240
Glu	Ala	Ala	Val	Glu	Ala	Ser	Lys	Gln	Glu	Ile	Ile	Arg	Arg	Tyr	Tyr
				245					250					255	
Gln	Thr	Val	Leu	Asp	Phe	Lys	Ala	Glu	Lys	Val	Gly	Glu	Ala	Ala	Val
			260					265					270		
Lys	Lys	Ile	Glu	Leu	Leu	Met	Asn	Asp	Leu	Gly	Ile	Thr	Pro	Ala	Asp
		275					280					285			
Arg	Lys	Val	Ala	Val	Val	Ala	Arg	Gln	Lys	Ala	Glu	Glu	Thr	Gly	Gly
	290					295					300				
Pro	Ala	Leu	Ala	Phe	Glu	Leu	Pro	Asn	Gly	Glu	Ile	Val	Thr	Gly	Lys
305					310					315					320
Asn	Ser	Glu	Leu	Phe	Gly	Pro	Thr	Ala	Ala	Ala	Leu	Ile	Asn	Ala	Ile
				325					330					335	
Lys	Lys	Ser	Ala	Asp	Ile	Ala	Lys	Glu	Val	Lys	Leu	Ile	Glu	Pro	Glu
			340					345					350		
Val	Val	Lys	Pro	Ile	Gln	Gly	Leu	Lys	Ile	Asp	His	Leu	Gly	Ser	Arg
		355					360					365			
Asn	Pro	Arg	Leu	His	Ser	Asn	Glu	Ile	Leu	Ile	Ala	Leu	Ala	Ile	Thr
	370					375					380				
Ala	Thr	Glu	Asn	Pro	Asp	Ala	Ala	Arg	Ala	Met	Glu	Glu	Leu	Gly	Asn
385					390					395					400
Leu	Lys	Gly	Ser	Glu	Ala	His	Ser	Thr	Ile	Ile	Leu	Thr	Asp	Glu	Asp
				405					410					415	
Lys	Asn	Val	Leu	Arg	Lys	Leu	Gly	Ile	Asn	Val	Thr	Phe	Asp	Pro	Tyr
			420					425					430		
Tyr	Gln	Tyr	Asp	Arg	Leu	Tyr	Arg	Lys							
		435					440								

(2) INFORMATION FOR SEQ ID NO:4781:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 299 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...299

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4781:

Ile	Leu	Lys	Ile	Ile	Pro	Leu	Asp	Ile	Ser	Ile	Arg	Val	Pro	Pro	Leu
1			5					10					15		
His	Lys	Ser	Ile	Leu	Ser	Gln	Lys	Arg	Lys	Lys	Asn	Asn	Tyr	Glu	Arg
			20				25					30			
Lys	Phe	Asn	Leu	Leu	Phe	Phe	Ala	Phe	Tyr	Phe	Gly	Arg	Ile	Lys	Arg
		35				40					45				
Arg	Cys	Lys	Met	Lys	Arg	Leu	Glu	Gln	Ile	Ile	Lys	Leu	Val	Ser	Glu
	50					55					60				
His	Glu	Lys	Ile	Asp	Val	Asn	Thr	Leu	Ser	Glu	Lys	Leu	Asn	Val	Ser
65				70						75				80	
Lys	Val	Thr	Ile	Arg	Lys	Asp	Leu	Asp	Lys	Leu	Glu	Ser	Lys	Gly	Leu
			85					90						95	
Leu	His	Arg	Glu	His	Gly	Tyr	Ala	Val	Leu	Asn	Ser	Gly	Asp	Asp	Leu
			100					105					110		
Asn	Val	Arg	Leu	Ser	Ile	Asn	Tyr	Glu	Ile	Lys	Arg	Lys	Ile	Val	Gln
		115					120					125			
Glu	Ala	Val	Lys	Leu	Val	Ser	Asp	Asn	Glu	Thr	Ile	Met	Ile	Glu	Ser
	130					135					140				
Gly	Ser	Thr	Cys	Ala	Leu	Leu	Ala	Glu	Glu	Ile	Cys	Lys	Gln	Lys	Arg
145					150					155					160
Asn	Val	Thr	Ile	Val	Thr	Asn	Ser	Phe	Phe	Ile	Ala	Asn	Phe	Val	Arg
			165					170						175	
Ala	Tyr	Asp	Ser	Cys	Arg	Ile	Ile	Val	Leu	Gly	Gly	Glu	Phe	Gln	Lys
		180						185					190		
Asp	Ser	Gln	Val	Thr	Val	Gly	Pro	Leu	Leu	Lys	Glu	Met	Ile	Gln	Thr
		195					200					205			
Phe	His	Val	Arg	Gln	Ala	Phe	Val	Gly	Thr	Asp	Gly	Tyr	Asp	Lys	Glu
	210					215					220				
Met	Gly	Phe	Thr	Gly	Lys	Asp	Leu	Met	Arg	Ser	Glu	Val	Val	Gln	Tyr
225					230					235					240
Ile	Ser	Ala	Ala	Ser	Asp	Lys	Val	Ile	Val	Leu	Thr	Asp	Ser	Ser	Lys
			245						250					255	
Phe	Asp	Lys	Arg	Gly	Thr	Val	Arg	Arg	Phe	Ala	Leu	Ser	Gln	Val	Tyr
			260					265					270		
Glu	Val	Ile	Thr	Asp	Glu	Lys	Leu	Ser	Lys	Gln	Asn	Ile	Ala	Thr	Leu
		275					280						285		

Glu Asn Ala Gly Ile Met Val Lys Val Val Ser
 290 295

(2) INFORMATION FOR SEQ ID NO:4782:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4782:

Pro	Leu	Lys	Ile	Lys	Gln	Ile	Phe	Arg	Ile	Phe	Arg	Leu	Val	Gly	Thr
1				5					10					15	
Asn	Phe	Ser	Phe	Phe	Glu	Tyr	Met	Ile	Gln	Ile	Val	Val	Arg	Ser	
			20				25					30			
Val	Lys	Asp	Tyr	Ser	Glu	Asn	Arg	Lys	Phe	Asp	Ala	Glu	Thr	Leu	Glu
			35				40					45			
Phe	Arg	Lys	Thr	Tyr	Ser	Lys	Met	Lys	Tyr	Gly	Arg	Asn	Asn	Val	Ile
			50				55				60				
Leu	Glu	Phe	Lys	Leu	Asn	Tyr	Asn	Asn	Ile	Val	Glu	Val	Ser	Phe	
65					70				75						

(2) INFORMATION FOR SEQ ID NO:4783:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 303 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...303

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4783:

Pro	Ile	Lys	Ile	Tyr	Arg	Arg	Pro	Asp	Lys	Met	Ala	Ile	Val	Ser	Ala
1				5					10					15	
Glu	Lys	Phe	Val	Gln	Ala	Ala	Arg	Asp	Asn	Gly	Tyr	Ala	Val	Gly	Gly

1				5					10					15		
Lys	Lys	Lys	Lys	Glu	Gly	Lys	Lys	Lys	Gly	Gly	Glu	Lys	Lys	Gly	Arg	
			20					25					30			
Glu	Gly	Lys	Glu	Glu	Glu	Gly	Gly	Val	Lys	Glu	Gly	Gly	Gly	Lys	Arg	
		35					40					45				
Arg	Lys	Lys	Arg	Val	Leu	Arg	Glu	Val	Trp	Gly	Lys	Arg	Gly	Lys	Glu	
	50					55					60					
Lys	Glu	Gly	Lys	Gly	Gly	Gly	Trp	Glu	Gly	Glu	Arg	Lys	Glu	Glu	Lys	
65					70					75					80	
Gly	Met	Gly	Val	Gly	Val	Gly	Glu	Ser	Glu	Lys	Lys					
				85					90							

(2) INFORMATION FOR SEQ ID NO:4785:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 295 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4785:

Lys	Ala	Lys	Met	Asn	Gly	Ile	Ile	Asn	Leu	Lys	Lys	Glu	Ala	Gly	Met	
1				5				10						15		
Thr	Ser	His	Asp	Ala	Val	Phe	Lys	Leu	Arg	Lys	Ile	Leu	Gly	Thr	Lys	
			20					25					30			
Lys	Ile	Gly	His	Gly	Gly	Thr	Leu	Asp	Pro	Asp	Val	Val	Gly	Val	Leu	
		35				40					45					
Pro	Ile	Ala	Val	Gly	Lys	Ala	Thr	Arg	Met	Val	Glu	Phe	Met	Gln	Asp	
	50				55					60						
Glu	Gly	Lys	Ile	Tyr	Glu	Gly	Glu	Ile	Thr	Leu	Gly	Tyr	Ser	Thr	Thr	
65				70						75					80	
Thr	Glu	Asp	Ala	Ser	Gly	Glu	Val	Val	Ala	Glu	Thr	Pro	Val	Leu	Ser	
			85					90						95		
Pro	Leu	Asp	Glu	Lys	Leu	Val	Asp	Glu	Ala	Ile	Ala	Ser	Leu	Thr	Gly	
		100						105					110			
Pro	Ile	Thr	Gln	Ile	Pro	Pro	Met	Tyr	Ser	Ala	Val	Lys	Val	Asn	Gly	
		115					120					125				
Arg	Lys	Leu	Tyr	Glu	Tyr	Ala	Arg	Ala	Gly	Gln	Glu	Val	Glu	Arg	Pro	
	130					135					140					
Glu	Arg	Gln	Val	Thr	Ile	Tyr	Gln	Phe	Glu	Arg	Thr	Ser	Pro	Ile	Ser	
145				150						155					160	
Tyr	Asp	Gly	Gln	Leu	Ala	Arg	Phe	Thr	Phe	Arg	Val	Lys	Cys	Ser	Lys	
			165					170						175		
Gly	Thr	Tyr	Ile	Arg	Thr	Leu	Ser	Val	Asp	Leu	Gly	Glu	Lys	Leu	Gly	
		180					185						190			
Tyr	Ala	Ala	His	Met	Ser	His	Leu	Thr	Arg	Thr	Ser	Ala	Ala	Gly	Leu	

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...68

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4787:

```
Val Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Lys Lys Xaa
1          5          10          15
Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Xaa Gly Xaa Xaa Gly Xaa
20          25          30
Gly Gly Gly Gly Gly Gly Gly Xaa Gly Gly Gly Gly Gly Gly Gly Gly
35          40          45
Gly Gly Xaa Gly Gly Gly Gly Gly Gly Gly Gly Gly Gly Xaa Gly Gly Xaa
50          55          60
Gly Gly Gly Gly
65
```

(2) INFORMATION FOR SEQ ID NO:4788:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 108 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4788:

```
Ile Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Asn Gly Gly
1          5          10          15
Lys Lys Ile Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys Lys
20          25          30
Lys Lys Gly Lys Lys Lys Lys Arg Gly Lys Lys Glu Gly Gly Gly Glu
35          40          45
Lys Gly Glu Gly Gly Lys Gly Gly Arg Arg Arg Gly Glu Gly Arg Gly
50          55          60
Gly Glu Lys Lys Glu Lys Lys Gly Val Glu Gly Gly Met Gly Lys Lys
65          70          75          80
Gly Glu Gly Lys Gly Gly Glu Gly Gly Arg Leu Gly Gly Gly Lys Lys
85          90          95
Gly Arg Lys Gly Asn Gly Gly Gly Cys Gly Gly Lys
100          105
```

(2) INFORMATION FOR SEQ ID NO:4789:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 333 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...333
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4789:

Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Thr	Val	Ile
1				5					10					15	
Phe	Phe	Gly	Leu	Leu	Ala	Thr	Asn	Thr	Val	Phe	Ala	Asp	Asn	Ser	Glu
		20					25						30		
Val	Trp	Gln	Phe	Val	Gln	Glu	Asn	Gly	Arg	Thr	Tyr	Tyr	Lys	Lys	Gly
	35						40					45			
Asp	Leu	Lys	Glu	Thr	Tyr	Trp	Arg	Val	Ile	Asp	Gly	Lys	Tyr	Tyr	Tyr
	50					55					60				
Phe	Asp	Ser	Leu	Ser	Gly	Glu	Met	Val	Val	Gly	Trp	Gln	Tyr	Ile	Pro
65					70					75					80
Phe	Pro	Ser	Lys	Gly	Ser	Thr	Ile	Gly	Pro	Tyr	Pro	Asn	Gly	Ile	Arg
			85					90						95	
Leu	Glu	Gly	Phe	Pro	Lys	Ser	Glu	Trp	Tyr	Tyr	Phe	Asp	Lys	Asn	Gly
		100						105					110		
Val	Leu	Gln	Glu	Phe	Val	Gly	Trp	Lys	Thr	Leu	Glu	Ile	Lys	Thr	Lys
		115					120					125			
Asp	Ser	Val	Gly	Arg	Lys	Tyr	Gly	Glu	Lys	Arg	Glu	Asp	Ser	Glu	Asp
	130					135					140				
Lys	Glu	Glu	Lys	Arg	Tyr	Tyr	Thr	Asn	Tyr	Tyr	Phe	Asn	Gln	Asn	His
145					150					155					160
Ser	Leu	Glu	Thr	Gly	Trp	Leu	Tyr	Asp	Gln	Ser	Asn	Trp	Tyr	Tyr	Leu
			165					170						175	
Ala	Lys	Thr	Glu	Ile	Asn	Gly	Glu	Asn	Tyr	Leu	Gly	Gly	Glu	Arg	Arg
			180					185					190		
Ala	Gly	Trp	Ile	Asn	Asp	Asp	Ser	Thr	Trp	Tyr	Tyr	Leu	Asp	Pro	Thr
	195					200						205			
Thr	Gly	Ile	Met	Gln	Thr	Gly	Trp	Gln	Tyr	Leu	Arg	Asn	Lys	Trp	Tyr
	210					215						220			
Tyr	Leu	Arg	Ser	Ser	Gly	Ala	Met	Ala	Thr	Gly	Trp	Tyr	Gln	Glu	Gly
225					230					235					240
Thr	Thr	Trp	Tyr	Tyr	Leu	Asp	Gln	Pro	Asn	Gly	Asp	Met	Lys	Thr	Gly
			245					250						255	
Trp	Gln	Asn	Leu	Gly	Asn	Lys	Trp	Tyr	Tyr	Leu	Arg	Ser	Ser	Gly	Ala
		260					265						270		
Met	Val	Thr	Gly	Trp	Val	Lys	Asp	Asp	Ser	Thr	Trp	Tyr	Tyr	Leu	Asn
	275					280						285			
Ala	Gly	Asn	Gly	Asp	Met	Lys	Thr	Gly	Trp	Phe	Gln	Val	Asn	Gly	Arg

290		295		300													
Trp	Tyr	Tyr	Ala	Tyr	Ser	Ser	Gly	Ala	Leu	Ala	Val	Asn	Thr	Thr	Val		
305					310					315					320		
Asp	Gly	Tyr	Ser	Val	Asn	Tyr	Asn	Gly	Glu	Trp	Val	Arg					
				325					330								

(2) INFORMATION FOR SEQ ID NO:4790:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...67
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4790:

Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys
1				5					10						15		
Lys	Lys	Arg	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys
			20					25					30				
Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Lys	Phe	Tyr	
			35				40						45				
Asn	Lys	Pro	Lys	Thr	Ala	Asp	His	Val	Val	Glu	Glu	Glu	Ala	His	Asp		
	50					55					60						
Asp	Trp	Ile															
65																	

(2) INFORMATION FOR SEQ ID NO:4791:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 471 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...471
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4791:

Val	Lys	Lys	Met	Thr	Lys	Thr	Leu	Pro	Lys	Asp	Phe	Ile	Phe	Gly	Gly
1				5					10					15	
Ala	Thr	Ala	Ala	Tyr	Gln	Ala	Glu	Gly	Ala	Thr	His	Thr	Asp	Gly	Lys
			20					25					30		
Gly	Pro	Val	Ala	Trp	Asp	Lys	Tyr	Leu	Glu	Asp	Asn	Tyr	Trp	Tyr	Thr
		35					40					45			
Ala	Glu	Pro	Ala	Ser	Asp	Phe	Tyr	Asn	Arg	Tyr	Pro	Val	Asp	Leu	Lys
	50					55					60				
Leu	Ala	Glu	Glu	Tyr	Gly	Val	Asn	Gly	Ile	Arg	Ile	Ser	Ile	Ala	Trp
65					70					75					80
Ser	Arg	Ile	Phe	Pro	Thr	Gly	Tyr	Gly	Gln	Val	Asn	Ala	Lys	Gly	Val
				85					90					95	
Glu	Phe	Tyr	His	Asn	Leu	Phe	Ala	Glu	Cys	His	Lys	Arg	His	Val	Glu
			100					105					110		
Pro	Phe	Val	Thr	Leu	His	His	Phe	Asp	Thr	Pro	Glu	Ala	Leu	His	Ser
		115					120					125			
Asn	Gly	Asp	Phe	Leu	Asn	Arg	Glu	Asn	Ile	Glu	His	Phe	Val	Asp	Tyr
	130					135					140				
Ala	Ala	Phe	Cys	Phe	Glu	Glu	Phe	Pro	Glu	Val	Asn	Tyr	Trp	Thr	Thr
145					150					155					160
Phe	Asn	Glu	Ile	Gly	Pro	Ile	Gly	Asp	Gly	Gln	Tyr	Leu	Val	Gly	Lys
				165					170					175	
Phe	Pro	Pro	Gly	Ile	Gln	Tyr	Asp	Leu	Ala	Lys	Val	Phe	Gln	Ser	His
			180					185					190		
His	Asn	Met	Met	Val	Ser	His	Ala	Arg	Ala	Val	Lys	Leu	Tyr	Lys	Glu
		195					200					205			
Lys	Gly	Tyr	Lys	Gly	Glu	Ile	Gly	Val	Val	His	Ala	Leu	Pro	Thr	Lys
	210					215					220				
Tyr	Pro	Leu	Asp	Pro	Glu	Asn	Pro	Ala	Asp	Val	Arg	Ala	Ala	Glu	Leu
225					230					235					240
Glu	Asp	Ile	Ile	His	Asn	Lys	Phe	Ile	Leu	Asp	Ala	Thr	Tyr	Leu	Gly
				245					250					255	
Arg	Tyr	Ser	Ala	Glu	Thr	Met	Glu	Gly	Val	Asn	His	Ile	Leu	Leu	Val
			260				265					270			
Asn	Gly	Gly	Ser	Leu	Asp	Leu	Arg	Glu	Glu	Asp	Phe	Thr	Ala	Leu	Glu
	275					280					285				
Ala	Ala	Lys	Asp	Leu	Asn	Asp	Phe	Leu	Gly	Ile	Asn	Tyr	Tyr	Met	Ser
	290					295					300				
Asp	Trp	Met	Glu	Ala	Phe	Asp	Gly	Glu	Thr	Glu	Ile	Ile	His	Asn	Gly
305					310					315					320
Lys	Gly	Glu	Lys	Gly	Ser	Ser	Lys	Tyr	Gln	Ile	Lys	Gly	Val	Gly	Arg
				325					330					335	
Arg	Val	Ala	Pro	Asp	Tyr	Val	Pro	Arg	Thr	Asp	Trp	Asp	Trp	Ile	Ile
			340					345					350		
Tyr	Pro	Gln	Gly	Leu	Tyr	Asp	Gln	Ile	Met	Arg	Val	Lys	Lys	Asp	Tyr
		355					360					365			
Pro	Asn	Tyr	Lys	Lys	Ile	Tyr	Ile	Thr	Glu	Asn	Gly	Leu	Gly	Tyr	Lys
	370					375					380				
Asp	Glu	Phe	Val	Asp	Asn	Thr	Val	Tyr	Asp	Asp	Gly	Arg	Ile	Asp	Tyr
385					390					395					400
Val	Lys	Gln	His	Leu	Glu	Ile	Leu	Ser	Asp	Ala	Ile	Ala	Asp	Gly	Ala
				405					410					415	
Asn	Val	Lys	Gly	Tyr	Phe	Ile	Trp	Ser	Leu	Met	Asp	Val	Phe	Ser	Trp
			420					425				430			
Ser	Asn	Gly	Tyr	Glu	Lys	Arg	Tyr	Gly	Leu	Phe	Tyr	Val	Asp	Phe	Glu

(2) INFORMATION FOR SEQ ID NO:4792:

(A) LENGTH: 85 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Streptococcus pneumoniae*

(A) NAME/KEY: misc_feature
(B) LOCATION 1...85

[illegible]

(A) LENGTH: 79 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Streptococcus pneumoniae*

(A) NAME/KEY: misc_feature
(B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4793:

Gly	Glu	Lys	Met	Ser	Tyr	Glu	Gln	Glu	Phe	Met	Lys	Glu	Phe	Glu	Ala
1				5					10					15	
Trp	Val	Asn	Thr	Gln	Ile	Met	Ile	Asn	Asp	Met	Ala	His	Lys	Glu	Ser
		20						25					30		
Gln	Lys	Val	Tyr	Glu	Glu	Asp	Gln	Asp	Glu	Arg	Ala	Lys	Asp	Ala	Met
		35					40					45			
Ile	Arg	Tyr	Glu	Ser	Arg	Leu	Asp	Ala	Tyr	Gln	Phe	Leu	Leu	Gly	Lys
	50					55					60				
Phe	Glu	Asn	Phe	Lys	Val	Gly	Lys	Gly	Phe	His	Asp	Leu	Pro	Glu	
65					70					75					

(2) INFORMATION FOR SEQ ID NO:4794:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4794:

Lys	Glu	Lys	Met	Thr	Lys	Lys	Val	Gly	Val	Gly	Gln	Ala	His	Ser	Lys
1				5					10					15	
Ile	Ile	Leu	Ile	Gly	Glu	His	Ala	Val	Val	Tyr	Gly	Tyr	Pro	Ala	Ile
		20						25					30		
Ser	Leu	Pro	Leu	Leu	Glu	Val	Glu	Val	Thr	Cys	Lys	Val	Val	Pro	Ala
		35					40					45			
Glu	Ser	Pro	Trp	Arg	Leu	Tyr	Glu	Glu	Asp	Thr	Leu	Ser	Met	Ala	Val
	50					55					60				
Tyr	Ala	Ser	Leu	Glu	Tyr	Leu	Asp	Ile	Thr	Glu	Ala	Cys	Ile	Arg	Cys
65					70					75				80	
Glu	Ile	Asp	Ser	Ala	Ile	Pro	Glu	Lys	Arg	Gly	Met	Gly	Ser	Ser	Ala
			85						90					95	
Ala	Ile	Ser	Ile	Ala	Ala	Ile	Arg	Ala	Val	Phe	Asp	Tyr	Tyr	Gln	Ala
		100						105					110		
Asp	Leu	Pro	His	Asp	Val	Leu	Glu	Ile	Leu	Val	Asn	Arg	Ala	Glu	Met
	115						120					125			
Ile	Ala	His	Met	Asn	Pro	Ser	Gly	Leu	Asp	Ala	Lys	Thr	Cys	Leu	Ser
	130					135					140				
Asp	Gln	Pro	Ile	Arg	Phe	Ile	Lys	Asn	Val	Gly	Phe	Thr	Glu	Leu	Glu
145				150					155					160	
Met	Asp	Leu	Ser	Ala	Tyr	Leu	Val	Ile	Ala	Asp	Thr	Gly	Val	Tyr	Gly
			165						170					175	
His	Thr	Arg	Glu	Ala	Ile	Gln	Val	Val	Gln	Asn	Lys	Gly	Lys	Asp	Ala
			180					185						190	

Leu	Pro	Phe	Leu	His	Ala	Leu	Gly	Glu	Leu	Thr	Gln	Gln	Ala	Glu	Val
		195					200					205			
Ala	Ile	Ser	Gln	Lys	Asp	Ala	Glu	Gly	Leu	Gly	Gln	Ile	Leu	Ser	Gln
	210					215					220				
Ala	His	Leu	His	Leu	Lys	Glu	Ile	Gly	Val	Ser	Ser	Pro	Glu	Ala	Asp
225					230					235					240
Phe	Leu	Val	Glu	Thr	Thr	Leu	Ser	His	Gly	Ala	Leu	Gly	Ala	Lys	Met
				245					250					255	
Ser	Gly	Gly	Gly	Leu	Gly	Gly	Cys	Ile	Ile	Ala	Leu	Val	Thr	Asn	Leu
			260					265					270		
Thr	His	Ala	Gln	Glu	Leu	Ala	Glu	Arg	Leu	Glu	Glu	Lys	Gly	Ala	Val
		275					280						285		
Gln	Thr	Trp	Ile	Glu	Ser	Leu									
	290					295									

(2) INFORMATION FOR SEQ ID NO:4795:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 363 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...363

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4795:

Gly	Arg	Lys	Met	Lys	Thr	Lys	Leu	Pro	Thr	Glu	Trp	Gln	Glu	Leu	Ser
1				5				10					15		
Asp	Gln	Leu	Gly	Phe	Gln	Glu	Phe	Thr	Pro	Ile	Gln	Thr	Gln	Leu	Phe
		20					25					30			
Asp	Pro	Leu	Leu	Thr	Gly	Glu	Asn	Leu	Leu	Gly	Val	Ser	Gln	Thr	Gly
	35					40					45				
Thr	Gly	Lys	Thr	Leu	Ala	Tyr	Leu	Leu	Pro	Ser	Leu	Leu	Arg	Leu	Gln
	50					55				60					
Lys	Lys	Lys	Ala	Gln	Gln	Leu	Leu	Ile	Leu	Ala	Pro	Asn	Thr	Glu	Leu
65				70					75					80	
Ala	Gly	Gln	Ile	Phe	Asp	Val	Cys	Lys	Thr	Trp	Ala	Glu	Ala	Ile	Gly
			85					90						95	
Leu	Thr	Ala	Gln	Leu	Phe	Leu	Ser	Gly	Ser	Ser	Gln	Lys	Arg	Gln	Ile
		100					105					110			
Glu	Arg	Leu	Lys	Lys	Gly	Pro	Glu	Ile	Leu	Ile	Gly	Thr	Pro	Gly	Arg
	115					120					125				
Ile	Phe	Glu	Leu	Ile	Lys	Leu	Lys	Lys	Ile	Lys	Met	Met	Asn	Val	Glu
	130				135				140						
Thr	Ile	Ile	Leu	Asp	Glu	Phe	Asp	Gln	Leu	Leu	Asp	Asp	Ser	Gln	Ile
145				150					155					160	
His	Phe	Val	Glu	Lys	Ile	Thr	His	Tyr	Ala	Pro	Arg	Asp	His	Gln	Leu
				165				170						175	

Val	Tyr	Met	Ser	Ala	Thr	Thr	Lys	Phe	Asp	Gln	Glu	Lys	Ile	Val	Pro
			180					185					190		
Asn	Thr	Arg	Thr	Ile	Asp	Leu	Ser	Asn	Gln	Lys	Leu	Asp	Asn	Ile	Gln
		195					200					205			
His	Phe	Tyr	Met	Gln	Val	Asp	Gln	Arg	His	Arg	Val	Asp	Ile	Leu	Arg
	210					215					220				
Lys	Leu	Ala	His	Val	Glu	Asp	Phe	Arg	Gly	Leu	Val	Phe	Phe	Asn	Ser
	225				230					235					240
Leu	Ser	Asp	Leu	Gly	Asn	Ala	Glu	Glu	Lys	Leu	Gln	Tyr	Arg	Asp	Ile
			245					250						255	
Leu	Ala	Val	Ser	Leu	Ala	Ser	Asp	Val	Asn	Val	Lys	Phe	Arg	Lys	Val
		260						265					270		
Ile	Leu	Glu	Lys	Phe	Lys	Asp	Asn	Gln	Leu	Thr	Leu	Leu	Leu	Ala	Thr
	275						280					285			
Asp	Leu	Leu	Ala	Arg	Gly	Ile	Asp	Ile	Asp	Ser	Leu	Glu	Cys	Val	Val
	290					295				300					
Asn	Phe	Asp	Ile	Pro	Arg	Asp	Ser	Glu	Thr	Tyr	Thr	His	Arg	Ala	Gly
	305				310					315					320
Arg	Thr	Gly	Arg	Met	Gly	Lys	Glu	Gly	Tyr	Val	Ile	Thr	Leu	Val	Thr
			325					330					335		
His	Pro	Glu	Glu	Ile	Lys	Lys	Leu	Lys	Lys	Phe	Ala	Ser	Ile	Arg	Glu
		340					345					350			
Ile	Val	Leu	Lys	Asn	Gln	Glu	Leu	Tyr	Ile	Lys					
		355				360									

(2) INFORMATION FOR SEQ ID NO:4796:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4796:

Ser	Met	Lys	Ile	Leu	Ile	Val	Glu	Asp	Glu	Glu	Met	Ile	Arg	Glu	Gly
1			5				10				15				
Val	Ser	Asp	Tyr	Leu	Thr	Asp	Cys	Gly	Tyr	Glu	Thr	Ile	Glu	Ala	Ala
		20					25				30				
Asp	Gly	Gln	Glu	Ala	Leu	Glu	Gln	Phe	Ser	Ser	Tyr	Glu	Val	Ala	Leu
	35					40					45				
Val	Leu	Leu	Asp	Ile	Gln	Met	Pro	Lys	Leu	Asn	Gly	Leu	Glu	Val	Leu
	50				55				60						
Ala	Glu	Ile	Arg	Lys	Thr	Ser	Gln	Val	Pro	Val	Leu	Met	Leu	Thr	Ala
	65				70				75				80		
Phe	Gln	Asp	Glu	Glu	Tyr	Lys	Met	Ser	Ala	Phe	Ala	Ser	Leu	Ala	Asp
		85					90						95		

Gly	Tyr	Leu	Glu	Lys	Pro	Phe	Ser	Leu	Ser	Leu	Leu	Lys	Val	Arg	Val
			100					105					110		
Asp	Ala	Ile	Phe	Lys	Arg	Tyr	Tyr	Asp	Thr	Gly	Arg	Ile	Phe	Ser	Tyr
		115					120					125			
Lys	Asp	Thr	Lys	Val	Asp	Phe	Glu	Ser	Tyr	Ser	Ala	Ser	Leu	Ala	Gly
		130				135					140				
Gln	Glu	Val	Pro	Ile	Asn	Ala	Lys	Glu	Leu	Glu	Ile	Leu	Asp	Tyr	Leu
145					150					155					160
Val	Lys	Asn	Glu	Gly	Arg	Ala	Leu	Thr	Arg	Ser	Gln	Ile	Ile	Asp	Ala
				165					170					175	
Val	Trp	Lys	Ala	Thr	Asp	Glu	Val	Pro	Phe	Asp	Arg	Val	Ile	Asp	Val
			180					185					190		
Tyr	Ile	Lys	Glu	Leu	Arg	Lys	Lys	Leu	Asp	Leu	Asp	Cys	Ile	Leu	Thr
		195					200					205			
Val	Arg	Asn	Val	Gly	Tyr	Lys	Leu	Glu	Arg	Lys					
		210				215									

(2) INFORMATION FOR SEQ ID NO:4797:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 175 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4797:

Lys	Met	Lys	Ile	Ala	Ile	Ile	Gly	Tyr	Ser	Gly	Ser	Gly	Lys	Ser	Thr
1				5					10				15		
Leu	Ala	Glu	Lys	Leu	Ser	Asn	Tyr	Tyr	Ser	Ile	Pro	Lys	Leu	His	Met
			20					25					30		
Asp	Thr	Leu	Gln	Phe	Gln	Pro	Gly	Trp	Gln	Asp	Ser	Asp	His	Glu	Trp
		35					40					45			
Met	Leu	Thr	Glu	Ile	Lys	Asn	Phe	Leu	Thr	Lys	His	Lys	Ala	Trp	Val
		50				55					60				
Ile	Asp	Gly	Asn	Tyr	Ser	Trp	Cys	Tyr	Tyr	Gln	Glu	Arg	Met	Gln	Glu
65				70						75				80	
Ala	Asp	Gln	Ile	Ile	Phe	Leu	Asn	Phe	Trp	Pro	Leu	Thr	Cys	Leu	Phe
			85						90				95		
Arg	Ala	Phe	Lys	Arg	Tyr	Leu	Lys	Tyr	Arg	Gly	Lys	Val	Arg	Glu	Ser
			100					105					110		
Met	Ala	Ala	Asp	Cys	Pro	Glu	Arg	Phe	Asp	Trp	Glu	Phe	Ile	Arg	Trp
		115					120					125			
Ile	Leu	Trp	Asp	Gly	Arg	Ser	Lys	Thr	Gln	Lys	Glu	Asn	Tyr	Gln	Lys
		130				135					140				
Leu	Cys	Gln	Glu	Tyr	Ser	His	Lys	Val	Thr	Ile	Leu	Arg	Asn	Gln	Arg
145					150					155					160

Glu Leu Asp Gln Phe Leu Asp Lys Lys Arg Lys Ser Tyr Asn Ser
165 170 175

(2) INFORMATION FOR SEQ ID NO:4798:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4798:

Ile	Lys	Lys	Ile	Pro	Leu	Gln	Asp	Gly	Val	Leu	Cys	Tyr	Asn	Arg	Asp
1				5					10					15	
Met	Lys	Thr	Asn	Asp	Ile	Val	Tyr	Gly	Val	His	Ala	Val	Thr	Glu	Ala
			20					25					30		
Leu	Leu	Ala	Asn	Thr	Gly	Asn	Lys	Leu	Tyr	Leu	Gln	Glu	Asp	Leu	Arg
		35				40					45				
Gly	Lys	Asn	Val	Glu	Lys	Val	Lys	Glu	Leu	Ala	Thr	Glu	Lys	Lys	Val
	50				55					60					
Ser	Ile	Ser	Trp	Thr	Ser	Lys	Lys	Ser	Leu	Ser	Glu	Met	Thr	Glu	Gly
65				70					75					80	
Ala	Val	His	Gln	Gly	Phe	Val	Leu	Arg	Val	Ser	Glu	Phe	Ala	Tyr	Ser
			85					90					95		
Glu	Leu	Asp	Tyr	Ile	Leu	Ala	Lys	Thr	Arg	Gln	Glu	Glu	Asn	Pro	Leu
		100					105						110		
Leu	Leu	Ile	Leu	Asp	Gly	Leu	Thr	Asp	Pro	His	Asn	Leu	Gly	Ser	Ile
	115					120						125			
Leu	Arg	Thr	Ala	Asp	Ala	Thr	Asn	Val	Ser	Gly	Val	Ile	Ile	Pro	Lys
	130				135						140				
His	Arg	Ala	Val	Gly	Val	Thr	Pro	Val	Val	Ala	Lys	Thr	Ala	Thr	Gly
145				150					155					160	
Ala	Ile	Glu	His	Val	Pro	Ile	Ala	Arg	Val	Thr	Asn	Leu	Asn	Gln	Thr
			165					170					175		
Leu	Tyr	Lys	Leu	Lys	Asp	Glu	Gly	Phe	Trp	Thr	Phe	Gly	Thr	Asp	Met
	180						185					190			
Asn	Gly	Thr	Pro	Cys	Tyr	Lys	Trp	Asn	Thr	Lys	Gly	Lys	Ile	Ala	Leu
	195					200					205				
Ile	Ile	Gly	Asn	Glu	Gly	Lys	Gly	Ile	Ser	Ser	Asn	Ile	Lys	Lys	Gln
	210				215						220				
Val	Asp	Glu	Met	Ile	Thr	Ile	Pro	Met	Asn	Gly	His	Val	Gln	Ser	Leu
225				230					235					240	
Asn	Ala	Ser	Val	Ala	Ala	Ala	Ile	Leu	Met	Tyr	Glu	Val	Phe	Arg	Asn
			245					250					255		
Arg	Leu														

(2) INFORMATION FOR SEQ ID NO:4799:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 110 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...110
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4799:

Ser	Glu	Lys	Ile	Leu	Gln	Arg	Leu	Glu	Val	Tyr	Lys	Asn	Tyr	Gln	His
1			5					10						15	
Leu	Tyr	Asp	Leu	Arg	Met	Thr	Ile	Leu	Leu	Asn	Leu	Ser	Thr	Leu	Tyr
		20					25					30			
Leu	Tyr	Asn	Gln	Asp	Lys	Asn	Met	Cys	Lys	Gln	Ile	Cys	Tyr	Thr	Leu
		35				40						45			
Leu	Glu	Asp	Ala	Lys	Asn	Lys	Lys	Ser	Tyr	Asp	Arg	Leu	Ala	Ile	Cys
	50					55				60					
Tyr	Val	Arg	Ile	Gly	Ile	Cys	Arg	Asp	Asn	Ala	Lys	Leu	Ile	Gln	Lys
65				70					75					80	
Gly	Phe	Ser	Leu	Leu	Glu	Leu	Thr	Glu	Glu	Thr	Ser	Met	Leu	Ser	His
			85					90					95		
Leu	Lys	Lys	Glu	Val	Glu	Ile	Tyr	Tyr	Gln	Ala	Lys	Glu	Arg		
			100				105						110		

(2) INFORMATION FOR SEQ ID NO:4800:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 206 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...206
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4800:

Gly Glu Lys Met Ser Ala Ile Glu Arg Ile Thr Lys Ala Ala His Leu

1				5					10					15	
Ile	Asp	Met	Asn	Asp	Ile	Ile	Arg	Glu	Gly	Asn	Pro	Thr	Leu	Arg	Ala
			20					25					30		
Ile	Ala	Glu	Glu	Val	Thr	Phe	Pro	Leu	Ser	Asp	Gln	Glu	Ile	Ile	Leu
		35					40					45			
Gly	Glu	Lys	Met	Met	Gln	Phe	Leu	Lys	His	Ser	Gln	Asp	Pro	Val	Met
	50				55						60				
Ala	Glu	Lys	Met	Gly	Leu	Arg	Gly	Gly	Val	Gly	Leu	Ala	Ala	Pro	Gln
65				70						75					80
Leu	Asp	Ile	Ser	Lys	Arg	Ile	Ile	Ala	Val	Leu	Val	Pro	Asn	Ile	Val
				85					90					95	
Glu	Glu	Gly	Glu	Thr	Pro	Gln	Glu	Ala	Tyr	Asp	Leu	Glu	Ala	Ile	Met
			100					105					110		
Tyr	Asn	Pro	Lys	Ile	Val	Ser	His	Ser	Val	Gln	Asp	Ala	Ala	Leu	Gly
		115					120					125			
Glu	Gly	Glu	Gly	Cys	Leu	Ser	Val	Asp	Arg	Asn	Val	Pro	Gly	Tyr	Val
	130					135					140				
Val	Arg	His	Ala	Arg	Val	Thr	Val	Asp	Tyr	Phe	Asp	Lys	Asp	Gly	Glu
145					150					155					160
Lys	His	Arg	Ile	Lys	Leu	Lys	Gly	Tyr	Asn	Ser	Ile	Val	Val	Gln	His
				165					170					175	
Glu	Ile	Asp	His	Ile	Asn	Gly	Ile	Met	Phe	Tyr	Asp	Arg	Ile	Asn	Glu
		180					185						190		
Lys	Asp	Pro	Phe	Ala	Val	Lys	Asp	Gly	Leu	Leu	Ile	Leu	Glu		
		195					200					205			

(2) INFORMATION FOR SEQ ID NO:4801:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 183 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...183

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4801:

Gln	Glu	Lys	Ile	Asn	Met	Ser	Arg	Ile	Gly	Asn	Lys	Val	Ile	Val	Leu
1				5					10					15	
Pro	Ala	Gly	Val	Glu	Leu	Ala	Asn	Asn	Asp	Asn	Val	Val	Thr	Val	Lys
			20					25					30		
Gly	Pro	Lys	Gly	Glu	Leu	Thr	Arg	Glu	Phe	Ser	Lys	Asp	Ile	Glu	Ile
		35					40					45			
Arg	Val	Glu	Gly	Thr	Glu	Val	Thr	Leu	His	Arg	Pro	Asn	Asp	Ser	Lys
	50					55					60				
Glu	Met	Lys	Thr	Ile	His	Gly	Thr	Thr	Arg	Ala	Leu	Leu	Asn	Asn	Met
65					70					75					80
Val	Val	Gly	Val	Ser	Glu	Gly	Phe	Lys	Lys	Glu	Leu	Glu	Met	Arg	Gly

				85					90					95			
Val	Gly	Tyr	Arg	Ala	Gln	Leu	Gln	Gly	Ser	Lys	Leu	Val	Leu	Ala	Val		
			100					105					110				
Gly	Lys	Ser	His	Pro	Asp	Glu	Val	Glu	Ala	Pro	Glu	Gly	Ile	Thr	Phe		
		115					120					125					
Glu	Leu	Pro	Asn	Pro	Thr	Thr	Ile	Val	Val	Ser	Gly	Ile	Ser	Lys	Glu		
	130						135				140						
Val	Val	Gly	Gln	Thr	Ala	Ala	Tyr	Val	Arg	Ser	Leu	Arg	Ser	Pro	Glu		
145					150					155					160		
Pro	Tyr	Lys	Gly	Lys	Gly	Ile	Arg	Tyr	Val	Gly	Glu	Phe	Val	Arg	Arg		
			165					170						175			
Lys	Glu	Gly	Lys	Thr	Gly	Lys											
			180														

(2) INFORMATION FOR SEQ ID NO:4802:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 263 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...263

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4802:

Lys	Glu	Lys	Ile	Met	Pro	Val	Met	Lys	Ile	Glu	Tyr	Tyr	Ser	Gln	Val
1				5				10					15		
Leu	Asp	Met	Glu	Trp	Gly	Met	Asn	Val	Leu	Tyr	Pro	Asp	Ala	Asn	Arg
		20					25					30			
Val	Arg	Glu	Pro	Glu	Cys	Glu	Asp	Ile	Pro	Val	Leu	Tyr	Leu	Leu	His
	35					40					45				
Gly	Met	Ser	Gly	Asn	His	Asn	Ser	Trp	Leu	Lys	Arg	Thr	Asn	Val	Glu
	50				55					60					
Arg	Leu	Leu	Arg	Gly	Thr	Asn	Leu	Ile	Val	Val	Met	Pro	Asn	Thr	Ser
65				70				75						80	
Asn	Gly	Trp	Tyr	Thr	Asp	Thr	Gln	Tyr	Gly	Phe	Asp	Tyr	Tyr	Thr	Ala

				85					90					95			
Leu	Ala	Glu	Glu	Leu	Pro	Gln	Val	Leu	Lys	Arg	Phe	Phe	Pro	Asn	Met		
		100						105					110				
Thr	Ser	Lys	Arg	Glu	Lys	Thr	Phe	Ile	Ala	Gly	Leu	Ser	Met	Gly	Gly		
	115					120						125					
Tyr	Gly	Cys	Phe	Lys	Leu	Ala	Leu	Ala	Thr	Asn	Arg	Phe	Ser	His	Ala		
	130					135				140							
Ala	Ser	Phe	Ser	Gly	Ala	Leu	Ser	Phe	Gln	Asn	Phe	Ser	Pro	Glu	Ser		
145					150				155					160			
Gln	Asn	Leu	Gly	Ser	Pro	Ala	Tyr	Trp	Arg	Gly	Val	Phe	Gly	Glu	Ile		
			165					170						175			

Arg	Asp	Trp	Thr	Thr	Ser	Pro	Tyr	Ser	Leu	Glu	Ser	Leu	Ala	Lys	Lys
			180					185					190		
Ser	Asp	Lys	Lys	Thr	Lys	Leu	Trp	Ala	Trp	Cys	Gly	Glu	Gln	Asp	Phe
		195					200					205			
Leu	Tyr	Glu	Ala	Asn	Asn	Leu	Ala	Val	Lys	Asn	Leu	Lys	Lys	Leu	Gly
		210				215					220				
Phe	Asp	Val	Thr	Tyr	Ser	His	Ser	Ala	Gly	Thr	His	Glu	Trp	Tyr	Tyr
225					230					235					240
Trp	Glu	Lys	Gln	Leu	Glu	Val	Phe	Leu	Thr	Thr	Leu	Pro	Ile	Asp	Phe
			245						250					255	
Lys	Leu	Glu	Glu	Arg	Leu	Thr									
			260												

(2) INFORMATION FOR SEQ ID NO:4803:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 121 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...121

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4803:

Arg	Val	Glu	Ile	Arg	Arg	Arg	Asn	Met	Thr	Gln	Ala	Glu	Arg	Ile	Arg
1				5					10					15	
Glu	Tyr	Tyr	Arg	Glu	His	Pro	Ala	Ala	Ser	Tyr	Asp	Glu	Val	Ala	Glu
			20				25					30			
Val	Val	Gly	Thr	Thr	Asn	Ser	Asn	Val	Arg	Ala	Asn	Leu	Ala	Lys	Asp
		35				40					45				
Ile	Lys	Ala	Gly	Arg	Cys	Val	Arg	Leu	Glu	Asp	Lys	Ser	Tyr	Asp	Tyr
	50				55					60					
Ser	Pro	Tyr	Tyr	Asn	His	Thr	Gln	Ala	Leu	Thr	Glu	Leu	Val	Asp	Trp
65				70					75					80	
Lys	Asn	Asp	Asn	Arg	Arg	Glu	Trp	Val	Asp	Met	Leu	Thr	Arg	Ala	Ala
			85					90					95		
Glu	Lys	Glu	Thr	Asp	Ser	Asn	Val	Met	Arg	Leu	Leu	Ile	Lys	Glu	Ala
			100				105						110		
Asn	Lys	Leu	Met	Lys	Glu	Val	Thr	Lys							
		115					120								

(2) INFORMATION FOR SEQ ID NO:4804:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...97
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4804:

```

Met Asn Glu Ile Cys His Leu Phe Ile Tyr Ser Val Leu Lys Gly Tyr
 1             5             10             15
Ser Leu Glu Gly Trp Lys Lys Ile Asn Gly Ser Trp Tyr Tyr Tyr Arg
      20             25             30
Gln His Asp Lys Gln Thr Gly Trp Gln Glu Ile Asn Asp Thr Trp Tyr
      35             40             45
Tyr Leu Asp Ser Ser Gly Lys Met Leu Thr Asp Trp Gln Lys Val Asn
 50             55             60
Gly Lys Trp Tyr Tyr Leu Asn Ser Asn Arg Ala Met Val Thr Gly Ser
65             70             75             80
Gln Thr Ile Asp Gly Lys Val Tyr Asn Phe Ala Ser Ser Gly Glu Trp
      85             90             95
Ile

```

(2) INFORMATION FOR SEQ ID NO:4805:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 278 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...278
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4805:

```

Glu Ile Glu Met Lys Leu Arg Arg Ser Asp Arg Met Val Val Ile Ser
 1             5             10             15
Asn Tyr Leu Ile Asn Asn Pro Tyr Lys Leu Thr Ser Leu Asn Thr Phe
      20             25             30
Ala Glu Lys Tyr Glu Ser Ala Lys Ser Ser Ile Ser Glu Asp Ile Val
      35             40             45
Ile Ile Lys Arg Ala Phe Glu Glu Ile Glu Ile Gly His Ile Gln Thr
 50             55             60
Val Thr Gly Ala Gly Gly Gly Val Ile Phe Thr Pro Ser Ile Ser Ser

```

65					70					75				80
Gln	Asp	Ala	Lys	Glu	Met	Val	Glu	Asp	Leu	Arg	Thr	Lys	Leu	Ser
				85					90					95
Ser	Asp	Arg	Ile	Leu	Pro	Gly	Gly	Tyr	Ile	Tyr	Leu	Ser	Asp	Leu
			100					105					110	
Ser	Thr	Pro	Ala	Ile	Leu	Lys	Asn	Ile	Gly	Arg	Ile	Ile	Ala	Lys
			115				120					125		
Phe	Met	Asp	Gln	Lys	Ile	Asp	Ala	Val	Met	Thr	Val	Ala	Thr	Lys
			130			135					140			
Val	Pro	Leu	Ala	Asn	Ala	Val	Ala	Asn	Val	Leu	Asn	Val	Ser	Phe
145				150					155					160
Ile	Val	Arg	Arg	Asp	Leu	Lys	Ile	Thr	Glu	Gly	Ser	Thr	Val	Ser
				165				170						175
Asn	Tyr	Val	Ser	Gly	Ser	Ser	Gly	Asp	Arg	Ile	Glu	Lys	Met	Phe
			180				185						190	
Ser	Lys	Arg	Ser	Leu	Lys	Ala	Gly	Ser	Arg	Val	Leu	Ile	Val	Asp
			195				200					205		
Phe	Leu	Lys	Gly	Gly	Gly	Thr	Val	Asn	Gly	Met	Ile	Ser	Leu	Leu
210					215					220				
Glu	Phe	Asp	Ser	Glu	Leu	Ala	Gly	Val	Ala	Val	Phe	Ala	Asp	Asn
225				230					235					240
Gln	Glu	Glu	Arg	Glu	Lys	Gln	Phe	Asp	Tyr	Lys	Ser	Leu	Leu	Lys
				245				250						255
Thr	Asn	Ile	Asp	Val	Lys	Asn	Gln	Ala	Ile	Asp	Val	Glu	Val	Gly
			260				265						270	
Ile	Phe	Asp	Glu	Asp	Lys									
			275											

(2) INFORMATION FOR SEQ ID NO:4806:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 364 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4806:

Gly	Glu	Glu	Met	Lys	Pro	Ser	Ile	His	Ser	Leu	Ala	His	Gln	Thr	Met
1				5				10					15		
Gln	Glu	Trp	Val	Leu	Glu	Gln	Gly	Glu	Lys	Lys	Phe	Arg	Ala	Asp	Gln
			20				25						30		
Ile	Trp	Glu	Trp	Leu	Tyr	Arg	Lys	Arg	Val	Gln	Ser	Phe	Glu	Glu	Met
			35			40					45				
Thr	Asn	Leu	Ser	Lys	Asp	Leu	Ile	Ala	Lys	Leu	Asn	Asp	Gln	Phe	Val
50				55				60							
Val	Asn	Pro	Leu	Lys	Gln	Gly	Ile	Val	Gln	Glu	Ser	Ala	Asp	Gly	Thr

65					70					75				80
Val	Lys	Tyr	Leu	Phe	Glu	Leu	Pro	Asp	Gly	Met	Leu	Ile	Glu	Thr
				85					90				95	
Leu	Met	Arg	Gln	His	Tyr	Gly	Leu	Ser	Val	Cys	Val	Thr	Thr	Gln
			100					105					110	
Gly	Cys	Asn	Ile	Gly	Cys	Thr	Phe	Cys	Ala	Ser	Gly	Leu	Ile	Lys
		115					120					125		
Gln	Arg	Asp	Leu	Asn	Asn	Gly	Glu	Ile	Val	Ala	Gln	Ile	Met	Leu
		130				135					140			
Gln	Lys	Tyr	Phe	Ala	Glu	Arg	Gly	Gln	Asp	Glu	Arg	Val	Ser	His
145					150				155					160
Val	Val	Met	Gly	Ile	Gly	Glu	Pro	Phe	Asp	Asn	Tyr	Asn	Asn	Val
			165					170						175
Asn	Phe	Phe	Arg	Thr	Ile	Asn	Asp	Asp	Lys	Gly	Met	Ala	Ile	Gly
			180				185						190	
Arg	His	Ile	Thr	Val	Ser	Thr	Ser	Gly	Leu	Ala	His	Lys	Ile	Arg
		195				200					205			
Phe	Ala	Asp	Glu	Gly	Val	Gln	Val	Asn	Leu	Ala	Val	Ser	Leu	His
210					215					220				
Pro	Asn	Asn	Glu	Leu	Arg	Ser	Ser	Ile	Met	Lys	Ile	Asn	Arg	Ala
225				230					235					240
Pro	Ile	Glu	Lys	Leu	Phe	Ala	Ala	Ile	Glu	Tyr	Tyr	Ile	Glu	Thr
			245					250					255	
Asn	Arg	Gly	Val	Thr	Phe	Glu	Tyr	Ile	Met	Leu	Asn	Glu	Val	Asn
		260					265					270		
Gly	Val	Glu	Gln	Ala	Leu	Glu	Leu	Thr	Glu	Leu	Leu	Lys	Asn	Ile
		275				280						285		
Lys	Leu	Ser	Tyr	Val	Asn	Leu	Ile	Pro	Tyr	Asn	Pro	Val	Ser	Glu
		290			295					300				
Asp	Gln	Tyr	Ser	Arg	Ser	Pro	Lys	Glu	Arg	Val	Leu	Ala	Phe	Tyr
305				310					315					320
Thr	Leu	Lys	Lys	Lys	Gly	Val	Asn	Cys	Val	Val	Arg	Gln	Glu	His
			325				330						335	
Thr	Asp	Ile	Asp	Ala	Ala	Cys	Gly	Gln	Leu	Arg	Ser	Asn	Thr	Met
		340				345						350		
Arg	Asp	Arg	Gln	Lys	Ala	Val	Ala	Val	Asn	Pro				
		355				360								

(2) INFORMATION FOR SEQ ID NO:4807:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 72 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...72

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4807:

Asp	Arg	Glu	Ile	Ser	Phe	Phe	Leu	Leu	Ile	Ser	Pro	Leu	Val	Gly	Ser
1				5					10					15	
Ser	Ser	Pro	Thr	Lys	Ile	Phe	Lys	Arg	Val	Asp	Leu	Pro	Ala	Pro	Phe
			20					25					30		
Phe	Pro	Thr	Arg	Ala	Ile	Arg	Ser	Arg	Ser	Ser	Thr	Cys	Arg	Leu	Ile
		35					40					45			
Leu	Ser	Lys	Arg	Thr	Ser	Pro	Ala	Lys	Glu	Arg	Ser	Ile	Leu	Leu	Ala
	50					55					60				
Cys	Lys	Ile	Ile	Ile	Gln	Val	Val								
65					70										

(2) INFORMATION FOR SEQ ID NO:4808:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 237 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...237

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4808:

Ala	Gly	Glu	Ile	Gly	Arg	Met	Asn	Lys	Gln	Glu	Leu	Ile	Lys	Arg	Ile
1				5					10					15	
Glu	Asp	Leu	Pro	Tyr	Thr	Glu	Gly	Pro	Ile	Ala	Asp	Thr	Ile	Glu	Ile
			20					25					30		
Asn	Arg	Asn	Trp	Ile	Leu	Lys	Ser	Ile	Glu	Gln	Leu	Ala	Glu	Ser	Glu
		35				40						45			
Ile	Gly	His	Ala	Asp	Glu	Ala	Pro	Arg	Tyr	Val	Lys	Asn	Ile	Leu	Ala
	50					55					60				
Arg	Leu	Arg	Glu	Leu	Pro	Leu	His	Asp	Arg	Glu	Phe	Trp	Leu	Lys	Ala
65					70					75					80
Ile	Met	Ser	Glu	Phe	Glu	Gln	Asp	Phe	Ser	His	Ala	Lys	Trp	Arg	Glu
				85					90					95	
Gly	Tyr	Glu	Gln	Gly	Lys	Ile	Glu	Gly	Met	Val	Glu	Arg	Glu	Lys	Val
			100					105					110		
Ile	Val	Pro	Gln	Cys	Val	Ala	Glu	Tyr	Ile	Glu	Phe	Lys	Lys	Lys	Asn
		115					120					125			
Asn	Phe	His	Val	Tyr	Gly	Ala	Met	Arg	Val	Ile	Glu	Asp	His	Tyr	Asp
	130					135					140				
Lys	Lys	Val	Pro	Asp	Trp	Phe	Tyr	Glu	Asn	Asn	Ile	Glu	Lys	Phe	Cys
145					150					155					160
Leu	Ala	Trp	Leu	Asp	Gly	Tyr	Glu	Val	Glu	Lys	Glu	Lys	Arg	Tyr	Phe
				165					170					175	
Val	Lys	Ile	Lys	Gly	Asn	Ile	Lys	Glu	Asn	Met	Leu	Val	Tyr	Gly	Glu
			180					185						190	

Leu	Leu	Lys	Arg	Tyr	Phe	Phe	Thr	Lys	Ser	Phe	Ser	Leu	Asp	Asp	Val
		195					200					205			
Ile	Tyr	Ser	His	Thr	Arg	Lys	Glu	Leu	Glu	Asn	Ala	Lys	Ile	Gly	Trp
	210					215				220					
Val	Phe	Asp	Cys	Glu	Gly	Phe	Glu	Ile	Glu	Glu	Val	Glu			
225					230					235					

(2) INFORMATION FOR SEQ ID NO:4809:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 325 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...325

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4809:

Lys	Gly	Glu	Ile	Met	Lys	Thr	Ser	Leu	Lys	Leu	Tyr	Phe	Thr	Ala	Leu
1				5					10					15	
Val	Ala	Ser	Phe	Leu	Leu	Leu	Leu	Gly	Ala	Cys	Ser	Thr	Asn	Ser	Ser
			20					25					30		
Thr	Ser	Gln	Thr	Glu	Thr	Ser	Ser	Ser	Ala	Pro	Thr	Glu	Val	Thr	Ile
		35				40						45			
Lys	Ser	Ser	Leu	Asp	Glu	Val	Lys	Leu	Ser	Lys	Val	Pro	Glu	Lys	Ile
	50				55					60					
Val	Thr	Phe	Asp	Leu	Gly	Ala	Ala	Asp	Thr	Ile	Arg	Ala	Leu	Gly	Phe
65				70				75						80	
Glu	Lys	Asn	Ile	Val	Gly	Met	Pro	Thr	Lys	Thr	Val	Pro	Thr	Tyr	Leu
			85					90						95	
Lys	Asp	Leu	Val	Gly	Thr	Val	Lys	Asn	Val	Gly	Phe	Met	Lys	Glu	Pro
		100					105						110		
Asp	Leu	Glu	Ala	Ile	Ala	Ala	Leu	Glu	Pro	Asp	Leu	Ile	Ile	Ala	Ser
		115					120					125			
Pro	Arg	Thr	Gln	Lys	Phe	Val	Asp	Lys	Phe	Lys	Glu	Ile	Ala	Pro	Thr
		130				135					140				
Val	Leu	Phe	Gln	Ala	Ser	Lys	Asp	Asp	Tyr	Trp	Thr	Ser	Thr	Lys	Ala
145				150						155					160
Asn	Ile	Glu	Ser	Leu	Ala	Ser	Ala	Phe	Gly	Glu	Thr	Gly	Thr	Gln	Lys
			165					170						175	
Ala	Lys	Glu	Glu	Leu	Ala	Lys	Leu	Asp	Lys	Ser	Ile	Gln	Glu	Val	Ala
		180					185					190			
Thr	Lys	Asn	Glu	Ser	Ser	Asp	Lys	Lys	Ala	Leu	Ala	Ile	Leu	Leu	Asn
		195				200						205			
Glu	Gly	Lys	Met	Ala	Ala	Phe	Gly	Ala	Lys	Ser	Arg	Phe	Ser	Phe	Leu
	210				215					220					
Tyr	Gln	Thr	Leu	Lys	Phe	Lys	Pro	Thr	Asp	Thr	Thr	Phe	Glu	Asp	Ser
225					230					235					240

Arg	His	Gly	Gln	Glu	Val	Ser	Phe	Glu	Ser	Val	Lys	Glu	Ile	Asn	Pro
				245					250					255	
Asp	Ile	Leu	Phe	Val	Ile	Asn	Arg	Thr	Leu	Ala	Ile	Gly	Gly	Asp	Asn
			260					265					270		
Ser	Ser	Asn	Asn	Gly	Val	Leu	Glu	Asn	Ala	Leu	Ile	Ala	Glu	Thr	Pro
		275					280					285			
Ala	Ala	Lys	Asn	Gly	Lys	Ile	Ile	Gln	Leu	Thr	Pro	Asp	Leu	Trp	Tyr
	290					295					300				
Leu	Ser	Gly	Gly	Gly	Leu	Glu	Ser	Thr	Lys	Leu	Met	Ile	Glu	Asp	Ile
305					310					315					320
Gln	Lys	Ala	Leu	Lys											
				325											

(2) INFORMATION FOR SEQ ID NO:4810:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4810:

Glu	Gly	Glu	Ile	Met	Thr	Leu	Leu	Gln	Leu	Gln	Asp	Val	Thr	Tyr	Arg
1				5				10						15	
Tyr	Lys	Asn	Thr	Ala	Glu	Ala	Val	Leu	Tyr	Gln	Ile	Asp	Tyr	Asn	Phe
			20					25					30		
Glu	Pro	Gly	Lys	Phe	Tyr	Ser	Ile	Ile	Gly	Glu	Ser	Gly	Ala	Gly	Lys
		35					40					45			
Ser	Thr	Leu	Leu	Ser	Leu	Leu	Ala	Gly	Leu	Asp	Ser	Pro	Val	Glu	Gly
	50					55					60				
Ser	Ile	Leu	Phe	Gln	Gly	Glu	Asp	Ile	Arg	Lys	Lys	Gly	Tyr	Ser	Tyr
65				70					75						80
His	Arg	Met	His	His	Ile	Ser	Leu	Val	Phe	Gln	Asn	Tyr	Asn	Leu	Ile
			85					90						95	
Asp	Tyr	Leu	Ser	Pro	Leu	Glu	Asn	Ile	Arg	Leu	Val	Asn	Lys	Lys	Ala
			100					105					110		
Ser	Lys	Asn	Thr	Leu	Leu	Glu	Leu	Gly	Leu	Asp	Glu	Ser	Gln	Ile	Lys
		115					120					125			
Arg	Asn	Val	Leu	Gln	Leu	Ser	Gly	Gly	Gln	Gln	Gln	Arg	Val	Ala	Ile
	130					135					140				
Ala	Arg	Ser	Leu	Val	Ser	Glu	Ala	Pro	Val	Ile	Leu	Ala	Asp	Glu	Pro
145					150					155					160
Thr	Gly	Asn	Leu	Asp	Pro	Lys	Thr	Ala	Gly	Asp	Ile	Val	Glu	Leu	Leu
			165						170					175	
Lys	Ser	Leu	Ala	Gln	Lys	Thr	Gly	Lys	Cys	Val	Ile	Val	Val	Thr	His
			180					185						190	

Ser Lys Glu Val Ala Gln Ala Ser Asp Ile Thr Leu Glu Leu Lys Asp
195 200 205
Lys Lys Leu Thr Glu Thr Arg Asn Thr Ser Lys
210 215

(2) INFORMATION FOR SEQ ID NO:4811:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 150 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4811:

Tyr Met Glu Ile Lys Asp Ile Leu Asn Val Ser Leu Ile Gln Thr Asp
1 5 10 15
Leu Gln Met Gln Ser Lys Glu Glu Val Phe Glu Ala Leu Ala Gln Leu
20 25 30
Leu Val Glu Thr Gly Tyr Val Ser Asp Arg Asp Gln Phe Ile Glu Val
35 40 45
Leu Tyr Gln Arg Glu Ala Glu Gly Gln Thr Gly Ile Gly Asn Tyr Ile
50 55 60
Ala Ile Pro His Ser Lys Ser Ser Ala Val Glu Lys Ala Gly Val Val
65 70 75 80
Ile Ala Ile Asn His Asn Glu Ile Pro Trp Glu Thr Ile Asp Gly Lys
85 90 95
Gly Val Lys Val Ile Val Leu Phe Ala Val Gly Asp Asp Thr Glu Ala
100 105 110
Ala Arg Glu His Leu Lys Thr Leu Ser Leu Phe Ala Arg Lys Leu Gly
115 120 125
Asn Asp Glu Val Val Ala Lys Leu Val Arg Ala Gln Thr Ser Asp Asp
130 135 140
Val Ile Ala Ala Phe Cys
145 150

(2) INFORMATION FOR SEQ ID NO:4812:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4812:

```

Asn Met Glu Ile Asn Val Ser Lys Leu Arg Thr Asp Leu Pro Gln Val
1           5           10           15
Gly Val Gln Pro Tyr Arg Gln Val His Ala His Ser Thr Gly Asn Pro
          20           25           30
His Ser Thr Val Gln Asn Glu Ala Asp Tyr His Trp Arg Lys Asp Pro
          35           40           45
Glu Leu Gly Phe Phe Ser His Ile Val Gly Asn Gly Cys Ile Met Leu
50           55           60
Gly
65
  
```

(2) INFORMATION FOR SEQ ID NO:4813:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 171 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4813:

```

His Met Glu Ile Ser Leu Leu Thr Asp Val Gly Gln Lys Arg Thr Asn
1           5           10           15
Asn Gln Asp Tyr Val Asn His Tyr Val Asn Arg Ala Gly Arg Thr Met
          20           25           30
Ile Ile Leu Ala Asp Gly Met Gly Gly His Arg Ala Gly Asn Ile Ala
          35           40           45
Ser Glu Met Ala Val Thr Asp Leu Gly Val Ala Trp Val Asp Thr Gln
          50           55           60
Ile Asp Thr Val Asn Glu Val Arg Glu Trp Phe Ala His Tyr Leu Glu
65           70           75           80
Ile Glu Asn Gln Lys Ile His Gln Leu Gly Gln Asp Glu Ala Tyr Arg
          85           90           95
Gly Met Gly Thr Thr Leu Glu Val Leu Ala Ile Ile Asp Asn Gln Ala
          100          105          110
Ile Tyr Ala His Ile Gly Asp Ser Arg Ile Gly Leu Ile Arg Gly Glu
          115          120          125
Glu Tyr His Gln Leu Thr Ser Asp His Ser Leu Val Asn Glu Leu Leu
  
```

130		135		140	
Lys	Ala	Gly	Gln	Leu	Thr
145		150		155	
Lys	Tyr	Tyr	His	Pro	Val
		165		170	

(2) INFORMATION FOR SEQ ID NO:4814:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...63
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4814:

Ala	Met	Glu	Met	Met	Glu	Leu	Pro	Ser	Gln	Asp	Ile	Leu	Ile	Phe	Thr
1			5					10					15		
Lys	Gln	Ile	Arg	His	Trp	Ile	Leu	Ser	Glu	Gln	Val	Ile	Ser	Gly	Glu
		20				25			30						
Arg	Lys	Leu	Phe	Phe	Arg	Glu	Asp	Thr	Pro	Lys	Glu	Ile	Leu	Asp	Met
	35				40			45							
Tyr	Glu	Asn	Ile	Lys	Ser	Lys	Leu	Asp	Cys	Ala	Tyr	Gln	Glu	Val	
50					55			60							

(2) INFORMATION FOR SEQ ID NO:4815:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 241 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...241
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4815:

Ser Lys Glu Ile Ile Met Thr Ala Thr Ser Leu Gly Leu Ser Asn Ile

1			5				10				15				
Glu	Ile	Val	Val	Arg	Ile	Val	Leu	Ser	Val	Val	Ile	Gly	Ser	Ile	Ile
			20					25					30		
Gly	Leu	Glu	Arg	Gly	Ser	Lys	Ser	Gln	Pro	Ala	Gly	Ile	Arg	Thr	Tyr
		35					40					45			
Ser	Ile	Val	Cys	Leu	Ala	Ala	Cys	Leu	Ile	Met	Met	Thr	Asn	Glu	Tyr
	50					55					60				
Val	Ser	Tyr	Lys	Phe	Gly	Thr	Gly	Asp	Pro	Thr	Arg	Leu	Gly	Ala	Gln
65				70						75					80
Val	Ile	Ser	Gly	Val	Gly	Phe	Leu	Gly	Ala	Gly	Thr	Ile	Leu	Ile	Thr
			85					90					95		
Asp	Lys	Lys	Lys	Ile	Thr	Gly	Leu	Thr	Thr	Ala	Ala	Gly	Ile	Trp	Ala
			100					105					110		
Ser	Ala	Gly	Ile	Gly	Leu	Ala	Ile	Gly	Val	Gly	Phe	Tyr	Glu	Gly	Ala
		115					120					125			
Leu	Leu	Val	Ala	Ile	Ser	Val	Trp	Gly	Val	Ile	Ser	Met	Phe	Gln	Pro
		130				135					140				
Leu	Lys	Lys	Tyr	Leu	Gln	Asn	Arg	Ser	Lys	Met	Ile	Glu	Leu	Tyr	Ile
145				150						155					160
Val	Val	Lys	Ser	Thr	Glu	Ala	Tyr	Asn	Arg	Val	Leu	Val	Tyr	Cys	Ala
			165					170						175	
Glu	Asn	Gly	Ile	Arg	Met	Thr	Asp	Ser	Arg	Thr	Ala	Phe	Gly	Asp	Val
		180					185						190		
Asn	Ser	Asp	Arg	Ile	Glu	Tyr	Phe	Asp	Val	Pro	Asp	Lys	Lys	Ile	Ala
		195					200					205			
Ser	Phe	Ile	Thr	Leu	Glu	Leu	Ser	Gly	Arg	Phe	Glu	His	Leu	Arg	Leu
	210					215				220					
Met	Glu	Glu	Ile	Ala	Asn	Ile	Val	Gly	Val	Ile	Tyr	Val	Glu	Glu	Ile
225					230					235					240
Ser															

(2) INFORMATION FOR SEQ ID NO:4816:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 443 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...443

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4816:

Glu	Lys	Glu	Met	Leu	Glu	Leu	Leu	Lys	Ser	Ile	Asp	Asp	Phe	Ala	Trp
1				5				10					15		
Gly	Pro	Pro	Leu	Leu	Ile	Leu	Leu	Val	Gly	Thr	Gly	Ile	Tyr	Leu	Thr
			20					25					30		
Met	Arg	Leu	Gly	Leu	Leu	Gln	Val	Leu	Arg	Leu	Pro	Lys	Ala	Phe	Gln

	35					40				45					
Leu	Ile	Phe	Ile	Gln	Asp	Lys	Gly	His	Gly	Asp	Val	Ser	Ser	Phe	Ala
50						55					60				
Ala	Leu	Cys	Thr	Ala	Leu	Ala	Ser	Thr	Val	Gly	Thr	Gly	Asn	Ile	Ile
65					70					75				80	
Gly	Val	Ala	Thr	Ala	Ile	Lys	Val	Gly	Gly	Pro	Gly	Ala	Leu	Phe	Trp
				85					90					95	
Met	Trp	Met	Ala	Ala	Phe	Phe	Gly	Met	Ala	Thr	Lys	Tyr	Ala	Glu	Gly
			100					105					110		
Leu	Leu	Ala	Ile	Lys	Tyr	Arg	Thr	Lys	Asp	Asp	His	Gly	Ala	Val	Ala
			115				120					125			
Gly	Gly	Pro	Met	His	Tyr	Ile	Leu	Leu	Gly	Met	Gly	Glu	Lys	Trp	Arg
			130			135					140				
Pro	Leu	Ala	Val	Leu	Phe	Ala	Val	Xaa	Gly	Val	Leu	Val	Ala	Leu	Leu
145					150					155				160	
Gly	Ile	Gly	Thr	Phe	Thr	Gln	Val	Asn	Ser	Ile	Thr	Glu	Ser	Ile	Gln
				165					170					175	
Asn	Thr	Thr	Thr	Ile	Ser	Pro	Ala	Ile	Thr	Ala	Leu	Val	Leu	Ser	Val
			180					185					190		
Phe	Val	Ala	Ile	Ala	Val	Phe	Gly	Gly	Leu	Lys	Ser	Ile	Ser	Lys	Val
		195				200					205				
Ser	Thr	Thr	Val	Val	Pro	Phe	Met	Ala	Ile	Ile	Tyr	Ile	Leu	Gly	Thr
	210					215					220				
Leu	Thr	Val	Ile	Phe	Phe	Asn	Ile	Gly	Lys	Ile	Pro	Gly	Thr	Ile	Ala
225					230					235				240	
Leu	Val	Phe	Thr	Ser	Ala	Phe	Ser	Pro	Leu	Ala	Ala	Val	Gly	Gly	Phe
				245				250					255		
Ala	Gly	Ala	Ser	Val	Arg	Met	Ala	Ile	Gln	Asn	Gly	Val	Ala	Arg	Gly
			260					265					270		
Val	Phe	Ser	Asn	Glu	Ser	Gly	Leu	Gly	Ser	Ala	His	Ile	Ala	Ala	Ala
		275				280					285				
Ala	Ala	Lys	Thr	Asn	Glu	Pro	Val	Glu	Gln	Gly	Leu	Ile	Ser	Met	Thr
	290				295					300					
Gly	Thr	Phe	Ile	Asp	Thr	Leu	Ile	Ile	Cys	Thr	Leu	Thr	Gly	Leu	Thr
305					310					315				320	
Ile	Leu	Val	Thr	Gly	Val	Trp	Ser	Gly	Asp	Leu	Asn	Gly	Val	Ala	Leu
				325					330					335	
Thr	Gln	Ser	Ala	Phe	Ser	Thr	Val	Phe	Ser	His	Phe	Gly	Pro	Ala	Leu
		340						345					350		
Leu	Thr	Ile	Phe	Leu	Val	Leu	Phe	Ala	Phe	Thr	Thr	Ile	Leu	Gly	Trp
		355				360						365			
Asn	Tyr	Tyr	Gly	Glu	Arg	Cys	Phe	Glu	Phe	Leu	Phe	Gly	Val	Arg	Phe
	370					375					380				
Ile	Trp	Leu	Tyr	Arg	Val	Val	Phe	Val	Leu	Met	Val	Leu	Leu	Gly	Gly
385					390				395					400	
Phe	Ile	Glu	Leu	Asp	Met	Val	Trp	Ile	Ile	Ala	Asp	Ile	Val	Asn	Ala
				405					410					415	
Leu	Met	Ala	Leu	Pro	Asn	Leu	Ile	Ala	Leu	Leu	Val	Leu	Ser	Pro	Val
		420						425					430		
Val	Ile	Ala	Glu	Thr	Lys	Lys	Tyr	Phe	Asp	Lys					
		435					440								

(2) INFORMATION FOR SEQ ID NO:4817:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 315 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...315

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4817:

```

Arg Gly Val Phe Met Ser Tyr Gln Asp Leu Lys Glu Cys Lys Ile Ile
1      5      10      15
Thr Ala Phe Ile Thr Pro Phe His Glu Asp Gly Ser Ile Asn Phe Asp
      20      25      30
Ala Ile Pro Ala Leu Ile Glu His Leu Leu Asp His His Thr Asp Gly
      35      40      45
Ile Leu Leu Ala Gly Thr Thr Ala Glu Ser Pro Thr Leu Thr His Asp
      50      55      60
Glu Glu Leu Glu Leu Phe Ala Ala Val Gln Lys Ile Val Asn Gly Arg
65      70      75      80
Val Pro Leu Ile Ala Gly Val Gly Thr Asn Asp Thr Arg Asp Ser Ile
      85      90      95
Glu Phe Val Lys Glu Val Ala Glu Phe Gly Gly Phe Ala Ala Gly Leu
      100     105     110
Ala Ile Val Pro Tyr Tyr Asn Lys Pro Ser Gln Glu Gly Met Tyr Gln
      115     120     125
His Phe Lys Ala Ile Ala Asp Ala Ser Asp Leu Pro Ile Ile Ile Tyr
      130     135     140
Asn Ile Pro Gly Arg Val Val Val Glu Leu Thr Pro Glu Thr Met Leu
145     150     155     160
Arg Leu Ala Asp His Pro Asn Ile Ile Gly Val Lys Glu Cys Thr Ser
      165     170     175
Leu Ala Asn Met Ala Tyr Leu Ile Glu His Lys Pro Glu Glu Phe Leu
      180     185     190
Val Tyr Thr Gly Glu Asp Gly Asp Ala Phe His Ala Met Asn Leu Gly
      195     200     205
Ala Asp Gly Val Ile Ser Val Ala Ser His Thr Asn Gly Asp Glu Met
      210     215     220
His Glu Met Phe Ile Ala Ile Ala Glu Ser Asp Met Lys Lys Ala Ala
225     230     235     240
Ala Ile Gln Arg Lys Phe Ile Pro Lys Val Asn Ala Leu Phe Ser Tyr
      245     250     255
Pro Ser Pro Ala Pro Val Lys Ala Val Leu Asn Tyr Met Gly Phe Glu
      260     265     270
Ala Gly Pro Thr Arg Leu Pro Leu Val Pro Ala Pro Glu Glu Asp Ala
      275     280     285
Lys Arg Ile Ile Lys Val Val Val Asp Gly Asp Tyr Glu Ala Thr Lys
      290     295     300
Ala Thr Val Thr Gly Val Leu Arg Pro Asp Tyr
305      310      315

```

(2) INFORMATION FOR SEQ ID NO:4818:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 257 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...257

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4818:

Arg	Glu	Pro	Leu	Ser	Leu	Gly	Trp	Ile	His	Ile	Cys	Asp	Ser	Lys	Met
1				5				10						15	
Ser	Asn	Val	Asp	Lys	Ile	Arg	Lys	Ile	His	Ile	Ile	Val	Cys	Trp	Met
			20				25					30			
Tyr	Ile	Phe	Leu	Ser	Phe	Arg	Ala	Ile	Ile	Asn	Asp	Thr	Glu	Tyr	Phe
		35				40					45				
Leu	Leu	Ile	Phe	Leu	Ala	Phe	Ile	Tyr	Ser	Ile	Val	Ser	Leu	Pro	Leu
	50					55				60					
Tyr	Ser	Val	Lys	Asn	Lys	Ile	Val	Ser	Ile	Cys	Leu	Ala	Ile	Asn	Ser
65				70						75				80	
Ile	Leu	Leu	Met	Ser	Phe	Pro	Ile	Leu	Ile	Asn	Lys	Phe	Phe	Pro	Glu
			85					90						95	
Ser	Phe	Leu	Thr	Tyr	Thr	Val	Leu	Ile	Ser	Val	Phe	Ile	Leu	Glu	Leu
		100					105					110			
Ala	Ile	Phe	His	Leu	Ile	Gly	Glu	Asp	Phe	Ala	Thr	Lys	Leu	Thr	Asn
		115				120					125				
Glu	Tyr	Lys	Lys	Ile	Ser	Gln	Phe	Arg	Ser	Lys	Val	Ser	Gln	Ser	Pro
	130					135					140				
Trp	Ile	Lys	Tyr	Leu	Glu	Ile	Ser	Ser	Phe	Ile	Leu	Thr	Ile	Phe	Pro
145				150					155					160	
Ser	Ile	Leu	Tyr	Gly	Thr	Val	Asp	Asn	His	Val	Leu	Thr	Leu	Ile	Phe
			165					170						175	
Leu	Ile	Lys	Ile	Cys	Ala	Asp	Thr	Thr	Ile	Lys	Phe	Leu	Phe	Ile	Arg
		180					185					190			
Leu	Phe	Asp	Thr	Ser	Thr	Leu	Met	Lys	Arg	Arg	Ile	Phe	Phe	Leu	Phe
		195				200					205				
Ala	Leu	Asp	Val	Ile	Val	Tyr	Leu	Phe	Leu	Gly	Tyr	Leu	Leu	Val	Ile
	210					215				220					
Gln	Lys	Ala	Gly	Tyr	Leu	Phe	Ser	Val	Leu	Leu	Leu	Phe	Ser	Asn	Phe
225				230					235					240	
Ser	Val	Pro	Phe	Ile	Lys	Glu	Lys	Glu	Tyr	Glu	Leu	Phe	Lys	Asn	Ser
			245					250						255	

Lys

(2) INFORMATION FOR SEQ ID NO:4819:

- (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...74

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4819:

```
Ser Phe Arg Ile Pro Phe Thr Val Pro Ile Ser Ser Leu Arg Pro Ser
1          5          10          15
Gly Ser Asn Ile Leu Val Ala Ser Ser Lys Ile Lys Ile Ala Gly Leu
          20          25          30
Arg Ala Thr Thr Pro Ala Met Ala Thr Arg Cys Phe Trp Pro Pro Asp
          35          40          45
Arg Arg Ala Gly Ser Leu Phe Leu Lys Ser Asn Met Pro Thr Lys Ala
          50          55          60
Arg Ala Ser Ser Thr Leu Phe Phe Ile Ser
65          70
```

(2) INFORMATION FOR SEQ ID NO:4820:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 442 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...442

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4820:

```
Ser Met Arg Ile Gly Leu Phe Thr Asp Thr Tyr Phe Pro Gln Val Ser
1          5          10          15
Gly Val Ala Thr Ser Ile Arg Thr Leu Lys Thr Glu Leu Glu Lys Gln
          20          25          30
Gly His Ala Val Phe Ile Phe Thr Thr Thr Asp Lys Asp Val Asn Arg
          35          40          45
Tyr Glu Asp Trp Gln Ile Ile Arg Ile Pro Ser Val Pro Phe Phe Ala
          50          55          60
Phe Lys Asp Arg Arg Phe Ala Tyr Arg Gly Phe Ser Lys Ala Leu Glu
```

65					70					75					80
Ile	Ala	Lys	Gln	Tyr	Gln	Leu	Asp	Ile	Ile	His	Thr	Gln	Thr	Glu	Phe
				85					90					95	
Ser	Leu	Gly	Leu	Leu	Gly	Ile	Trp	Ile	Ala	Arg	Glu	Leu	Lys	Ile	Pro
			100					105					110		
Val	Ile	His	Thr	Tyr	His	Thr	Gln	Tyr	Glu	Asp	Tyr	Val	His	Tyr	Ile
		115					120					125			
Ala	Lys	Gly	Met	Leu	Ile	Arg	Pro	Ser	Met	Val	Lys	Tyr	Leu	Val	Arg
		130				135					140				
Gly	Phe	Leu	His	Asp	Val	Asp	Gly	Val	Ile	Cys	Pro	Ser	Glu	Ile	Val
145					150					155					160
Arg	Asp	Leu	Leu	Ser	Asp	Tyr	Lys	Val	Lys	Val	Glu	Lys	Arg	Val	Ile
				165					170					175	
Pro	Thr	Gly	Ile	Glu	Leu	Ala	Lys	Phe	Glu	Arg	Pro	Glu	Ile	Lys	Gln
			180					185					190		
Glu	Asn	Leu	Lys	Glu	Leu	Arg	Ser	Lys	Leu	Gly	Ile	Gln	Asp	Gly	Glu
		195					200					205			
Lys	Thr	Leu	Leu	Ser	Leu	Ser	Arg	Ile	Ser	Tyr	Glu	Lys	Asn	Ile	Gln
		210				215					220				
Ala	Val	Leu	Val	Ala	Phe	Ala	Asp	Val	Leu	Lys	Glu	Glu	Asp	Lys	Val
225				230						235					240
Lys	Leu	Val	Val	Ala	Gly	Asp	Gly	Pro	Tyr	Leu	Asn	Asp	Leu	Lys	Glu
				245					250					255	
Gln	Ala	Gln	Asn	Leu	Glu	Ile	Gln	Asp	Ser	Val	Ile	Phe	Thr	Gly	Met
			260				265						270		
Ile	Ala	Pro	Ser	Glu	Thr	Ala	Leu	Tyr	Tyr	Lys	Ala	Ala	Asp	Phe	Phe
		275				280						285			
Ile	Ser	Ala	Ser	Thr	Ser	Glu	Thr	Gln	Gly	Leu	Thr	Tyr	Leu	Glu	Ser
	290				295						300				
Leu	Ala	Ser	Gly	Thr	Pro	Val	Ile	Ala	His	Gly	Asn	Pro	Tyr	Leu	Asn
305				310					315						320
Asn	Leu	Ile	Ser	Asp	Lys	Met	Phe	Gly	Thr	Leu	Tyr	Tyr	Gly	Glu	His
			325					330					335		
Asp	Leu	Ala	Gly	Ala	Ile	Leu	Glu	Ala	Leu	Ile	Ala	Thr	Pro	Asp	Met
		340				345						350			
Asn	Glu	His	Thr	Leu	Ser	Glu	Lys	Leu	Tyr	Glu	Ile	Ser	Ala	Glu	Asn
		355				360					365				
Phe	Gly	Lys	Arg	Val	His	Glu	Phe	Tyr	Leu	Asp	Ala	Ile	Ile	Ser	Asn
	370				375					380					
Asn	Phe	Gln	Lys	Asp	Leu	Ala	Lys	Asp	Asp	Thr	Val	Ser	Gln	Arg	Ile
385				390					395						400
Phe	Lys	Thr	Val	Leu	Tyr	Leu	Pro	Gln	Gln	Val	Val	Ala	Val	Pro	Val
			405					410						415	
Lys	Gly	Ser	Arg	Met	Leu	Lys	Ala	Ser	Lys	Thr	Gln	Leu	Ile	Ser	
		420				425						430			
Met	Arg	Asp	Tyr	Trp	Lys	Asp	His	Glu	Glu						
	435				440										

(2) INFORMATION FOR SEQ ID NO:4821:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...69

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4821:

```
Leu Lys Pro Leu Leu His Ala Asp Glu Thr Ser Tyr Arg Val Leu Glu
1      5      10      15
Ser Asp Ser Gln Leu Thr Tyr Tyr Trp Thr Phe Leu Ser Gly Lys Ala
      20      25      30
Glu Asn Gln Ala Ile Thr Leu Tyr His His Asp Gln Arg Arg Ser Gly
      35      40      45
Leu Val Val Gln Glu Phe Leu Gly Asp Tyr Ser Gly Tyr Val His Cys
      50      55      60
Asp Met Leu Arg Gln
65
```

(2) INFORMATION FOR SEQ ID NO:4822:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 378 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4822:

```
Leu Phe Arg Met Arg Glu Asn Met Lys Ile Val Ile Ala Pro Asp Ser
1      5      10      15
Phe Lys Glu Ser Leu Thr Ala Gln Gln Val Ala Glu Ala Ile Lys Arg
      20      25      30
Gly Phe Gln Gln Ser Ile Ala Asp Val Glu Cys Leu Leu Cys Pro Val
      35      40      45
Gly Asp Gly Gly Glu Gly Thr Val Asp Ala Ile Arg His Ser Leu Asp
      50      55      60
Leu Lys Glu Lys Trp Ile Gln Val Thr Asp Pro Ser Gly Gln Lys Glu
      65      70      75      80
Ala Met Arg Tyr Phe Gln Lys Gly Glu Leu Ala Leu Phe Glu Val Ala
      85      90      95
Asp Leu Val Gly Leu Gly Lys Ile Pro Leu Glu Lys Arg Asn Pro Leu
      100     105     110
Gln Ile Gln Thr Cys Gly Ile Gly Glu Leu Ile Leu His Leu Ile Ser
```


(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...272

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4824:

Lys	Thr	Arg	Met	Ser	Glu	Ile	Gly	Phe	Lys	Tyr	Ser	Ile	Leu	Ala	Ser
1				5					10					15	
Gly	Ser	Ser	Gly	Asn	Ser	Phe	Tyr	Leu	Glu	Thr	Ser	Lys	Lys	Lys	Leu
			20					25					30		
Leu	Val	Asp	Ala	Gly	Leu	Ser	Gly	Lys	Lys	Ile	Thr	Ser	Leu	Leu	Ala
		35					40					45			
Glu	Ile	Asn	Arg	Lys	Pro	Glu	Asp	Leu	Asp	Ala	Ile	Leu	Ile	Thr	His
	50					55					60				
Glu	His	Ser	Asp	His	Ile	His	Gly	Val	Gly	Val	Leu	Ala	Arg	Lys	Tyr
65					70					75					80
Gly	Met	Asp	Leu	Tyr	Ala	Asn	Glu	Lys	Thr	Trp	Gln	Ala	Met	Glu	Asn
				85					90					95	
Ser	Lys	Tyr	Leu	Gly	Lys	Val	Asp	Ser	Ser	Gln	Lys	His	Ile	Phe	Glu
			100					105					110		
Met	Gly	Lys	Thr	Lys	Thr	Phe	Gly	Asp	Ile	Asp	Ile	Glu	Ser	Phe	Gly
		115					120					125			
Val	Ser	His	Asp	Ala	Val	Ala	Pro	Gln	Phe	Tyr	Arg	Phe	Met	Lys	Asp
	130					135					140				
Asp	Lys	Ser	Phe	Val	Leu	Leu	Thr	Asp	Thr	Gly	Tyr	Val	Ser	Asp	Arg
145					150					155					160
Met	Ala	Gly	Ile	Val	Glu	Asn	Ala	Asp	Gly	Tyr	Leu	Ile	Glu	Ala	Asn
			165						170					175	
His	Asp	Val	Glu	Ile	Leu	Arg	Ser	Gly	Ser	Tyr	Ala	Trp	Arg	Leu	Lys
		180						185					190		
Gln	Arg	Ile	Leu	Ser	Asp	Leu	Gly	His	Leu	Ser	Asn	Glu	Asp	Gly	Ala
	195					200						205			
Glu	Ala	Met	Ile	Arg	Thr	Leu	Gly	Asn	Arg	Thr	Lys	Lys	Ile	Tyr	Leu
	210					215					220				
Gly	His	Leu	Ser	Lys	Glu	Asn	Asn	Ile	Lys	Glu	Leu	Ala	His	Met	Thr
225					230					235					240
Met	Val	Asn	Gln	Leu	Ala	Gln	Ala	Asp	Leu	Gly	Val	Gly	Val	Asp	Phe
			245						250					255	
Lys	Val	Tyr	Asp	Thr	Ser	Pro	Asp	Thr	Ala	Thr	Pro	Leu	Thr	Glu	Ile
			260					265					270		

(2) INFORMATION FOR SEQ ID NO:4825:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 391 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...391

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4825:

Glu	Asn	Arg	Met	Ala	Lys	Lys	Pro	Lys	Lys	Leu	Glu	Glu	Ile	Ser	Lys
1				5				10						15	
Lys	Phe	Gly	Ala	Glu	Arg	Glu	Lys	Ala	Leu	Asn	Asp	Ala	Leu	Lys	Leu
		20						25					30		
Ile	Glu	Lys	Asp	Phe	Gly	Lys	Gly	Ser	Ile	Met	Arg	Leu	Gly	Glu	Arg
		35					40					45			
Ala	Glu	Gln	Lys	Val	Gln	Val	Met	Ser	Ser	Gly	Ser	Leu	Ala	Leu	Asp
	50					55					60				
Ile	Ala	Leu	Gly	Ser	Gly	Gly	Tyr	Pro	Lys	Gly	Arg	Ile	Ile	Glu	Ile
65					70					75				80	
Tyr	Gly	Pro	Glu	Ser	Ser	Gly	Lys	Thr	Thr	Val	Ala	Leu	His	Ala	Val
				85				90						95	
Ala	Gln	Ala	Gln	Lys	Glu	Gly	Gly	Ile	Ala	Ala	Phe	Ile	Asp	Ala	Glu
			100					105					110		
His	Ala	Leu	Asp	Pro	Ala	Tyr	Ala	Ala	Ala	Leu	Gly	Val	Asn	Ile	Asp
	115					120						125			
Glu	Leu	Leu	Leu	Ser	Gln	Pro	Asp	Ser	Gly	Glu	Gln	Gly	Leu	Glu	Ile
	130					135					140				
Ala	Gly	Lys	Leu	Ile	Asp	Ser	Gly	Ala	Val	Asp	Leu	Val	Val	Val	Asp
145					150					155					160
Ser	Val	Ala	Ala	Leu	Val	Pro	Arg	Ala	Glu	Ile	Asp	Gly	Asp	Ile	Gly
				165					170					175	
Asp	Ser	His	Val	Gly	Leu	Gln	Ala	Arg	Met	Met	Ser	Gln	Ala	Met	Arg
		180						185					190		
Lys	Leu	Gly	Ala	Ser	Ile	Asn	Lys	Thr	Lys	Thr	Ile	Ala	Ile	Phe	Ile
	195						200					205			
Asn	Gln	Leu	Arg	Glu	Lys	Val	Gly	Val	Met	Phe	Gly	Asn	Pro	Glu	Thr
	210					215					220				
Thr	Pro	Gly	Gly	Arg	Ala	Leu	Lys	Phe	Tyr	Ala	Ser	Val	Arg	Leu	Asp
225					230					235					240
Val	Arg	Gly	Asn	Thr	Gln	Ile	Lys	Gly	Thr	Gly	Asp	Gln	Lys	Glu	Thr
				245					250					255	
Asn	Val	Gly	Lys	Glu	Thr	Lys	Ile	Lys	Val	Val	Lys	Asn	Lys	Val	Ala
		260						265					270		
Pro	Pro	Phe	Lys	Glu	Ala	Val	Val	Glu	Ile	Met	Tyr	Gly	Glu	Gly	Ile
		275						280				285			
Ser	Lys	Thr	Gly	Glu	Leu	Leu	Lys	Ile	Ala	Ser	Asp	Leu	Asp	Ile	Ile
	290					295					300				
Lys	Lys	Ala	Gly	Ala	Trp	Tyr	Ser	Tyr	Lys	Asp	Glu	Lys	Ile	Gly	Gln
305					310					315					320
Gly	Ser	Glu	Asn	Ala	Lys	Lys	Tyr	Leu	Ala	Glu	His	Pro	Glu	Ile	Phe
				325					330					335	
Asp	Glu	Ile	Asp	Lys	Gln	Val	Arg	Ser	Lys	Phe	Gly	Leu	Ile	Asp	Gly

			340					345					350			
Glu	Glu	Val	Ser	Glu	Gln	Asp	Thr	Glu	Asn	Lys	Lys	Asp	Glu	Pro	Lys	
			355					360					365			
Lys	Glu	Glu	Ala	Val	Asn	Glu	Glu	Val	Thr	Leu	Asp	Leu	Gly	Asp	Glu	
		370				375					380					
Leu	Glu	Ile	Glu	Ile	Glu	Glu										
385					390											

(2) INFORMATION FOR SEQ ID NO:4826:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 271 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...271

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4826:

Lys	Asp	Arg	Met	Met	Gln	Ala	Leu	Thr	Asn	Pro	Phe	Pro	Ile	Gly	Ser	
1				5					10					15		
Ser	Ser	Leu	Ile	His	Cys	Met	Thr	Asn	Glu	Ile	Ser	Cys	Glu	Met	Leu	
			20					25					30			
Ala	Asn	Gly	Ile	Leu	Ala	Leu	Gly	Cys	Lys	Pro	Val	Met	Ala	Asp	Asp	
		35					40					45				
Pro	Arg	Glu	Val	Leu	Asp	Phe	Thr	Lys	Gln	Ser	Gln	Ala	Leu	Phe	Ile	
	50					55					60					
Asn	Leu	Gly	His	Leu	Ser	Ala	Glu	Lys	Glu	Lys	Ala	Ile	Arg	Met	Ala	
65				70					75					80		
Ala	Leu	Tyr	Ala	Asn	Gln	Ser	Ser	Leu	Pro	Met	Val	Val	Asp	Ala	Val	
			85					90					95			
Gly	Val	Thr	Thr	Ser	Ser	Ile	Arg	Lys	Ser	Leu	Val	Lys	Asp	Leu	Leu	
		100						105					110			
Asp	Tyr	Arg	Pro	Thr	Val	Leu	Lys	Gly	Asn	Met	Ser	Glu	Ile	Arg	Ser	
	115					120					125					
Leu	Val	Gly	Leu	Lys	His	His	Gly	Val	Gly	Val	Asp	Ala	Ser	Ala	Lys	
	130				135						140					
Asp	Gln	Glu	Thr	Glu	Asp	Leu	Leu	Gln	Val	Leu	Lys	Asp	Trp	Cys	Gln	
145				150					155					160		
Thr	Tyr	Pro	Gly	Met	Pro	Phe	Leu	Val	Thr	Gly	Pro	Lys	Asp	Leu	Ile	
			165					170					175			
Val	Ser	Glu	Asn	Gln	Val	Ala	Val	Leu	Glu	Asn	Gly	Cys	Thr	Glu	Leu	
		180						185					190			
Asp	Trp	Ile	Thr	Gly	Thr	Gly	Asp	Leu	Val	Gly	Ala	Leu	Thr	Ala	Val	
	195					200					205					
Phe	Leu	Ser	Gln	Gly	Lys	Thr	Gly	Phe	Glu	Ala	Ser	Cys	Leu	Ala	Val	
210				215					220							
Ser	Tyr	Leu	Asn	Ile	Ala	Ala	Glu	Lys	Ile	Val	Val	Gln	Gly	Met	Gly	

225		230		235		240									
Leu	Glu	Glu	Phe	Arg	Tyr	Gln	Val	Leu	Asn	Gln	Leu	Ser	Leu	Leu	Arg
		245		250		255									
Arg	Asp	Glu	Asn	Trp	Leu	Asp	Thr	Ile	Lys	Gly	Glu	Val	Tyr	Glu	
		260		265		270									

(2) INFORMATION FOR SEQ ID NO:4827:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 245 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...245

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4827:

Gly	Gln	Arg	Met	Ile	Glu	Tyr	Lys	Asn	Val	Ala	Leu	Arg	Tyr	Thr	Glu
1				5				10						15	
Lys	Asp	Val	Leu	Arg	Asp	Val	Asn	Leu	Gln	Ile	Glu	Asp	Gly	Glu	Phe
		20					25						30		
Met	Val	Leu	Val	Gly	Pro	Ser	Gly	Ser	Gly	Lys	Thr	Thr	Met	Leu	Lys
		35					40						45		
Met	Ile	Asn	Arg	Leu	Leu	Glu	Pro	Thr	Asp	Gly	Asn	Ile	Tyr	Met	Asp
		50				55				60					
Gly	Lys	Arg	Ile	Lys	Asp	Tyr	Asp	Glu	Arg	Glu	Leu	Arg	Leu	Ser	Thr
65				70				75						80	
Gly	Tyr	Val	Leu	Gln	Ala	Ile	Ala	Leu	Phe	Pro	Asn	Leu	Thr	Val	Ala
			85					90						95	
Glu	Asn	Ile	Ala	Leu	Ile	Pro	Glu	Met	Lys	Gly	Trp	Ser	Lys	Glu	Glu
		100					105						110		
Ile	Thr	Lys	Lys	Thr	Glu	Glu	Leu	Leu	Ala	Lys	Val	Gly	Leu	Pro	Val
		115					120					125			
Ala	Glu	Tyr	Gly	His	Arg	Leu	Pro	Ser	Glu	Leu	Ser	Gly	Gly	Glu	Gln
		130				135					140				
Gln	Arg	Val	Gly	Ile	Val	Arg	Ala	Met	Ile	Gly	Gln	Pro	Lys	Ile	Leu
145				150						155					160
Leu	Met	Asp	Glu	Pro	Phe	Ser	Ala	Leu	Asp	Ala	Ile	Ser	Arg	Lys	Gln
			165					170						175	
Leu	Gln	Val	Leu	Thr	Lys	Glu	Leu	His	Lys	Glu	Phe	Gly	Met	Thr	Thr
		180					185						190		
Ile	Phe	Val	Thr	His	Asp	Thr	Asp	Glu	Ala	Leu	Lys	Leu	Ala	Asp	Arg
		195				200						205			
Ile	Ala	Val	Leu	Gln	Asp	Gly	Glu	Ile	Arg	Gln	Val	Ser	Asn	Pro	Glu
	210				215				220						
Thr	Ile	Leu	Lys	Ala	Pro	Ala	Thr	Asp	Phe	Val	Ala	Asp	Leu	Phe	Gly
225				230					235						240
Gly	Ser	Ile	His	Asp											

(2) INFORMATION FOR SEQ ID NO:4828:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 120 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4828:

```

Asn Lys Arg Ile Tyr Asn Asp Phe Gln Ala Ser Lys Met Asn Leu Asn
1      5      10      15
Ile Tyr Thr Ser Pro Leu Leu Ala Phe Val Phe Val Phe Ile Gly Glu
      20      25      30
Phe Val Ala Tyr Thr Leu Tyr Gly Ile Ser Leu Leu Ala Leu Ile Gly
      35      40      45
Leu Ala Arg Asn Phe Gly Glu Ala Gly Gln Asn Leu Ala Ser Tyr Leu
      50      55      60
Gln Thr Leu His Gln Ser Leu Thr Asp Lys Thr Ser Asp Phe Arg Leu
65      70      75      80
Ile Leu Gly Leu Leu Ala Phe Gly Phe Ile Leu Asn Thr Val Phe Arg
      85      90      95
Trp Thr Arg Lys Val Glu Lys Arg Pro Ile Arg Thr Leu Gly Phe Tyr
      100     105     110
Arg Glu Ile Ser Ser Ala Ile Phe
      115     120

```

(2) INFORMATION FOR SEQ ID NO:4829:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4829:

Val	Gly	Arg	Ile	Ile	Arg	Ser	Gly	Val	Lys	Met	Glu	His	Leu	Gly	Lys
1			5					10					15		
Val	Phe	Arg	Glu	Phe	Arg	Thr	Ser	Gly	Asn	Tyr	Ser	Leu	Lys	Glu	Ala
		20						25				30			
Ala	Gly	Glu	Ser	Cys	Ser	Thr	Ser	Gln	Leu	Ser	Arg	Phe	Glu	Leu	Gly
		35					40					45			
Glu	Ser	Asp	Leu	Ala	Val	Ser	Arg	Phe	Phe	Glu	Ile	Leu	Asp	Asn	Ile
	50					55					60				
His	Val	Thr	Ile	Glu	Asn	Phe	Met	Asp	Lys	Ala	Arg	Asn	Phe	His	Asn
65					70				75					80	
His	Glu	His	Val	Ser	Met	Met	Ala	Gln	Ile	Ile	Pro	Leu	Tyr	Tyr	Ser
			85					90						95	
Asn	Asp	Ile	Ala	Gly	Phe	Gln	Lys	Leu	Gln	Arg	Glu	Gln	Leu	Glu	Lys
			100					105					110		
Ser	Lys	Ser	Ser	Thr	Thr	Pro	Leu	Tyr	Phe	Glu	Leu	Asn	Trp	Ile	Leu
		115					120					125			
Leu	Gln	Gly	Leu	Ile	Cys	Gln	Arg	Asp	Ala	Ser	Tyr	Asp	Met	Lys	Gln
	130					135					140				
Asp	Asp	Leu	Asp	Lys	Val	Ala	Asp	Tyr	Leu	Phe	Lys	Thr	Glu	Glu	Trp
145				150					155						160
Thr	Met	Tyr	Glu	Leu	Ile	Leu	Phe	Gly	Asn	Leu	Tyr	Ser	Phe	Tyr	Asp
			165					170						175	
Val	Asp	Tyr	Val	Thr	Arg	Ile	Gly	Arg	Glu	Val	Met	Glu	Arg	Glu	Glu
		180						185					190		
Phe	Tyr	Gln	Glu	Ile	Ser	Arg	His	Lys	Arg	Leu	Val	Leu	Ile	Leu	Ala
		195					200					205			
Leu	Asn	Cys	Tyr	Gln	His	Cys	Leu	Glu	His	Ser	Ser	Phe	Tyr	Asn	Ala
	210					215					220				
Asn	Tyr	Phe	Glu	Ala	Tyr	Thr	Glu	Lys	Ile	Ile	Asp	Lys	Gly	Ile	Lys
225					230				235						240
Leu	Tyr	Glu	Arg	Asn	Val	Phe	His	Tyr	Leu	Lys	Gly	Phe	Ala	Leu	Tyr
			245						250					255	
Gln	Lys	Gly	Gln	Cys	Lys	Glu	Gly	Cys	Lys	Gln	Met	Gln	Glu	Ala	Ile
		260					265						270		
His	Ile	Phe	Asp	Val	Leu	Gly	Leu	Pro	Glu	Gln	Val	Ala	Tyr	Tyr	Gln
	275					280						285			
Glu	His	Tyr	Glu	Lys	Phe	Val	Lys	Ser							
	290					295									

(2) INFORMATION FOR SEQ ID NO:4830:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 96 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...96

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4830:

Pro	Met	Arg	Ile	Met	Gly	Leu	Asp	Val	Gly	Ser	Lys	Thr	Val	Gly	Val
1				5					10					15	
Ala	Ile	Ser	Asp	Pro	Leu	Gly	Phe	Thr	Ala	Gln	Gly	Leu	Glu	Ile	Ile
			20					25					30		
Gln	Ile	Asn	Glu	Glu	Gln	Gly	Gln	Phe	Gly	Ser	Asp	Arg	Val	Lys	Glu
		35					40					45			
Leu	Val	Asp	Thr	Tyr	Lys	Val	Glu	Arg	Phe	Val	Val	Gly	Leu	Pro	Lys
	50					55					60				
Asn	Met	Asn	Asn	Thr	Ser	Gly	Pro	Arg	Val	Glu	Ala	Ser	Gln	Ala	Tyr
65					70					75				80	
Gly	Ala	Lys	Leu	Glu	Glu	Phe	Phe	Gly	Leu	Pro	Val	Asp	Tyr	Gln	Glu
			85						90					95	

(2) INFORMATION FOR SEQ ID NO:4831:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4831:

Asn	Ala	Arg	Met	Lys	Ala	Leu	Cys	Ile	Phe	Leu	Leu	Asn	Met	Leu	Ala
1				5					10					15	
Trp	Thr	Val	Leu	Ala	Met	Ile	Ile	Arg	Gly	Gly	Leu	Asp	Gly	Phe	Asp
			20					25					30		
Arg	His	Thr	Trp	Ser	Thr	Ile	Leu	Ile	Ala	Ser	Leu	Phe	Gly	Val	Tyr
		35				40						45			
Asp	Tyr	Lys	Pro	Ile	Asp	Lys	Asn	Arg	Lys	Lys	Ser	Lys	Arg	Lys	Lys
	50					55					60				
Lys	Lys														
65															

(2) INFORMATION FOR SEQ ID NO:4832:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 190 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...190

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4832:

Glu	Gln	Arg	Met	Thr	Lys	Arg	Cys	Ser	Trp	Val	Lys	Met	Thr	Asn	Pro	
1				5					10					15		
Leu	Tyr	Ile	Ala	Tyr	His	Asp	Glu	Glu	Trp	Gly	Gln	Pro	Leu	His	Asp	
			20					25					30			
Asp	Gln	Ala	Leu	Phe	Glu	Leu	Leu	Cys	Met	Glu	Thr	Tyr	Gln	Ala	Gly	
			35				40						45			
Leu	Ser	Trp	Glu	Thr	Val	Leu	Asn	Lys	Arg	Gln	Ala	Phe	Arg	Glu	Ala	
			50				55				60					
Phe	His	Ser	Tyr	Gln	Ile	His	Ser	Val	Ala	Glu	Met	Thr	Asp	Thr	Glu	
65					70					75					80	
Leu	Glu	Ala	Met	Leu	Glu	Asn	Pro	Ala	Ile	Ile	Arg	Asn	Arg	Ala	Lys	
				85					90					95		
Ile	Phe	Ala	Thr	Arg	Ala	Asn	Ala	Gln	Ala	Phe	Leu	Gln	Leu	Gln	Ala	
			100					105					110			
Glu	Tyr	Gly	Ser	Phe	Asp	Ala	Tyr	Leu	Trp	Ser	Phe	Val	Glu	Gly	Lys	
			115				120						125			
Ile	Val	Val	Asn	Asp	Val	Pro	Asp	Tyr	Arg	Gln	Ala	Pro	Ala	Lys	Thr	
			130				135				140					
Pro	Leu	Ser	Glu	Lys	Leu	Ala	Lys	Asp	Leu	Lys	Lys	Arg	Gly	Phe	Lys	
145					150					155					160	
Phe	Thr	Gly	Pro	Val	Ala	Val	Leu	Ser	Phe	Leu	Gln	Ala	Ala	Gly	Leu	
				165					170					175		
Val	Asp	Asp	His	Glu	Asn	Asp	Cys	Glu	Trp	Lys	Gly	Leu	Lys			
			180					185					190			

(2) INFORMATION FOR SEQ ID NO:4833:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 290 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...290

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4833:

Glu Glu Arg Ile Lys Lys Leu Ala Lys Arg Ile Ser Arg Lys Glu Trp

1		5		10		15									
Gly	Met	Ile	Leu	Leu	Ala	Ile	Leu	Phe	Thr	Cys	Phe	Ser	Val	Tyr	Leu
		20						25					30		
Glu	Leu	Glu	Val	Pro	Thr	Tyr	Ile	Ser	Lys	Ile	Thr	Asp	Leu	Leu	Gly
		35					40					45			
Ser	Gln	Glu	Thr	Asn	Leu	Asp	Glu	Leu	Trp	Gln	Pro	Ala	Ser	Met	Met
	50					55					60				
Met	Gly	Met	Ser	Phe	Leu	Ala	Phe	Leu	Ser	Val	Val	Ala	Val	Gly	Phe
65					70					75					80
Phe	Ala	Ser	Arg	Val	Ala	Ala	Ser	Tyr	Thr	Ser	Arg	Leu	Arg	Ser	Asp
				85					90					95	
Ile	Phe	Asn	Arg	Val	Leu	Asp	Tyr	Ser	Gln	Thr	Glu	Ile	Lys	Lys	Phe
		100						105					110		
Ser	Ile	Pro	Ser	Leu	Leu	Thr	Arg	Thr	Thr	Asn	Asp	Ile	Thr	Gln	Val
		115					120					125			
Gln	Met	Leu	Ile	Thr	Met	Gly	Leu	Gln	Val	Val	Thr	Arg	Gly	Ser	Ile
	130					135					140				
Met	Ala	Ile	Trp	Ala	Ile	Gly	Lys	Ile	Leu	Gly	His	Ser	Glu	Tyr	Trp
145					150					155					160
Leu	Trp	Ala	Val	Leu	Val	Val	Val	Ile	Val	Asn	Val	Leu	Met	Thr	Thr
			165						170					175	
Val	Leu	Met	Thr	Leu	Ala	Phe	Pro	Lys	Gln	Ser	Leu	Ile	Gln	Gly	Leu
		180						185					190		
Thr	Asp	Lys	Leu	Asn	Ser	Ile	Thr	Arg	Glu	Ser	Leu	Thr	Gly	Ile	Arg
		195					200					205			
Val	Val	Arg	Ala	Tyr	Asn	Ala	Glu	Asp	Tyr	Gln	Asn	Glu	Lys	Phe	Ala
	210					215					220				
Ala	Val	Asn	Asp	Glu	Leu	Thr	Arg	Leu	Asn	Leu	Phe	Val	Asn	Arg	Leu
225					230					235					240
Met	Ala	Ile	Leu	Asn	Pro	Ile	Met	Met	Gly	Ile	Ser	Ser	Gly	Leu	Ser
				245					250					255	
Val	Ala	Ile	Tyr	Trp	Ile	Gly	Ala	Tyr	Val	Ile	Asn	Asp	Ala	Ala	Pro
		260					265					270			
Ile	Ala	Arg	Leu	Pro	Leu	Phe	Ser	Asp	Met	Ile	Val	Phe	Met	Ser	Tyr
		275					280					285			
Ala	Met														
	290														

(2) INFORMATION FOR SEQ ID NO:4834:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 94 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...94

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4834:

Lys	Arg	Arg	Met	Arg	Asn	Met	Ala	Leu	Thr	Ala	Gly	Ile	Val	Gly	Leu
1				5					10					15	
Pro	Asn	Val	Gly	Lys	Ser	Thr	Leu	Phe	Asn	Ala	Ile	Thr	Lys	Ala	Gly
		20					25						30		
Ala	Glu	Ala	Ala	Asn	Tyr	Pro	Phe	Ala	Thr	Ile	Asp	Pro	Asn	Val	Gly
		35					40					45			
Met	Val	Glu	Asp	Pro	Asp	Glu	Arg	Leu	Gln	Lys	Leu	Thr	Glu	Met	Ile
	50					55					60				
Thr	Pro	Lys	Lys	Thr	Val	Pro	Thr	Thr	Phe	Glu	Phe	Thr	Asp	Ile	Ala
65					70					75					80
Gly	Ile	Val	Lys	Gly	Ala	Phe	Lys	Arg	Arg	Arg	Ala	Arg	Glu		
				85					90						

(2) INFORMATION FOR SEQ ID NO:4835:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 354 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...354

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4835:

Thr	Arg	Arg	Ile	Thr	Met	Val	Glu	Leu	Gly	Ile	Ser	Thr	Phe	Gly	Glu
1				5					10					15	
Ile	Thr	Glu	Leu	Glu	Gly	Thr	Gly	Gln	Thr	Tyr	Ser	His	Ala	Glu	Arg
		20					25					30			
Ile	Arg	Gln	Leu	Val	Ala	Glu	Ile	Glu	Leu	Ala	Asp	Lys	Val	Gly	Leu
	35					40					45				
Asp	Val	Tyr	Gly	Ile	Gly	Glu	His	His	Arg	Ala	Asp	Phe	Ala	Val	Ser
	50					55					60				
Ala	Pro	Glu	Ile	Val	Leu	Ala	Ala	Gly	Ala	Val	Asn	Thr	Lys	Lys	Ile
65					70				75						80
Arg	Leu	Thr	Ser	Ala	Val	Ser	Ile	Leu	Ser	Ser	Met	Asp	Pro	Ile	Arg
			85					90						95	
Leu	Phe	Gln	Gln	Tyr	Ala	Thr	Ile	Asp	Ala	Leu	Ser	Asn	Gly	Arg	Ser
		100						105					110		
Glu	Ile	Met	Ala	Gly	Arg	Gly	Ser	Phe	Thr	Glu	Ser	Phe	Pro	Leu	Phe
		115					120					125			
Gly	Tyr	Asp	Leu	Lys	Asp	Tyr	Asp	Ser	Leu	Phe	Asp	Glu	Lys	Leu	Asp
	130					135					140				
Leu	Leu	Gln	Leu	Val	Asn	Glu	Lys	Thr	Lys	Leu	Asp	Trp	Gln	Gly	Arg
145					150					155					160
Leu	Thr	Gln	Thr	Ile	Ala	Gly	Lys	Glu	Val	Tyr	Pro	Arg	Pro	Val	Gln
			165					170						175	
Asp	Lys	Leu	Pro	Met	Trp	Ile	Ala	Thr	Gly	Gly	His	Val	Glu	Ser	Thr

		100					105				110				
Ala	Ile	Pro	Leu	Ala	Ile	Phe	Ile	Ser	Leu	Ser	Glu	Val	Ile	Ile	Leu
		115					120				125				
His	Thr	Asn	Pro	Gln	Thr	Phe	Phe	Leu	Ser	Phe	Leu	Leu	Phe	Val	Val
		130					135				140				
Phe	Leu	Val	Ala	Gln	Lys	Ser	Leu	Phe	Lys	Thr	Ile	Ala	Ile	Val	Arg
		145			150				155						160
Gln	Phe	Asp	Leu	Glu	Phe	Phe	Ala	Thr	Pro	Lys	Asp	Val	Leu	Asn	Tyr
		165						170					175		
Ile	Asn	Ser	Tyr	Asp	Glu	Gly	Glu	Arg	Gln	Ala	Asn	Leu	Glu	Gln	Ser
		180					185					190			
Phe	Arg	Ile	Leu	Phe	Gln	Leu	His	Gln	Tyr	Val	Leu	Pro	Ala	Leu	Tyr
		195					200				205				
Ile	Phe	Leu	Ile	Ile	Ile	Ser	Phe	Leu	Thr	Gly	Glu	Ile	Gln	Leu	Leu
		210				215				220					
Ala	Phe	Leu	Leu	Val	Gly	Ala	Ile	His	Val	Tyr	Ile	Asn	Val	Met	Gln
		225			230				235						240
Leu	Pro	Met	Val	Lys	Arg	Tyr	Phe	Lys							
				245											

(2) INFORMATION FOR SEQ ID NO:4837:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4837:

Lys	Arg	Arg	Ile	Leu	Met	Gly	Lys	Leu	Ser	Ser	Ile	Leu	Leu	Gly	Thr
1				5				10						15	
Val	Ser	Gly	Ala	Ala	Leu	Ala	Leu	Phe	Leu	Thr	Ser	Asp	Lys	Gly	Lys
		20					25					30			
Gln	Val	Cys	Ser	Gln	Ala	Gln	Asp	Phe	Leu	Asp	Asp	Leu	Arg	Glu	Asp
		35				40					45				
Pro	Glu	Tyr	Ala	Lys	Glu	Gln	Val	Cys	Glu	Lys	Leu	Thr	Glu	Val	Lys
		50				55				60					
Glu	Gln	Ala	Thr	Asp	Phe	Val	Leu	Lys	Thr	Lys	Glu	Gln	Val	Glu	Ser
		65			70				75					80	
Gly	Glu	Ile	Thr	Val	Asp	Ser	Ile	Leu	Ala	Gln	Ala	Lys	Ser	Tyr	Ala
			85				90					95			
Phe	Gln	Ala	Thr	Glu	Ala	Ser	Lys	Asn	Gln	Leu	Asn	Asn	Leu	Lys	Glu
		100					105					110			
Gln	Trp	Gln	Glu	Lys	Ala	Glu	Ala	Leu	Asp	Asp	Ser	Glu	Glu	Ile	Val
		115				120						125			
Ile	Asp	Ile	Thr	Glu	Glu										

(A) LENGTH: 280 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Streptococcus pneumoniae*

(A) NAME/KEY: misc_feature
(B) LOCATION 1...280

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4838:

3725

(2) INFORMATION FOR SEQ ID NO:4839:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 101 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...101

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4839:

```

Val Ser Thr Leu Arg Ser Tyr Ser Pro Gly Gly Val Leu Asn Ala Leu
1          5          10          15
Ala Thr Ala Leu Asn Pro Gly Lys Gly Leu Thr Pro Ser Thr His Arg
          20          25          30
Leu Gln Arg Gly Leu Pro Gly Tyr Leu Ile Leu Phe Ala Pro His Ala
          35          40          45
Phe Glu Pro Gln Arg Gln Leu Gln Ala Arg Glu Pro Leu Ser Pro Pro
          50          55          60
Val Phe Leu His Ile Ser Thr His Phe Thr Ala Thr His Gly Ile Pro
65          70          75          80
Leu Ser Pro Leu Ala Leu Lys Leu Asn Ser Phe Gln Ser Leu Leu Trp
          85          90          95
Leu Ser His Ser Leu
          100

```

(2) INFORMATION FOR SEQ ID NO:4840:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 164 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4840:

Tyr	Thr	Leu	Ile	Ser	Lys	Thr	Leu	Leu	Glu	Ile	Arg	Leu	Asn	Ser	Leu
1				5					10					15	
Ile	Asp	Leu	Arg	Met	Phe	Tyr	Phe	Ile	Ser	Leu	Tyr	Phe	Arg	Leu	Glu
		20						25					30		
Asn	Lys	Glu	Ser	His	Lys	Ser	Gln	Glu	Ile	Gly	Asn	Leu	Ile	Arg	Val
		35					40					45			
Tyr	Asn	Arg	Ser	Lys	Arg	Glu	Glu	Ala	Glu	Ser	Glu	Pro	Leu	Asn	Leu
	50					55					60				
Tyr	Val	Glu	Asp	Glu	Lys	Gly	Asn	Leu	Leu	Ala	Gly	Leu	Ile	Ala	Glu
65					70					75					80
Thr	Phe	Gly	Asn	Trp	Leu	Glu	Leu	Glu	Ile	Glu	Tyr	Leu	Phe	Val	Lys
			85						90					95	
Glu	Glu	Leu	Arg	Gly	Gln	Gly	Ile	Gly	Ser	Lys	Leu	Leu	Gln	Gln	Ala
			100					105					110		
Glu	Ser	Glu	Ala	Lys	Asn	Arg	Asn	Cys	Cys	Phe	Ala	Phe	Val	Asn	Thr
		115					120					125			
Tyr	Gln	Phe	Gln	Ala	Pro	Asp	Phe	Tyr	Gln	Lys	His	Gly	Tyr	Lys	Glu
	130					135					140				
Val	Phe	Ser	Leu	Gln	Asp	Tyr	Leu	Tyr	Ile	Arg	Gln	Arg	Tyr	Tyr	Tyr
145					150					155					160
Gln	Lys	Asn	Leu												

(2) INFORMATION FOR SEQ ID NO:4841:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 100 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4841:

Phe	Phe	Leu	Ile	Ile	Asn	Ile	Phe	Leu	Pro	Arg	Phe	Phe	Cys	His	Thr
1				5					10					15	
Leu	Leu	Leu	Val	Phe	Phe	Tyr	Phe	Ser	Tyr	Tyr	Asn	Ile	Asn	Met	Asn
		20						25					30		
Met	Lys	Ile	Thr	Leu	Ile	Pro	Glu	Arg	Cys	Ile	Ala	Cys	Gly	Leu	Cys
		35					40					45			
Gln	Thr	Tyr	Ser	Asp	Leu	Phe	Asp	Tyr	His	Asp	Asn	Gly	Ile	Val	Arg
	50					55					60				
Phe	Tyr	Asp	Asp	Pro	Asp	Gln	Leu	Glu	Lys	Glu	Ile	Ser	Pro	Ser	Gln
65					70					75					80
Asp	Val	Leu	Glu	Ala	Val	Lys	Asn	Cys	Pro	Thr	Arg	Ala	Leu	Ile	Gly
				85					90					95	
Asn	Gln	Glu	Ala												
			100												

(2) INFORMATION FOR SEQ ID NO:4842:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 83 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...83

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4842:

Gln	Gly	Leu	Met	Glu	Val	Gln	Ala	Ser	Ser	Asn	Leu	Lys	Glu	Phe	Leu
1			5					10					15		
Ser	Lys	Gln	Asn	His	Gln	Ala	Lys	Ile	Ser	Ser	Thr	Asp	Glu	Val	Gln
		20					25					30			
Val	Leu	Phe	Leu	Lys	Lys	Thr	Pro	Lys	Ile	Ile	Ser	Leu	Val	Lys	Glu
		35				40					45				
Trp	Asn	Pro	Thr	Ile	Asp	Leu	Ile	Gly	Phe	Lys	Leu	Leu	Val	Asp	Val
	50					55				60					
Thr	Glu	Asp	His	Leu	Val	Asp	Ile	Ala	Arg	Lys	Ile	Leu	Ser	Arg	Ile
65				70					75					80	
Lys	Gln	Ile													

(2) INFORMATION FOR SEQ ID NO:4843:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1080 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1080

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4843:

Phe	Leu	Leu	Ile	Leu	Gln	Tyr	Val	Tyr	Trp	Ser	Val	Tyr	Met	Gln	Thr
1			5					10					15		
Lys	Thr	Lys	Lys	Leu	Ile	Val	Ser	Leu	Ser	Ser	Leu	Val	Leu	Ser	Gly

465					470					475				480
Leu	Val	Asp	Met	Gly	Arg	Val	Lys	Val	Ile	Ala	Gly	Leu	Leu	Arg
				485					490					495
Asp	Asp	Gln	Glu	Ile	Ser	Ser	Thr	Ile	Arg	Ser	Ile	Glu	Gln	Val
														Phe
				500					505				510	
Lys	Leu	Val	Asp	Gln	Gly	Glu	Gly	Phe	Tyr	Gln	Asp	Gly	Ser	Tyr
														Ile
				515				520				525		
Asp	His	Thr	Asn	Val	Ala	Tyr	Thr	Gly	Ala	Tyr	Gly	Asn	Val	Leu
														Ile
				530				535				540		
Asp	Gly	Leu	Ser	Gln	Leu	Leu	Pro	Val	Ile	Gln	Lys	Thr	Lys	Asn
														Pro
545					550					555				560
Ile	Asp	Lys	Asp	Lys	Met	Gln	Thr	Met	Tyr	His	Trp	Ile	Asp	Lys
				565					570					575
Phe	Ala	Pro	Leu	Leu	Val	Asn	Gly	Glu	Leu	Met	Asp	Met	Ser	Arg
														Gly
				580				585					590	
Arg	Ser	Ile	Ser	Arg	Ala	Asn	Ser	Glu	Gly	His	Val	Ala	Ala	Val
														Glu
				595				600					605	
Val	Leu	Arg	Gly	Ile	His	Arg	Ile	Ala	Asp	Met	Ser	Glu	Gly	Glu
														Thr
				610				615				620		
Lys	Gln	Arg	Leu	Gln	Ser	Leu	Val	Lys	Thr	Ile	Val	Gln	Ser	Asp
														Ser
625					630					635				640
Tyr	Tyr	Asp	Val	Phe	Lys	Asn	Leu	Lys	Thr	Tyr	Lys	Asp	Ile	Ser
				645					650					Leu
														655
Met	Gln	Ser	Leu	Leu	Ser	Asp	Ala	Gly	Val	Ala	Ser	Val	Pro	Arg
				660				665						Thr
														670
Ser	Tyr	Leu	Ser	Ala	Phe	Asn	Lys	Met	Asp	Lys	Thr	Ala	Met	Tyr
														Asn
				675				680						685
Ala	Glu	Lys	Gly	Phe	Gly	Phe	Gly	Leu	Ser	Leu	Phe	Ser	Ser	Arg
														Thr
				690				695						700
Leu	Asn	Tyr	Glu	His	Met	Asn	Lys	Glu	Asn	Lys	Arg	Gly	Trp	Tyr
														Thr
705					710					715				720
Ser	Asp	Gly	Met	Phe	Tyr	Leu	Tyr	Asn	Gly	Asp	Leu	Ser	His	Tyr
				725					730					735
Asp	Gly	Tyr	Trp	Pro	Thr	Val	Asn	Pro	Tyr	Lys	Met	Pro	Gly	Thr
				740				745						750
Glu	Thr	Asp	Ala	Lys	Arg	Ala	Asp	Ser	Asp	Thr	Gly	Lys	Val	Leu
				755				760						765
Ser	Ala	Phe	Val	Gly	Thr	Ser	Lys	Leu	Asp	Asp	Ala	Asn	Ala	Thr
														Ala
				770				775						780
Thr	Met	Asp	Phe	Thr	Asn	Trp	Asn	Gln	Thr	Leu	Thr	Ala	His	Lys
														Ser
785					790					795				800
Trp	Phe	Met	Leu	Lys	Asp	Lys	Ile	Ala	Phe	Leu	Gly	Ser	Asn	Ile
				805					810					Gln
														815
Asn	Thr	Ser	Thr	Asp	Thr	Ala	Ala	Thr	Thr	Ile	Asp	Gln	Arg	Lys
				820				825						Leu
Glu	Ser	Ser	Asn	Pro	Tyr	Lys	Val	Tyr	Val	Asn	Asp	Lys	Glu	Ala
														Ser
				835				840						845
Leu	Thr	Glu	Gln	Glu	Lys	Asp	Tyr	Pro	Glu	Thr	Gln	Ser	Val	Phe
														Leu
				850				855						860
Glu	Ser	Ser	Asp	Ser	Lys	Lys	Asn	Ile	Gly	Tyr	Phe	Phe	Phe	Lys
														Lys
865					870					875				880
Ser	Ser	Ile	Ser	Met	Ser	Lys	Ala	Leu	Gln	Lys	Gly	Ala	Trp	Lys
				885					890					895
Ile	Asn	Glu	Gly	Gln	Ser	Asp	Lys	Glu	Val	Glu	Asn	Glu	Phe	Leu
				900				905						910
Ile	Ser	Gln	Ala	His	Lys	Gln	Asn	Gly	Asp	Ser	Tyr	Gly	Tyr	Met
														Leu

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 471 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...471
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4845:

Arg	Glu	Leu	Met	Met	Lys	Tyr	Leu	Glu	Gly	Glu	Glu	Ile	Thr	Asn	Glu
1				5					10					15	
Glu	Leu	Lys	Ala	Gly	Ile	Arg	Lys	Ala	Thr	Ile	Asn	Val	Glu	Phe	Phe
			20					25					30		
Pro	Val	Leu	Cys	Gly	Ser	Ala	Phe	Lys	Asn	Lys	Gly	Val	Gln	Leu	Met
		35					40						45		
Leu	Asp	Ala	Val	Ile	Asp	Tyr	Leu	Pro	Ser	Pro	Leu	Asp	Ile	Pro	Ala
	50					55					60				
Ile	Lys	Gly	Ile	Asn	Pro	Asp	Thr	Asp	Ala	Glu	Glu	Thr	Arg	Pro	Ala
65					70					75					80
Ser	Asp	Glu	Glu	Pro	Phe	Ala	Ala	Leu	Ala	Phe	Lys	Ile	Met	Thr	Asp
				85					90					95	
Pro	Phe	Val	Gly	Arg	Leu	Thr	Phe	Phe	Arg	Val	Tyr	Ser	Gly	Val	Leu
			100					105					110		
Gln	Ser	Gly	Ser	Tyr	Val	Leu	Asn	Thr	Ser	Lys	Gly	Lys	Arg	Glu	Arg
		115					120					125			
Ile	Gly	Arg	Ile	Leu	Gln	Met	His	Ala	Asn	Ser	Arg	Gln	Glu	Ile	Asp
	130					135					140				
Thr	Val	Tyr	Ser	Gly	Asp	Ile	Ala	Ala	Ala	Val	Gly	Leu	Lys	Asp	Thr
145					150					155					160
Thr	Thr	Gly	Asp	Ser	Leu	Thr	Asp	Glu	Lys	Ser	Lys	Ile	Ile	Leu	Glu
				165					170					175	
Ser	Ile	Asn	Val	Pro	Glu	Pro	Val	Ile	Gln	Leu	Met	Val	Glu	Pro	Lys
			180						185				190		
Ser	Lys	Ala	Asp	Gln	Asp	Lys	Met	Gly	Ile	Ala	Leu	Gln	Lys	Leu	Ala
		195					200					205			
Glu	Glu	Asp	Pro	Thr	Phe	Arg	Val	Glu	Thr	Asn	Val	Glu	Thr	Gly	Glu
	210					215						220			
Thr	Val	Ile	Ser	Gly	Met	Gly	Glu	Leu	His	Leu	Asp	Val	Leu	Val	Asp
225					230					235					240
Arg	Met	Arg	Arg	Glu	Phe	Lys	Val	Glu	Ala	Asn	Val	Gly	Ala	Pro	Gln
				245					250					255	
Val	Ser	Tyr	Arg	Glu	Thr	Phe	Arg	Ala	Ser	Thr	Gln	Ala	Arg	Gly	Phe
			260					265					270		
Phe	Lys	Arg	Gln	Ser	Gly	Gly	Lys	Gly	Gln	Phe	Gly	Asp	Val	Trp	Ile
		275					280					285			
Glu	Phe	Thr	Pro	Asn	Glu	Glu	Gly	Lys	Gly	Phe	Glu	Phe	Glu	Asn	Ala
	290					295					300				
Ile	Val	Gly	Gly	Val	Val	Pro	Arg	Glu	Phe	Ile	Pro	Ala	Val	Glu	Lys

305		310		315		320									
Gly	Leu	Val	Glu	Ser	Met	Ala	Asn	Gly	Val	Leu	Ala	Gly	Tyr	Pro	Met
		325						330						335	
Val	Asp	Val	Lys	Ala	Lys	Leu	Tyr	Asp	Gly	Ser	Tyr	His	Asp	Val	Asp
		340						345						350	
Ser	Ser	Glu	Thr	Ala	Phe	Lys	Ile	Ala	Ala	Ser	Leu	Ser	Leu	Lys	Glu
		355					360						365		
Ala	Ala	Lys	Ser	Ala	Gln	Pro	Ala	Ile	Leu	Glu	Pro	Met	Met	Leu	Val
		370				375					380				
Thr	Ile	Thr	Val	Pro	Glu	Glu	Asn	Leu	Gly	Asp	Val	Met	Gly	His	Val
385				390						395					400
Thr	Ala	Arg	Arg	Gly	Arg	Val	Asp	Gly	Met	Glu	Ala	His	Gly	Asn	Ser
				405				410						415	
Gln	Ile	Val	Arg	Ala	Tyr	Val	Pro	Leu	Ala	Glu	Met	Phe	Gly	Tyr	Ala
		420					425						430		
Thr	Val	Leu	Arg	Ser	Ala	Ser	Gln	Gly	Arg	Gly	Thr	Phe	Met	Met	Val
		435					440					445			
Phe	Asp	His	Tyr	Glu	Asp	Val	Pro	Lys	Ser	Val	Gln	Glu	Glu	Ile	Ile
	450				455					460					
Lys	Lys	Asn	Lys	Gly	Glu	Asp									
465				470											

(2) INFORMATION FOR SEQ ID NO:4846:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 202 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...202
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4846:

Thr	Gln	Leu	Met	Ser	Ile	Ser	Gln	Asn	Gln	Asn	Val	Thr	Leu	Thr	Asn
1			5				10						15		
His	Cys	Phe	Phe	Gln	Ser	Arg	Thr	Tyr	Ser	Gln	Ser	Leu	Asp	Val	Val
		20					25					30			
Gln	Leu	Leu	Gln	Asp	Val	Ser	Thr	Val	Val	Ser	Leu	Lys	Ser	Thr	Thr
		35				40					45				
Lys	Thr	Ile	Leu	Leu	Val	Ser	Lys	Lys	Lys	Thr	Ser	Asn	Pro	Leu	Phe
	50				55				60						
Pro	Gly	Val	Glu	Met	Phe	Arg	Lys	Gln	Leu	Asp	Glu	Gly	Leu	Ala	Gly
65				70				75						80	
Asp	Asn	Val	Gly	Val	Leu	Leu	Arg	Gly	Val	Gln	Arg	Asp	Glu	Ile	Glu
		85					90						95		
Arg	Gly	Gln	Val	Ile	Ala	Lys	Pro	Gly	Ser	Ile	Asn	Pro	His	Thr	Lys
		100					105					110			
Phe	Lys	Gly	Glu	Val	Tyr	Ile	Leu	Thr	Lys	Glu	Glu	Gly	Gly	Arg	His

		115					120				125						
Thr	Pro	Phe	Phe	Asn	Asn	Tyr	Arg	Pro	Gln	Phe	Tyr	Phe	Arg	Thr	Thr		
	130					135					140						
Asp	Val	Thr	Gly	Ser	Ile	Glu	Leu	Pro	Ala	Gly	Thr	Glu	Met	Val	Met		
145					150					155					160		
Pro	Gly	Asp	Asn	Val	Thr	Ile	Asp	Val	Glu	Leu	Ile	His	Pro	Ile	Ala		
			165						170					175			
Val	Glu	Gln	Gly	Thr	Thr	Phe	Ser	Ile	Arg	Glu	Gly	Gly	Arg	Thr	Val		
		180						185					190				
Gly	Ser	Gly	Met	Val	Thr	Glu	Ile	Glu	Ala								
	195						200										

(2) INFORMATION FOR SEQ ID NO:4847:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1169 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4847:

Met	Val	Thr	Leu	Leu	Asp	Leu	Phe	Ser	Glu	Asn	Asp	Gln	Ile	Lys	Lys		
1				5					10					15			
Trp	His	Gln	Asn	Leu	Thr	Asp	Lys	Lys	Arg	Gln	Leu	Ile	Leu	Gly	Leu		
			20					25					30				
Ser	Thr	Ser	Thr	Lys	Ala	Leu	Ala	Ile	Ala	Ser	Ser	Leu	Glu	Lys	Glu		
		35				40					45						
Asp	Arg	Ile	Val	Leu	Leu	Met	Ser	Thr	Tyr	Gly	Glu	Ala	Glu	Gly	Leu		
50						55					60						
Val	Ser	Asp	Leu	Ile	Ser	Ile	Leu	Gly	Glu	Glu	Leu	Val	Tyr	Pro	Phe		
65				70					75						80		
Leu	Val	Asp	Asp	Ala	Pro	Met	Val	Glu	Phe	Leu	Met	Ser	Ser	Gln	Glu		
			85					90						95			
Lys	Ile	Ile	Ser	Arg	Val	Glu	Ala	Leu	Arg	Phe	Leu	Thr	Asp	Ser	Ser		
			100				105						110				
Lys	Lys	Gly	Ile	Leu	Val	Cys	Asn	Ile	Ala	Ala	Ser	Arg	Leu	Ile	Leu		
		115					120					125					
Pro	Ser	Pro	Asn	Ala	Phe	Lys	Asp	Ser	Ile	Val	Lys	Ile	Ser	Val	Gly		
	130					135					140						
Glu	Glu	Tyr	Asp	Gln	His	Ala	Phe	Ile	His	Gln	Leu	Lys	Glu	Asn	Gly		
145				150					155					160			
Tyr	Arg	Lys	Val	Thr	Gln	Val	Gln	Thr	Gln	Gly	Glu	Phe	Ser	Leu	Arg		
			165					170					175				
Gly	Asp	Ile	Leu	Asp	Ile	Phe	Glu	Ile	Ser	Gln	Leu	Glu	Pro	Cys	Arg		
		180					185						190				
Ile	Glu	Phe	Phe	Gly	Asp	Glu	Ile	Asp	Gly	Ile	Arg	Ser	Phe	Glu	Val		

		195					200				205				
Glu	Thr	Gln	Leu	Ser	Lys	Glu	Asn	Lys	Thr	Glu	Leu	Thr	Ile	Phe	Pro
	210						215				220				
Ala	Ser	Asp	Met	Leu	Leu	Arg	Glu	Lys	Asp	Tyr	Gln	Arg	Gly	Gln	Ser
225					230					235					240
Ala	Leu	Glu	Lys	Gln	Ile	Ser	Lys	Thr	Leu	Ser	Pro	Ile	Leu	Lys	Ser
				245					250					255	
Tyr	Leu	Glu	Glu	Ile	Leu	Ser	Ser	Phe	His	Gln	Lys	Gln	Ser	His	Ala
		260						265					270		
Asp	Ser	Arg	Lys	Phe	Leu	Ser	Leu	Cys	Tyr	Asp	Lys	Thr	Trp	Thr	Val
		275					280					285			
Phe	Asp	Tyr	Ile	Glu	Lys	Asp	Thr	Pro	Ile	Phe	Phe	Asp	Asp	Tyr	Gln
	290					295				300					
Lys	Leu	Met	Asn	Gln	Tyr	Glu	Val	Phe	Glu	Arg	Glu	Leu	Ala	Gln	Tyr
305				310					315						320
Phe	Thr	Glu	Glu	Leu	Gln	Asn	Ser	Lys	Ala	Phe	Ser	Asp	Met	Gln	Tyr
				325					330					335	
Phe	Ser	Asp	Ile	Glu	Gln	Ile	Tyr	Lys	Lys	Gln	Ser	Pro	Val	Thr	Phe
		340						345					350		
Phe	Ser	Asn	Leu	Gln	Lys	Gly	Leu	Gly	Asn	Leu	Lys	Phe	Asp	Lys	Ile
		355				360						365			
Tyr	Gln	Phe	Asn	Gln	Tyr	Pro	Met	Gln	Glu	Phe	Phe	Asn	Gln	Phe	Ser
	370					375					380				
Phe	Leu	Lys	Glu	Glu	Ile	Glu	Arg	Tyr	Lys	Lys	Met	Asp	Tyr	Thr	Ile
385				390					395						400
Ile	Leu	Gln	Ser	Ser	Asn	Ser	Met	Gly	Ser	Lys	Thr	Leu	Glu	Asp	Met
				405				410						415	
Leu	Glu	Glu	Tyr	Gln	Ile	Lys	Leu	Asp	Ser	Arg	Asp	Lys	Thr	Asn	Ile
		420					425						430		
Cys	Lys	Glu	Ser	Val	Asn	Leu	Ile	Glu	Gly	Asn	Leu	Arg	His	Gly	Phe
	435					440						445			
His	Phe	Val	Asp	Glu	Lys	Ile	Leu	Leu	Ile	Thr	Glu	His	Glu	Ile	Phe
	450					455					460				
Gln	Lys	Lys	Leu	Lys	Arg	Arg	Phe	Arg	Arg	Gln	His	Val	Ser	Asn	Ala
465				470						475					480
Glu	Arg	Leu	Lys	Asp	Tyr	Asn	Glu	Leu	Glu	Lys	Gly	Asp	Tyr	Val	Val
				485				490						495	
His	His	Ile	His	Gly	Ile	Gly	Gln	Tyr	Leu	Gly	Ile	Glu	Thr	Ile	Glu
		500						505					510		
Ile	Lys	Gly	Ile	His	Arg	Asp	Tyr	Val	Ser	Val	Gln	Tyr	Gln	Asn	Gly
		515				520						525			
Asp	Gln	Ile	Ser	Ile	Pro	Val	Glu	Gln	Ile	His	Leu	Leu	Ser	Lys	Tyr
	530					535					540				
Ile	Ser	Ser	Asp	Gly	Lys	Ala	Pro	Lys	Leu	Asn	Lys	Leu	Asn	Asp	Gly
545				550					555					560	
His	Phe	Lys	Lys	Ala	Lys	Gln	Lys	Val	Lys	Asn	Gln	Val	Glu	Asp	Ile
				565				570						575	
Ala	Asp	Asp	Leu	Ile	Lys	Leu	Tyr	Ser	Glu	Arg	Ser	Gln	Leu	Lys	Gly
		580					585					590			
Phe	Ala	Phe	Ser	Ala	Asp	Asp	Asp	Asp	Gln	Asp	Ala	Phe	Asp	Asp	Ala
	595					600					605				
Phe	Pro	Tyr	Val	Glu	Thr	Asp	Asp	Gln	Leu	Arg	Ser	Ile	Glu	Glu	Ile
	610					615					620				
Lys	Arg	Asp	Met	Gln	Ala	Ser	Gln	Pro	Met	Asp	Arg	Leu	Leu	Val	Gly
625				630					635					640	
Asp	Val	Gly	Phe	Gly	Lys	Thr	Glu	Val	Ala	Met	Arg	Ala	Ala	Phe	Lys
				645				650						655	

Ala	Val	Asn	Asp	His	Lys	Gln	Val	Val	Ile	Leu	Val	Pro	Thr	Thr	Val
			660					665					670		
Leu	Ala	Gln	Gln	His	Tyr	Thr	Asn	Phe	Lys	Glu	Arg	Phe	Gln	Asn	Phe
		675					680					685			
Ala	Val	Asn	Ile	Asp	Val	Leu	Ser	Arg	Phe	Arg	Ser	Lys	Lys	Glu	Gln
	690					695					700				
Thr	Ala	Thr	Leu	Glu	Lys	Leu	Lys	Asn	Gly	Gln	Val	Asp	Ile	Leu	Ile
705					710						715				720
Gly	Thr	His	Arg	Val	Leu	Ser	Lys	Asp	Val	Val	Phe	Ala	Asp	Leu	Gly
				725					730					735	
Leu	Met	Ile	Ile	Asp	Glu	Glu	Gln	Arg	Phe	Gly	Val	Lys	His	Lys	Glu
			740					745					750		
Thr	Leu	Lys	Glu	Leu	Lys	Lys	Gln	Val	Asp	Val	Leu	Thr	Leu	Thr	Ala
		755					760					765			
Thr	Pro	Ile	Pro	Arg	Thr	Leu	His	Met	Ser	Met	Leu	Gly	Ile	Arg	Asp
	770					775					780				
Leu	Ser	Val	Ile	Glu	Thr	Pro	Pro	Thr	Asn	Arg	Tyr	Pro	Val	Gln	Thr
785					790					795					800
Tyr	Val	Leu	Glu	Lys	Asn	Asp	Ser	Val	Ile	Arg	Asp	Ala	Val	Leu	Arg
				805					810					815	
Glu	Met	Glu	Arg	Gly	Gly	Gln	Val	Tyr	Tyr	Leu	Tyr	Asn	Lys	Val	Asp
			820					825					830		
Thr	Ile	Val	Gln	Lys	Val	Ser	Glu	Leu	Gln	Glu	Leu	Ile	Pro	Glu	Ala
		835					840					845			
Ser	Ile	Gly	Tyr	Val	His	Gly	Arg	Met	Ser	Glu	Val	Gln	Leu	Glu	Asn
	850					855					860				
Thr	Leu	Leu	Asp	Phe	Ile	Glu	Gly	Gln	Tyr	Asp	Ile	Leu	Val	Thr	Thr
865					870					875					880
Thr	Ile	Ile	Glu	Thr	Gly	Val	Asp	Ile	Pro	Asn	Ala	Asn	Thr	Leu	Phe
			885					890						895	
Ile	Glu	Asn	Ala	Asp	His	Met	Gly	Leu	Ser	Thr	Leu	Tyr	Gln	Leu	Arg
		900					905						910		
Gly	Arg	Val	Gly	Arg	Ser	Asn	Arg	Ile	Ala	Tyr	Ala	Tyr	Leu	Met	Tyr
		915				920						925			
Arg	Pro	Glu	Lys	Ser	Ile	Ser	Glu	Val	Ser	Glu	Lys	Arg	Leu	Glu	Ala
	930					935					940				
Ile	Lys	Gly	Phe	Thr	Glu	Leu	Gly	Ser	Gly	Phe	Lys	Ile	Ala	Met	Arg
945					950					955					960
Asp	Leu	Ser	Ile	Arg	Gly	Ala	Gly	Asn	Leu	Leu	Gly	Lys	Ser	Gln	Ser
			965					970						975	
Gly	Phe	Ile	Asp	Ser	Val	Gly	Phe	Glu	Leu	Tyr	Ser	Gln	Leu	Leu	Glu
		980						985					990		
Glu	Ala	Ile	Ala	Lys	Arg	Asn	Gly	Asn	Ala	Asn	Ala	Asn	Thr	Arg	Thr
		995					1000					1005			
Lys	Gly	Asn	Ala	Glu	Leu	Ile	Leu	Gln	Ile	Asp	Ala	Tyr	Leu	Pro	Asp
	1010					1015					1020				
Thr	Tyr	Ile	Ser	Asp	Gln	Arg	His	Lys	Ile	Glu	Ile	Tyr	Lys	Lys	Ile
1025					1030					1035					1040
Arg	Gln	Ile	Asp	Asn	Arg	Val	Asn	Tyr	Glu	Glu	Leu	Gln	Glu	Glu	Leu
			1045					1050						1055	
Ile	Asp	Arg	Phe	Gly	Glu	Tyr	Pro	Asp	Val	Val	Ala	Tyr	Leu	Leu	Glu
		1060						1065					1070		
Ile	Gly	Leu	Val	Lys	Ser	Tyr	Leu	Asp	Lys	Val	Phe	Val	Gln	Arg	Val
	1075					1080					1085				
Glu	Arg	Lys	Asp	Asn	Lys	Ile	Thr	Ile	Gln	Phe	Glu	Lys	Val	Thr	Gln
	1090					1095					1100				
Arg	Leu	Phe	Leu	Ala	Gln	Asp	Tyr	Phe	Lys	Ala	Leu	Ser	Val	Thr	Asn

1105		1110		1115		1120
Leu	Lys	Ala	Gly	Ile	Ala	Glu
		1125		1130		1135
Asp	Val	Gln	Asn	Lys	Lys	Asp
		1140		1145		1150
Phe	Gly	Glu	Ser	Leu	Leu	Glu
		1155		1160		1165
Ile						

(2) INFORMATION FOR SEQ ID NO:4848:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 145 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...145
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4848:

Thr	Lys	Leu	Ile	Val	Thr	Cys	Ser	Glu	Arg	Gly	Arg	Tyr	Met	Ile	Lys
1			5					10					15		
Ile	Tyr	Thr	Val	Ser	Ser	Cys	Thr	Ser	Cys	Lys	Lys	Ala	Lys	Thr	Trp
		20					25					30			
Leu	Asn	Ala	His	Gln	Leu	Ser	Tyr	Lys	Glu	Gln	Asn	Leu	Gly	Lys	Glu
		35				40					45				
Gly	Ile	Thr	Arg	Glu	Glu	Leu	Leu	Asp	Ile	Leu	Thr	Lys	Thr	Asp	Asn
	50				55				60						
Gly	Ile	Ala	Ser	Ile	Val	Ser	Ser	Lys	Asn	Arg	Tyr	Ala	Lys	Ala	Leu
65				70					75						80
Gly	Val	Asp	Ile	Glu	Asp	Leu	Ser	Val	Asn	Glu	Val	Leu	Asn	Leu	Ile
			85					90					95		
Met	Glu	Thr	Pro	Arg	Ile	Leu	Lys	Ser	Pro	Ile	Leu	Val	Asp	Glu	Lys
			100				105						110		
Arg	Leu	Gln	Val	Gly	Tyr	Lys	Glu	Asp	Asp	Ile	Arg	Thr	Phe	Leu	Pro
		115				120					125				
Arg	Ser	Val	Arg	Asn	Val	Glu	Asn	Ala	Glu	Ala	Arg	Leu	Arg	Ala	Ala
	130					135					140				
Leu															
145															

(2) INFORMATION FOR SEQ ID NO:4849:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 77 amino acids
 - (B) TYPE: amino acid

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...77
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4849:

Lys	Ser	Met	Ile	His	Ile	Ile	Val	Asn	Thr	Phe	Ile	Glu	Lys	Asp	Met
1				5				10					15		
Thr	Gly	Ala	Val	Val	Glu	Val	Leu	Tyr	Ala	Ser	Ala	Asp	Gln	Asp	Lys
			20				25					30			
Val	Gln	Ala	Lys	Tyr	Glu	Glu	Leu	Ala	Ala	Gln	Tyr	Pro	Glu	Asn	Tyr
		35				40					45				
Leu	Ala	Ile	Tyr	Asp	Val	Pro	Leu	Asp	Thr	Asp	Leu	Asn	Thr	Leu	Asp
	50				55				60						
His	Tyr	Pro	Ser	Val	Phe	Ile	Glu	Lys	Glu	Glu	Phe	Glu			
65				70				75							

(2) INFORMATION FOR SEQ ID NO:4850:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 147 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...147
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4850:

Thr	Pro	Met	Ile	Glu	Ile	Lys	Arg	Ile	Gln	Gln	Gln	Pro	Asp	Leu	Ala
1			5				10					15			
Gln	Ala	Ile	Tyr	Ala	Val	Met	Ala	Ala	Val	Tyr	Leu	Val	Ser	Pro	Trp
		20				25				30					
Thr	Leu	Glu	Gln	Ile	Gln	Ala	Asp	Leu	Ser	Gln	Asp	Gln	Thr	Trp	Tyr
		35			40					45					
Ala	Leu	Ala	Tyr	Asp	Gly	Ala	Glu	Val	Ile	Gly	Phe	Leu	Ala	Val	Gln
	50				55				60						
Glu	Asn	Leu	Phe	Glu	Ala	Glu	Val	Leu	Gln	Ile	Ala	Val	Lys	Gly	Ala
65				70				75				80			
Tyr	Gln	Gly	Gln	Gly	Ile	Ala	Ser	Ala	Leu	Phe	Ala	Gln	Leu	Pro	Thr

				85				90					95				
Asp	Lys	Glu	Ile	Phe	Leu	Glu	Val	Arg	Lys	Ser	Asn	Gln	Arg	Ala	Gln		
			100					105					110				
Ala	Phe	Tyr	Lys	Lys	Glu	Lys	Met	Ala	Val	Ile	Ala	Asp	Arg	Lys	Ala		
		115					120					125					
Tyr	Tyr	His	Asp	Pro	Val	Glu	Asp	Ala	Ile	Ile	Met	Lys	Arg	Glu	Ile		
	130					135					140						
Asp	Glu	Gly															
145																	

(2) INFORMATION FOR SEQ ID NO:4851:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 176 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...176

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4851:

Ile	Asp	Met	Met	Ser	Glu	Val	Gln	Arg	Ala	Ala	Arg	Ile	Leu	Tyr	Met		
1				5					10					15			
Leu	Arg	Val	Asn	Phe	Asn	Gly	Leu	Tyr	Arg	Val	Asn	Ser	Lys	Asn	Gln		
			20					25					30				
Phe	Asn	Val	Pro	Tyr	Gly	Arg	Tyr	Lys	Asn	Pro	Lys	Ile	Val	Asp	Glu		
		35				40					45						
Glu	Leu	Ile	Ser	Ala	Ile	Ser	Val	Tyr	Leu	Asn	Asn	Asn	Gln	Leu	Glu		
	50				55					60							
Ile	Lys	Val	Gly	Asp	Phe	Glu	Lys	Ala	Ile	Val	Asp	Val	Arg	Thr	Gly		
65				70					75					80			
Asp	Phe	Val	Tyr	Phe	Asp	Pro	Pro	Tyr	Ile	Pro	Leu	Ser	Glu	Thr	Ser		
			85					90					95				
Ala	Phe	Thr	Ser	Tyr	Thr	His	Glu	Gly	Phe	Ser	Phe	Ala	Asp	Gln	Val		
		100					105					110					
Arg	Leu	Arg	Asp	Ala	Phe	Lys	Arg	Leu	Ser	Asp	Thr	Gly	Ala	Tyr	Val		
	115					120					125						
Met	Leu	Ser	Asn	Ser	Ser	Ser	Ala	Leu	Val	Glu	Glu	Leu	Tyr	Lys	Asp		
	130				135				140								
Phe	Asn	Ile	His	Tyr	Val	Glu	Ala	Thr	Arg	Thr	Asn	Gly	Ala	Lys	Ser		
145			150					155					160				
Ser	Ser	Arg	Gly	Lys	Ile	Ser	Glu	Ile	Ile	Val	Thr	Asn	Tyr	Glu	Lys		
			165				170						175				

(2) INFORMATION FOR SEQ ID NO:4852:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 221 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...221

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4852:

```
Ile Ser Met Ile Asp Phe Tyr Phe Phe Leu Val Gly Ser Ile Leu Ala
1          5          10          15
Ser Phe Leu Gly Leu Val Ile Asp Arg Phe Pro Glu Gln Ser Ile Ile

          20          25          30
Ser Ser Ala Ser His Cys Asp Ser Cys Gln Thr Arg Leu Arg Pro Leu
35          40          45
Asp Leu Ile Pro Ile Leu Ser Gln Val Phe Asn Arg Phe Arg Cys Arg
50          55          60
Tyr Cys Lys Val Arg Tyr Pro Val Trp Tyr Ala Leu Phe Glu Leu Val
65          70          75          80
Leu Gly Leu Leu Phe Leu Leu Tyr Ser Trp Glu Leu Leu Ser Leu Gly
85          90          95
Gln Val Val Leu Ile Thr Ala Gly Leu Thr Leu Gly Ile Tyr Asp Phe
100          105          110
His His Gln Glu Tyr Pro Leu Leu Val Trp Met Thr Phe His Leu Ile
115          120          125
Leu Ile Ala Ser Ser Gly Trp Asn Leu Val Met Val Ser Phe Leu Ala
130          135          140
Leu Gly Ile Leu Ala His Phe Ile Asp Ile Arg Met Gly Ala Gly Asp
145          150          155          160
Phe Leu Phe Leu Ala Ser Cys Ala Leu Val Phe Ser Val Thr Glu Leu
165          170          175
Leu Ile Leu Ile Gln Phe Ala Ser Ala Thr Gly Ile Leu Ala Phe Leu
180          185          190
Leu Gln Lys Lys Lys Glu Arg Leu Pro Phe Val Pro Phe Leu Leu Leu
195          200          205
Ala Thr Cys Leu Ile Ile Phe Gly Lys Leu Leu Leu Val
210          215          220
```

(2) INFORMATION FOR SEQ ID NO:4853:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 247 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...247

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4853:

```

Asn Lys Met Ile Leu Lys Lys Glu Ile Thr Met Lys Pro Glu Thr Phe
1          5          10          15
Tyr Asn Leu Leu Ala Glu Gln Asn Leu Pro Leu Ser Asn Gln Gln Lys
20          25          30
Glu Gln Phe Glu Arg Tyr Phe Glu Leu Leu Val Glu Trp Asn Glu Lys
35          40          45
Ile Asn Leu Thr Ala Ile Thr Asp Lys Glu Glu Val Tyr Leu Lys His
50          55          60
Phe Tyr Asp Ser Ile Ala Pro Ile Leu Gln Gly Leu Ile Pro Asn Glu
65          70          75          80
Thr Ile Lys Leu Leu Asp Ile Gly Ala Gly Ala Gly Phe Pro Ser Leu
85          90          95
Pro Met Lys Ile Leu Tyr Pro Glu Leu Asp Val Thr Ile Ile Asp Ser
100         105         110
Leu Asn Lys Arg Ile Asn Phe Leu Gln Leu Leu Ala Gln Glu Leu Asp
115         120         125
Leu Asn Gly Val His Phe Tyr His Gly Arg Ala Glu Asp Phe Ala Gln
130         135         140
Asp Lys Asn Phe Arg Ala Gln Tyr Asp Phe Val Thr Ala Arg Ala Val
145         150         155         160
Ala Arg Met Gln Val Leu Ser Glu Leu Thr Ile Pro Tyr Leu Lys Val
165         170         175
Gly Gly Lys Leu Leu Ala Leu Lys Ala Ser Asn Ala Pro Glu Glu Leu
180         185         190
Leu Glu Ala Lys Asn Ala Leu Asn Leu Leu Phe Ser Lys Val Glu Asp
195         200         205
Asn Leu Arg Tyr Ala Leu Pro Asn Arg Asp Pro Arg Tyr Ile Thr Val
210         215         220
Val Glu Lys Lys Lys Glu Thr Pro Asn Lys Tyr Pro Arg Lys Ala Gly
225         230         235         240
Met Pro Asn Lys Arg Pro Leu
245
  
```

(2) INFORMATION FOR SEQ ID NO:4854:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 337 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...337

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4854:

[illegible]

(2) INFORMATION FOR SEO ID NO:4855:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 243 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...243
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4855:

```

Glu Lys Met Ile Met Ser Ile Tyr Lys Leu Tyr Lys Asp Ile Glu Arg
1      5      10      15
Lys Thr Met Ser Pro Ala Lys Lys Ala Met Ala Lys Asn Asp Tyr Phe
20      25      30
Ala Phe Tyr Val Gly Arg Pro Leu Ser Tyr Leu Leu Thr Val Pro Phe
35      40      45
Leu Lys Thr Asn Ile Thr Pro Asn Gln Val Ser Tyr Leu Ser Ile Ala
50      55      60
Pro Leu Ile Leu Gly Phe Leu Thr Met Thr Phe Thr Thr Asn Phe Ile
65      70      75      80
Leu Leu Leu Leu Ala Trp Phe Leu Phe Phe Leu Trp Asn Leu Leu Asp
85      90      95
Gly Val Asp Gly Asn Leu Ala Arg Tyr Arg Glu Gln Tyr Ser Lys Asp
100     105     110
Gly Ser Val Val Asp Ala Met Ala Gly Tyr Val Ala Met Val Leu Thr
115     120     125
Tyr Phe Gly Ala Gly Ile Val Ala Thr His Leu Asn Gly Ser Asp Met
130     135     140
Tyr Val Ile Leu Gly Ala Leu Ser Gly Ile Ser Leu Ile Phe Pro Arg
145     150     155     160
Leu Val Met His Lys Tyr Ile Asn Thr Val Ala Arg Asn Glu Ser Val
165     170     175
Asn Asn Ile Lys Asp Lys Ser Asn Phe Ser Thr Ile Lys Leu Leu Ala
180     185     190
Leu Asn Met Thr Ser Ile Thr Gly Ile Pro Gln Val Leu Leu Leu Val
195     200     205
Thr Ile Leu Thr Asn Gln Trp Glu Phe Phe Thr Leu Val Tyr Phe Thr
210     215     220
Ile Asn Phe Leu Leu Met Ile Phe Ser Leu Tyr Ser Leu Phe Lys Lys
225     230     235     240
Glu Asn Val

```

(2) INFORMATION FOR SEQ ID NO:4856:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 227 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...227

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4856:

```
Glu Lys Met Ile Ser Lys Arg Leu Glu Leu Val Ala Ser Phe Val Ser
1           5           10           15
Gln Gly Ala Ile Leu Leu Asp Val Gly Ser Asp His Ala Tyr Leu Pro
          20           25           30
Ile Glu Leu Val Glu Arg Gly Gln Ile Lys Ser Ala Ile Ala Gly Glu
          35           40           45
Val Val Glu Gly Pro Tyr Gln Ser Ala Val Lys Asn Val Glu Ala His
          50           55           60
Gly Leu Lys Glu Lys Ile Gln Val Arg Leu Ala Asn Gly Leu Ala Ala
65          70          75          80
Phe Glu Glu Thr Asp Gln Val Ser Val Ile Thr Ile Ala Gly Met Gly
          85          90          95
Gly Arg Leu Ile Ala Arg Ile Leu Glu Gly Leu Gly Lys Leu Ala
          100         105         110
Asn Val Glu Arg Leu Ile Leu Gln Pro Asn Asn Arg Glu Asp Asp Leu
          115         120         125
Arg Ile Trp Leu Gln Asp His Gly Phe Gln Ile Val Ala Glu Ser Ile
          130         135         140
Leu Glu Glu Ala Gly Lys Phe Tyr Glu Ile Leu Val Val Glu Ala Gly
145         150         155         160
Gln Met Lys Leu Ser Ala Ser Asp Val Arg Phe Gly Pro Phe Leu Ser
          165         170         175
Lys Glu Val Ser Pro Val Phe Val Gln Lys Trp Gln Lys Glu Ala Glu
          180         185         190
Lys Leu Glu Phe Ala Leu Gly Gln Ile Pro Glu Lys Asn Leu Glu Glu
          195         200         205
Arg Gln Val Leu Val Asp Lys Ile Gln Ala Ile Lys Glu Val Leu His
          210         215         220
Val Ser Lys
225
```

(2) INFORMATION FOR SEQ ID NO:4857:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...67

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4857:

```
Leu Met Val Met Ile Lys Leu Leu Lys Leu Tyr Lys Lys Asp Pro Leu
1          5          10          15
Leu Gly Lys Ile Asn Ala Ile Lys Asn Gly Ala Val Ala Val Ile Pro
20          25          30
Asp Asn Thr Pro Leu Ala Ala Ser Cys Thr Pro Ala Pro Leu Ser Ile
35          40          45
Asn Tyr Thr Ile Glu Glu Tyr Leu Asn Leu Leu Gly Asn Ala Cys Lys
50          55          60
Asn Ala Lys
65
```

(2) INFORMATION FOR SEQ ID NO:4858:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...67

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4858:

```
Leu Glu Val Met Lys Met Ala Thr Asp Lys Asn Arg Ile Met Ile Ser
1          5          10          15
Leu Asp Asp Lys Asn Leu Glu Lys Leu Glu Asn Leu Val Glu Asp Ala
20          25          30
Arg Asp Arg Arg Gly Met Arg Leu Thr Lys Ser Gln Val Ile Glu Leu
35          40          45
Leu Leu Asn Thr Val Asp Tyr Phe Asp Asp Ile Met Gly Ala Ile Tyr
50          55          60
Ser Lys Lys
65
```

(2) INFORMATION FOR SEQ ID NO:4859:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1102 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1102

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4859:

Tyr	Arg	Val	Met	Lys	Asn	Ser	Asn	Glu	Ala	Glu	Met	Lys	Leu	Leu	Tyr
1				5				10					15		
Thr	Asp	Ile	Arg	Thr	Ser	Leu	Thr	Glu	Ile	Leu	Thr	Arg	Glu	Ala	Glu
			20					25					30		
Glu	Leu	Val	Ala	Ala	Gly	Lys	Arg	Val	Phe	Tyr	Ile	Ala	Pro	Asn	Ser
		35				40						45			
Leu	Ser	Phe	Glu	Lys	Glu	Arg	Ala	Val	Leu	Glu	Tyr	Leu	Ser	Gln	Gln
	50					55					60				
Ala	Ser	Phe	Ser	Ile	Thr	Val	Thr	Arg	Phe	Ala	Gln	Met	Ala	Arg	Tyr
65					70					75				80	
Leu	Val	Leu	Asn	Asp	Leu	Pro	Ala	Lys	Thr	Thr	Leu	Asp	Asp	Ile	Gly
			85						90					95	
Leu	Gly	Leu	Ala	Phe	Tyr	Lys	Cys	Leu	Ala	Glu	Leu	Asp	Pro	Lys	Asp
		100						105					110		
Leu	Arg	Val	Tyr	Gly	Ala	Ile	Lys	Gln	Asp	Pro	Gln	Leu	Ile	Gln	Gln
	115						120					125			
Leu	Ile	Glu	Leu	Tyr	His	Glu	Met	Thr	Lys	Ser	Gln	Met	Ser	Phe	Leu
	130					135					140				
Asp	Leu	Glu	Asn	Leu	Thr	Asp	Glu	Asp	Lys	Arg	Ala	Asp	Leu	Leu	Leu
145					150					155					160
Ile	Phe	Glu	Lys	Val	Thr	Ala	Tyr	Leu	Asn	Gln	Gly	Gln	Leu	Ala	Gln
			165						170					175	
Gly	Ser	Gln	Leu	Ser	His	Leu	Ile	Glu	Ala	Ile	Glu	Asn	Asp	Lys	Val
		180						185				190			
Ser	Ser	Asp	Phe	Asn	Gln	Ile	Ala	Leu	Val	Ile	Asp	Gly	Phe	Thr	Arg
		195					200					205			
Phe	Ser	Ala	Glu	Glu	Glu	Arg	Val	Val	Asp	Leu	Leu	His	Gly	Lys	Gly
	210					215					220				
Val	Glu	Ile	Val	Ile	Gly	Ala	Tyr	Ala	Ser	Lys	Lys	Ala	Tyr	Thr	Ser
225					230					235					240
Pro	Phe	Ser	Glu	Gly	Asn	Leu	Tyr	Gln	Ala	Ser	Val	Lys	Phe	Leu	His
			245						250					255	
His	Leu	Ala	Ser	Lys	Tyr	Gln	Thr	Pro	Ala	Gln	Asp	Cys	Ser	Gln	Thr
		260						265					270		
His	Glu	Lys	Met	Asp	Ser	Phe	Asp	Lys	Ala	Ser	Arg	Leu	Leu	Glu	Ser
	275						280					285			
Ser	Tyr	Asp	Phe	Ser	Glu	Leu	Ala	Leu	Asp	Val	Asp	Glu	Lys	Asp	Arg
	290					295					300				
Glu	Asn	Leu	Gln	Ile	Trp	Ser	Cys	Leu	Thr	Gln	Lys	Glu	Glu	Leu	Glu
305					310					315					320
Leu	Val	Ala	Arg	Ser	Ile	Arg	Gln	Lys	Leu	His	Glu	Asn	Ser	Asp	Leu
			325						330					335	
Ser	Tyr	Lys	His	Phe	Arg	Ile	Leu	Leu	Gly	Asp	Val	Ala	Ser	Tyr	Gln
		340					345						350		
Leu	Ser	Leu	Lys	Thr	Ile	Phe	Asp	Gln	Tyr	Gln	Ile	Pro	Phe	Tyr	Leu
	355					360						365			
Gly	Arg	Ser	Glu	Ala	Met	Ala	His	His	Pro	Leu	Thr	Gln	Phe	Val	Glu
	370					375					380				

Ser	Ile	Leu	Ala	Leu	Lys	Arg	Tyr	Arg	Phe	Arg	Gln	Glu	Asp	Leu	Ile	385	390	395	400
Asn	Leu	Leu	Arg	Thr	Asp	Leu	Tyr	Thr	Asp	Leu	Ser	Gln	Ser	Asp	Ile	405	410	415	
Asp	Ala	Phe	Glu	Gln	Tyr	Ile	Arg	Tyr	Leu	Gly	Ile	Asn	Gly	Leu	Pro	420	425	430	
Ala	Phe	Gln	Gln	Thr	Phe	Thr	Lys	Ser	His	His	Gly	Lys	Phe	Asn	Leu	435	440	445	
Glu	Arg	Leu	Asn	Val	Leu	Arg	Leu	Arg	Ile	Leu	Ala	Pro	Leu	Glu	Thr	450	455	460	
Leu	Phe	Ala	Ser	Arg	Lys	Gln	Lys	Ala	Glu	Asn	Leu	Leu	Gln	Lys	Trp	465	470	475	480
Ser	Val	Phe	Leu	Lys	Glu	Gly	Ala	Val	Thr	Lys	Gln	Leu	Gln	Asp	Leu	485	490	495	
Thr	Thr	Thr	Leu	Glu	Ala	Val	Glu	Gln	Glu	Arg	Gln	Thr	Glu	Val	Trp	500	505	510	
Lys	Ala	Phe	Cys	His	Val	Leu	Glu	Gln	Phe	Ala	Thr	Val	Phe	Ala	Gly	515	520	525	
Ser	Gln	Val	Ser	Leu	Glu	Asp	Phe	Leu	Ala	Leu	Leu	His	Ser	Gly	Met	530	535	540	
Ser	Leu	Ser	Gln	Tyr	Arg	Thr	Ile	Pro	Ala	Thr	Val	Asp	Thr	Val	Leu	545	550	555	560
Val	Gln	Ser	Tyr	Asp	Leu	Ile	Ala	Pro	Leu	Thr	Ala	Asp	Phe	Val	Tyr	565	570	575	
Ala	Ile	Gly	Leu	Thr	Gln	Asp	Asn	Leu	Pro	Lys	Ile	Ser	Gln	Asn	Thr	580	585	590	
Ser	Leu	Leu	Thr	Asp	Glu	Glu	Arg	Gln	Asn	Leu	Asn	Gln	Thr	Thr	Glu	595	600	605	
Glu	Gly	Val	Gln	Leu	Leu	Ile	Ala	Ser	Ser	Glu	Asn	Leu	Lys	Lys	Asn	610	615	620	
Arg	Tyr	Thr	Met	Leu	Ser	Leu	Val	Asn	Ser	Ala	Arg	Lys	Gln	Leu	Phe	625	630	635	640
Leu	Ser	Ala	Pro	Ser	Leu	Phe	Asn	Glu	Ser	Glu	Ser	Lys	Glu	Ser	Ala	645	650	655	
Tyr	Leu	Gln	Glu	Leu	Ile	His	Phe	Gly	Phe	Arg	Arg	Arg	Glu	Lys	Arg	660	665	670	
Met	Asn	His	Lys	Gly	Leu	Ser	Lys	Glu	Asp	Met	Gly	Ser	Tyr	His	Ser	675	680	685	
Leu	Leu	Ser	Ser	Leu	Val	Ala	Tyr	His	Gln	Gln	Gly	Glu	Met	Ser	Asp	690	695	700	
Thr	Glu	Gln	Asp	Leu	Thr	Phe	Val	Lys	Val	Leu	Ser	Arg	Val	Ile	Gly	705	710	715	720
Lys	Lys	Leu	Asp	Leu	Gln	Gly	Leu	Glu	Asn	Pro	Ala	Ile	Pro	Thr	Ser	725	730	735	
Pro	Ser	Ser	Lys	Thr	Leu	Thr	Lys	Asp	Thr	Leu	Gln	Ala	Leu	Tyr	Pro	740	745	750	
Ala	Lys	Gln	Glu	Phe	Tyr	Leu	Ser	Thr	Ser	Gly	Leu	Thr	Glu	Phe	Tyr	755	760	765	
Leu	Asn	Glu	Tyr	Ser	Tyr	Phe	Leu	Arg	Tyr	Val	Leu	Gly	Leu	Gln	Glu	770	775	780	
Glu	Leu	Arg	Leu	Arg	Pro	Asp	Ala	Arg	Ser	His	Gly	Asn	Phe	Leu	His	785	790	795	800
Arg	Ile	Phe	Glu	Arg	Ala	Leu	Gln	Leu	Pro	Asn	Glu	Asp	Ser	Phe	Asp	805	810	815	
Gln	Arg	Leu	Glu	Gln	Ala	Ile	Gln	Glu	Thr	Ser	Gln	Glu	Arg	Glu	Phe	820	825	830	
Glu	Ala	Ile	Tyr	Gln	Glu	Ser	Leu	Glu	Ala	Gln	Phe	Thr	Lys	Glu	Val				

			20					25					30				
Lys	Glu	His	Asp	Leu	Leu	Cys	Tyr	Leu	Cys	Gly	Gly	Gly	Ala	Ile	Gly		
		35					40					45					
Ala	Leu	Arg	Asn	Lys	Gly	Phe	Ile	Pro	Trp	Asp	Asp	Asp	Leu	Asp	Phe		
	50					55					60						
Phe	Met	Pro	Arg	Lys	Asp	Tyr	Glu	Lys	Leu	Ala	Glu	Leu	Trp	Pro	Arg		
65					70					75					80		
Tyr	Ala	Asp	Glu	Arg	Tyr	Phe	Leu	Ser	Lys	Ser	Tyr	Lys	Asp	Phe	Val		
				85					90					95			
Asp	Arg	Asn	Leu	Phe	Ile	Thr	Ile	Arg	Asp	Lys	Glu	Thr	Thr	Cys	Ile		
			100					105					110				
Lys	Pro	Tyr	Gln	Gln	Asp	Leu	Asp	Leu	Pro	His	Gly	Leu	Ala	Leu	Asp		
	115						120					125					
Val	Leu	Pro	Leu	Asp	Tyr	Tyr	Pro	Lys	Asp	Pro	Ala	Glu	Arg	Lys	Lys		
	130					135					140						
Gln	Val	Arg	Trp	Ala	Leu	Ile	Tyr	Ser	Leu	Phe	Cys	Ala	Gln	Thr	Ile		
145					150					155					160		
Pro	Glu	Lys	His	Gly	Ala	Leu	Met	Lys	Trp	Gly	Ser	Arg	Ile	Leu	Leu		
				165					170					175			
Gly	Leu	Thr	Pro	Lys	Ser	Leu	Arg	Tyr	Arg	Ile	Trp	Lys	Lys	Ala	Glu		
		180					185						190				
Lys	Glu	Met	Thr	Lys	Tyr	Asp	Leu	Ala	Asp	Cys	Asp	Gly	Ile	Thr	Glu		
	195						200					205					
Leu	Cys	Ser	Gly	Pro	Gly	Tyr	Met	Arg	Asn	Lys	Tyr	Pro	Ile	Thr	Ser		
	210					215					220						
Phe	Glu	Asp	Asn	Leu	Phe	Leu	Pro	Phe	Glu	Gly	Thr	Lys	Met	Pro	Ile		
225					230					235					240		
Pro	Ile	Gly	Tyr	Asp	Val	Tyr	Leu	Arg	Thr	Ala	Phe	Gly	Asp	Tyr	Met		
				245					250					255			
Thr	Pro	Pro	Pro	Ala	Asp	Lys	Gln	Val	Pro	His	His	Asp	Val	Val	Ile		
			260				265						270				
Ala	Asp	Met	Asp	Lys	Ser	Tyr	Thr	Glu	Tyr	Lys	Gly	Glu	Tyr	Gly	Gly		
	275						280					285					

(2) INFORMATION FOR SEQ ID NO:4861:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 404 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...404
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4861:

Tyr	Arg	Thr	Ile	Phe	Tyr	Met	Asn	Asp	Lys	Thr	Glu	Val	Asn	Met	Thr
1				5					10					15	

Ile	Gly	Ile	Asp	Lys	Ile	Gly	Phe	Ala	Thr	Ser	Gln	Tyr	Val	Leu	Lys
			20					25					30		
Leu	Gln	Asp	Leu	Ala	Glu	Ala	Arg	Gly	Ile	Asp	Pro	Glu	Lys	Leu	Ser
		35					40					45			
Lys	Gly	Leu	Leu	Leu	Lys	Glu	Leu	Ser	Ile	Ala	Pro	Leu	Thr	Glu	Asp
	50					55					60				
Ile	Val	Thr	Leu	Ala	Ala	Ser	Ala	Ser	Asp	Ser	Ile	Leu	Thr	Glu	Gln
65					70				75						80
Glu	Arg	Gln	Glu	Val	Asp	Met	Val	Ile	Val	Ala	Thr	Glu	Ser	Gly	Ile
				85					90					95	
Asp	Gln	Ser	Lys	Ala	Ala	Ala	Val	Phe	Val	His	Gly	Leu	Leu	Gly	Ile
			100					105					110		
Gln	Pro	Phe	Ala	Arg	Ser	Phe	Glu	Ile	Lys	Glu	Ala	Cys	Tyr	Gly	Ala
		115					120					125			
Thr	Ala	Ala	Leu	His	Tyr	Ala	Lys	Leu	His	Val	Glu	Asn	Ser	Pro	Glu
						135					140				
Ser	Lys	Val	Leu	Val	Ile	Ala	Ser	Asp	Ile	Ala	Lys	Tyr	Gly	Ile	Glu
145					150				155						160
Thr	Pro	Gly	Glu	Pro	Thr	Gln	Gly	Ala	Gly	Ser	Val	Ala	Met	Leu	Ile
				165					170					175	
Thr	Gln	Asn	Pro	Arg	Met	Met	Ala	Phe	Asn	Asn	Asp	Asn	Val	Ala	Gln
			180					185					190		
Thr	Arg	Asp	Ile	Met	Asp	Phe	Trp	Arg	Pro	Asn	Tyr	Ser	Thr	Thr	Pro
		195					200					205			
His	Val	Asn	Gly	Val	Tyr	Ser	Thr	Gln	Gln	Tyr	Leu	Asp	Ser	Leu	Lys
	210					215					220				
Thr	Thr	Trp	Leu	Glu	Tyr	Gln	Lys	Arg	Tyr	Gln	Leu	Thr	Leu	Asp	Asp
225					230				235						240
Phe	Ala	Ala	Val	Cys	Phe	His	Leu	Pro	Tyr	Pro	Lys	Leu	Ala	Leu	Lys
				245					250					255	
Gly	Leu	Lys	Lys	Ile	Met	Asp	Lys	Ser	Leu	Pro	Gln	Glu	Lys	Lys	Asp
			260				265					270			
Leu	Leu	Gln	Lys	His	Phe	Asp	Gln	Ser	Ile	Leu	Tyr	Ser	Gln	Lys	Val
		275					280					285			
Gly	Asn	Ile	Tyr	Thr	Gly	Ser	Leu	Phe	Leu	Gly	Leu	Leu	Ser	Leu	Leu
	290					295					300				
Glu	Asn	Thr	Asp	Ser	Leu	Lys	Ala	Gly	Asp	Lys	Ile	Ala	Leu	Tyr	Ser
305					310				315						320
Tyr	Gly	Ser	Gly	Ala	Val	Ala	Glu	Phe	Phe	Ser	Gly	Glu	Leu	Val	Glu
				325					330					335	
Gly	Tyr	Glu	Ala	Tyr	Leu	Asp	Lys	Asp	Arg	Leu	Asn	Lys	Leu	Asn	Gln
			340				345					350			
Arg	Thr	Ala	Leu	Ser	Val	Ala	Asp	Tyr	Glu	Lys	Val	Phe	Phe	Glu	Glu
			355				360					365			
Val	Asn	Leu	Asp	Glu	Thr	Asn	Ser	Ala	Gln	Phe	Ala	Gly	Tyr	Glu	Asn
	370					375					380				
Gln	Asp	Phe	Ala	Leu	Val	Glu	Ile	Leu	Asp	His	Gln	Arg	Arg	Tyr	Ser
385					390					395					400
Lys	Val	Glu	Lys												

(2) INFORMATION FOR SEQ ID NO:4862:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 317 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...317

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4862:

```

Leu Leu Ala Ile Val Thr Val Asn Asn Ile Leu Val Ala Ser Asn Phe
1      5      10      15
Ser Pro Arg Leu Glu Ile Lys Arg Ile Ser Leu Tyr Asn Lys Tyr Leu
20      25      30
Tyr Arg Lys His Leu Leu Glu Arg Tyr Leu Cys Phe His Ile His Phe
35      40      45
Pro Phe Phe His Val Phe Gly Trp Tyr Arg Lys Pro Leu Ser Lys Arg
50      55      60
Phe Glu Leu Asn Trp Phe Gln Leu Leu Phe Thr Ser Ile Phe Leu Ile
65      70      75      80
Ser Leu Ser Met Val Pro Ile Ala Ile Gln Asn Ser Ser Gln Glu Thr
85      90      95
Tyr Pro Leu Glu Thr Phe Ile Asp Asn Val Tyr Glu Pro Leu Thr Asp
100     105     110
Lys Val Val Gln Asp Leu Ser Glu His Ala Thr Ile Val Asp Gly Thr
115     120     125
Leu Thr Tyr Thr Gly Thr Val Ser Gln Ala Ser Ser Ile Val Ile Gly
130     135     140
Pro Ser Gln Ile Lys Glu Leu Pro Lys Asp Leu Gln Leu His Phe Asp
145     150     155     160
Thr Asn Glu Leu Val Ile Ser Lys Glu Ser Lys Glu Leu Thr Arg Ile
165     170     175
Ser Tyr Arg Ala Ile Gln Thr Glu Ser Phe Lys Ser Lys Asp Ser Leu
180     185     190
Thr Gln Ala Ile Ser Lys Asp Trp Tyr Gln Gln Asn Arg Val Tyr Ile
195     200     205
Ser Leu Phe Leu Val Leu Gly Ala Ser Phe Leu Phe Gly Leu Asn Phe
210     215     220
Phe Ile Val Ser Leu Gly Ala Ser Leu Leu Leu Tyr Ile Thr Lys Lys
225     230     235     240
Ser Arg Leu Phe Ser Phe Arg Thr Phe Lys Glu Cys Tyr His Phe Ile
245     250     255
Leu Asn Cys Leu Gly Leu Pro Thr Leu Ile Thr Leu Ile Leu Gly Leu
260     265     270
Phe Gly Gln Asn Met Thr Thr Leu Ile Thr Val Gln Asn Ile Leu Phe
275     280     285
Val Leu Tyr Leu Val Thr Ile Phe Tyr Lys Thr His Phe Arg Asp Pro
290     295     300
Asn Tyr His Lys Tyr Gly Asp Phe Tyr Ala Arg Tyr Asp
305     310     315

```

(2) INFORMATION FOR SEQ ID NO:4863:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...68
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4863:

```

Lys Ser Ala Phe Phe Ser Thr Lys Ile Arg Leu Ser Ile Asn Ser Tyr
1      5      10      15
Ser Phe Ile Ser Ala Leu Ala Ile Phe Pro Asn Ser Leu Glu Val Val
      20      25      30
Ile Leu Asn Pro Ala Thr Phe Pro Arg Gln Phe Arg Lys His Leu Leu
      35      40      45
Val His Leu Val Leu Tyr Arg Val Lys Arg Ser Gly Gly Pro Phe Gln
      50      55      60
Pro Glu Ser Phe
65

```

(2) INFORMATION FOR SEQ ID NO:4864:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 448 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...448
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4864:

```

Val Cys Gln Met Lys Ser Trp Lys Asn Trp Leu Ile Lys Ile Asn Tyr
1      5      10      15
Cys Val Tyr Lys Lys Lys Arg Lys Gly Arg Met Arg Lys Phe Leu Ile
      20      25      30
Ile Leu Leu Leu Pro Ser Phe Leu Thr Ile Ser Lys Val Val Ser Thr
      35      40      45
Glu Lys Glu Val Val Tyr Thr Ser Lys Glu Ile Tyr Tyr Leu Ser Gln

```

50		55		60											
Ser	Asp	Phe	Gly	Ile	Tyr	Phe	Arg	Glu	Lys	Leu	Ser	Ser	Pro	Met	Val
65					70					75					80
Tyr	Gly	Glu	Val	Pro	Val	Tyr	Ala	Asn	Glu	Asp	Leu	Val	Val	Glu	Ser
				85					90					95	
Gly	Lys	Leu	Thr	Pro	Lys	Thr	Ser	Phe	Gln	Ile	Thr	Glu	Trp	Arg	Leu
			100					105					110		
Asn	Lys	Gln	Gly	Ile	Pro	Val	Phe	Lys	Leu	Ser	Asn	His	Gln	Phe	Ile
		115					120					125			
Ala	Ala	Asp	Lys	Arg	Phe	Leu	Tyr	Asp	Gln	Ser	Glu	Val	Thr	Pro	Thr
	130					135					140				
Ile	Lys	Lys	Val	Trp	Leu	Glu	Ser	Asp	Phe	Lys	Leu	Tyr	Asn	Ser	Pro
145					150					155					160
Tyr	Asp	Leu	Lys	Glu	Val	Lys	Ser	Ser	Leu	Ser	Ala	Tyr	Ser	Gln	Val
				165				170					175		
Ser	Ile	Asp	Lys	Thr	Met	Phe	Val	Glu	Gly	Arg	Glu	Phe	Leu	His	Ile
			180					185					190		
Asp	Gln	Ala	Gly	Trp	Val	Ala	Lys	Glu	Ser	Thr	Ser	Glu	Glu	Asp	Asn
	195						200					205			
Arg	Met	Ser	Lys	Val	Gln	Glu	Met	Leu	Ser	Glu	Lys	Tyr	Gln	Lys	Asp
	210					215					220				
Ser	Phe	Ser	Ile	Tyr	Val	Lys	Gln	Leu	Thr	Thr	Gly	Lys	Glu	Ala	Gly
225					230					235					240
Ile	Asn	Gln	Asp	Glu	Lys	Met	Tyr	Ala	Ala	Ser	Val	Leu	Lys	Leu	Ser
			245					250					255		
Tyr	Leu	Tyr	Tyr	Thr	Gln	Glu	Lys	Ile	Asn	Glu	Gly	Leu	Tyr	Gln	Leu
		260					265						270		
Asp	Thr	Thr	Val	Lys	Tyr	Val	Ser	Ala	Val	Asn	Asp	Phe	Pro	Gly	Ser
	275					280						285			
Tyr	Lys	Pro	Glu	Gly	Ser	Gly	Ser	Leu	Pro	Lys	Lys	Glu	Asp	Asn	Lys
	290					295				300					
Glu	Tyr	Ser	Leu	Lys	Asp	Leu	Ile	Thr	Lys	Val	Ser	Lys	Glu	Ser	Asp
305					310					315					320
Asn	Val	Ala	His	Asn	Leu	Leu	Gly	Tyr	Tyr	Ile	Ser	Asn	Gln	Ser	Asp
			325					330						335	
Ala	Thr	Phe	Lys	Ser	Lys	Met	Ser	Ala	Ile	Met	Gly	Asp	Asp	Trp	Asp
	340						345					350			
Pro	Lys	Glu	Lys	Leu	Ile	Ser	Ser	Lys	Met	Ala	Gly	Lys	Phe	Met	Glu
	355					360					365				
Ala	Ile	Tyr	Asn	Gln	Asn	Gly	Phe	Val	Leu	Glu	Ser	Leu	Thr	Lys	Thr
	370				375					380					
Asp	Phe	Asp	Ser	Gln	Arg	Ile	Ala	Lys	Gly	Val	Ser	Val	Lys	Val	Ala
385					390				395						400
His	Lys	Ile	Gly	Asp	Ala	Asp	Glu	Phe	Lys	His	Asp	Thr	Gly	Val	Val
			405					410					415		
Tyr	Ala	Asp	Ser	Pro	Phe	Ile	Leu	Ser	Ile	Phe	Thr	Lys	Asn	Ser	Asp
	420						425					430			
Tyr	Asp	Thr	Ile	Ser	Lys	Ile	Ala	Lys	Asp	Val	Tyr	Glu	Val	Leu	Lys
	435					440						445			

(2) INFORMATION FOR SEQ ID NO:4865:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 295 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...295
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4865:

Arg	Cys	Gln	Met	Ala	Val	Ser	Leu	Asn	Asp	Ile	Lys	Thr	Lys	Ile	Ala	1	5	10	15
Ser	Thr	Lys	Asn	Thr	Ser	Gln	Ile	Thr	Asn	Ala	Met	Gln	Met	Val	Ser	20	25	30	
Ala	Ala	Lys	Leu	Gly	Arg	Ser	Glu	Glu	Ala	Ala	Arg	Asn	Phe	Gln	Val	35	40	45	
Tyr	Ala	Gln	Lys	Val	Arg	Lys	Leu	Leu	Thr	Asp	Ile	Leu	His	Gly	Asn	50	55	60	
Gly	Ala	Gly	Ala	Ser	Thr	Asn	Pro	Met	Leu	Ile	Ser	Arg	Ser	Val	Lys	65	70	75	80
Lys	Thr	Gly	Tyr	Ile	Val	Ile	Thr	Ser	Asp	Arg	Gly	Leu	Val	Gly	Gly	85	90	95	
Tyr	Asn	Ser	Ser	Ile	Leu	Lys	Ala	Val	Met	Glu	Leu	Lys	Glu	Glu	Tyr	100	105	110	
His	Pro	Asp	Gly	Lys	Gly	Phe	Glu	Met	Ile	Cys	Ile	Gly	Gly	Met	Gly	115	120	125	
Ala	Asp	Phe	Phe	Lys	Ala	Arg	Gly	Ile	Gln	Pro	Leu	Tyr	Glu	Leu	Arg	130	135	140	
Gly	Leu	Ala	Asp	Gln	Pro	Ser	Phe	Asp	Gln	Val	Arg	Lys	Ile	Ile	Ser	145	150	155	160
Lys	Thr	Val	Glu	Met	Tyr	Gln	Asn	Glu	Leu	Phe	Asp	Glu	Leu	Tyr	Val	165	170	175	
Cys	Tyr	Asn	His	His	Val	Asn	Thr	Leu	Thr	Ser	Gln	Met	Arg	Val	Glu	180	185	190	
Gln	Met	Leu	Pro	Ile	Val	Asp	Leu	Asp	Pro	Asn	Glu	Ala	Asp	Glu	Glu	195	200	205	
Tyr	Ser	Leu	Thr	Phe	Glu	Leu	Glu	Thr	Ser	Arg	Glu	Glu	Ile	Leu	Glu	210	215	220	
Gln	Leu	Leu	Pro	Gln	Phe	Ala	Glu	Ser	Met	Ile	Tyr	Gly	Ala	Ile	Ile	225	230	235	240
Asp	Ala	Lys	Thr	Ala	Glu	Asn	Ala	Ala	Gly	Met	Thr	Ala	Met	Gln	Thr	245	250	255	
Ala	Thr	Asp	Asn	Ala	Lys	Lys	Val	Ile	Asn	Asp	Leu	Thr	Ile	Gln	Tyr	260	265	270	
Asn	Arg	Ala	Arg	Gln	Ala	Ala	Ile	Thr	Gln	Glu	Ile	Thr	Glu	Ile	Val	275	280	285	
Ala	Gly	Ala	Ser	Ala	Leu	Glu										290	295		

(2) INFORMATION FOR SEQ ID NO:4866:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 302 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...302

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4866:

Val	Thr	Lys	Met	Leu	Phe	Asp	Gln	Ile	Ala	Ser	Asn	Lys	Arg	Lys	Thr
1				5					10					15	
Trp	Ile	Leu	Leu	Leu	Val	Phe	Phe	Leu	Leu	Leu	Ala	Leu	Val	Gly	Tyr
			20					25					30		
Ala	Val	Gly	Tyr	Leu	Phe	Ile	Arg	Ser	Gly	Leu	Gly	Gly	Leu	Val	Ile
		35					40					45			
Ala	Leu	Ile	Ile	Gly	Phe	Ile	Tyr	Ala	Leu	Ser	Met	Ile	Phe	Gln	Ser
	50					55					60				
Thr	Glu	Ile	Val	Met	Ser	Met	Asn	Gly	Ala	Arg	Glu	Val	Asp	Glu	Gln
65					70					75					80
Thr	Ala	Pro	Asp	Leu	Tyr	His	Val	Val	Glu	Asp	Met	Ala	Leu	Val	Ala
				85				90					95		
Gln	Ile	Pro	Met	Pro	Arg	Val	Phe	Ile	Ile	Asp	Asp	Pro	Ala	Leu	Asn
			100					105					110		
Ala	Phe	Ala	Thr	Gly	Ser	Asn	Pro	Gln	Asn	Ala	Ala	Val	Ala	Ala	Thr
		115					120					125			
Ser	Gly	Leu	Leu	Ala	Ile	Met	Asn	Arg	Glu	Glu	Leu	Glu	Ala	Val	Met
	130					135					140				
Gly	His	Glu	Val	Ser	His	Ile	Arg	Asn	Tyr	Asp	Ile	Arg	Ile	Ser	Thr
145					150				155					160	
Ile	Ala	Val	Ala	Leu	Ala	Ser	Ala	Ile	Thr	Met	Leu	Ser	Gly	Met	Ala
			165						170					175	
Gly	Arg	Met	Met	Trp	Trp	Gly	Gly	Ala	Gly	Arg	Arg	Arg	Ser	Asp	Asp
		180					185						190		
Asp	Arg	Asp	Gly	Asn	Gly	Leu	Glu	Ile	Ile	Met	Leu	Val	Val	Ser	Leu
		195				200						205			
Leu	Ala	Ile	Val	Leu	Ala	Pro	Leu	Ala	Ala	Thr	Leu	Val	Gln	Leu	Ala
	210					215					220				
Ile	Ser	Arg	Gln	Arg	Glu	Phe	Leu	Ala	Asp	Ala	Ser	Ser	Val	Glu	Leu
225				230					235					240	
Thr	Arg	Asn	Pro	Gln	Gly	Met	Ile	Asn	Ala	Leu	Asp	Lys	Leu	Asp	Asn
			245						250					255	
Ser	Lys	Pro	Met	Ser	Arg	His	Val	Asp	Asp	Ala	Ser	Ser	Ala	Leu	Tyr
		260					265						270		
Ile	Asn	Asp	Pro	Lys	Lys	Gly	Gly	Gly	Phe	Gln	Lys	Leu	Phe	Tyr	Thr
	275					280						285			
His	Pro	Pro	Ile	Ser	Glu	Arg	Ile	Glu	Arg	Leu	Lys	Gln	Met		
	290					295						300			

(2) INFORMATION FOR SEQ ID NO:4867:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 217 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...217
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4867:

```

Glu Asn Lys Met Ala Phe Ile Glu Lys Gly Gln Glu Ile Asp Met Glu
1      5      10      15
Val Ile Lys Ala Glu Thr Gln Leu Ser Ala Glu Ala Leu Arg Leu Lys
      20      25      30
Glu Ser Arg Asp Arg Glu Leu Ala Asp Ile Ile Ser Gly Glu Asp Asp
      35      40      45
Arg Ile Leu Leu Val Ile Gly Pro Cys Ser Ser Asp Asn Glu Glu Ala
      50      55      60
Val Leu Glu Tyr Ala Arg Arg Leu Ser Ala Leu Gln Lys Lys Val Ala
65      70      75      80
Asp Lys Ile Phe Met Val Met Arg Val Tyr Thr Ala Lys Pro Arg Thr
      85      90      95
Asn Gly Asp Gly Tyr Lys Gly Leu Val His Gln Pro Asp Thr Ser Lys
      100     105     110
Ala Pro Ser Leu Ile Asn Gly Leu Gln Ala Val Arg Gln Leu His Tyr
      115     120     125
Arg Val Ile Thr Glu Thr Gly Leu Thr Thr Ala Asp Glu Met Leu Tyr
      130     135     140
Pro Ser Asn Leu Ile Leu Val Asp Asp Leu Val Ser Tyr His Ala Val
145     150     155     160
Gly Ala Arg Ser Val Glu Asp Gln Glu His Arg Phe Val Ala Ser Gly
      165     170     175
Ile Asp Ala Pro Val Gly Met Lys Asn Pro Thr Ser Gly Asn Leu Gly
      180     185     190
Val Met Phe Asn Ala Ile Tyr Ala Ala Gln Asn Lys Gln Thr Ser Leu
      195     200     205
Ile Met Gly Arg Lys Leu Glu His Gln
210     215

```

(2) INFORMATION FOR SEQ ID NO:4868:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 292 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4868:

```
Glu Asn Lys Met Lys Ile Ile Val Pro Ala Thr Ser Ala Asn Ile Gly
1      5      10      15
Pro Gly Phe Asp Ser Val Gly Val Ala Val Thr Lys Tyr Leu Gln Ile
      20      25      30
Glu Val Cys Glu Glu Arg Asp Glu Trp Leu Ile Glu His Gln Ile Gly
      35      40      45
Lys Trp Ile Pro His Asp Glu Arg Asn Leu Leu Leu Lys Ile Ala Leu
      50      55      60
Gln Ile Val Pro Asp Leu Gln Pro Arg Arg Leu Lys Met Thr Ser Asp
      65      70      75      80
Val Pro Leu Ala Arg Gly Leu Gly Ser Ser Ser Ser Val Ile Val Ala
      85      90      95
Gly Ile Glu Leu Ala Asn Gln Leu Gly Gln Leu Asn Leu Ser Asp His
      100     105     110
Glu Lys Leu Gln Leu Ala Thr Lys Ile Glu Gly His Pro Asp Asn Val
      115     120     125
Ala Pro Ala Ile Tyr Gly Asn Leu Val Ile Ala Ser Ser Val Glu Gly
      130     135     140
Gln Val Ser Ala Ile Val Ala Asp Phe Pro Glu Cys Asp Phe Leu Ala
      145     150     155     160
Tyr Ile Pro Asn Tyr Glu Leu Arg Thr Arg Asp Ser Arg Ser Val Leu
      165     170     175
Pro Lys Lys Leu Ser Tyr Lys Glu Ala Val Ala Ala Ser Ser Ile Ala
      180     185     190
Asn Val Ala Val Ala Ala Leu Leu Ala Gly Asp Met Val Thr Ala Gly
      195     200     205
Gln Ala Ile Glu Gly Asp Leu Phe His Glu Arg Tyr Arg Gln Asp Leu
      210     215     220
Val Arg Glu Phe Ala Met Ile Lys Gln Val Thr Lys Glu Asn Gly Ala

225      230      235      240
Tyr Ala Thr Tyr Leu Ser Gly Ala Gly Pro Thr Val Met Val Leu Ala
      245     250     255
Ser His Asp Lys Met Pro Thr Ile Lys Ala Glu Leu Glu Lys Gln Pro
      260     265     270
Phe Lys Gly Lys Leu His Asp Leu Arg Val Asp Thr Gln Gly Val Arg
      275     280     285
Val Glu Ala Lys
      290
```

(2) INFORMATION FOR SEQ ID NO:4869:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 411 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...411

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4869:

Lys	Ser	Lys	Ile	Gly	Ala	Phe	Met	Gln	Tyr	Ser	Glu	Ile	Met	Ile	Arg	1	5	10	15
Tyr	Gly	Glu	Leu	Ser	Thr	Lys	Gly	Lys	Asn	Arg	Met	Arg	Phe	Ile	Asn	20	25	30	
Lys	Leu	Arg	Asn	Asn	Ile	Ser	Asp	Val	Leu	Ser	Ile	Tyr	Pro	Gln	Val	35	40	45	
Lys	Val	Thr	Ala	Asp	Arg	Asp	Arg	Ala	His	Ala	Tyr	Leu	Asn	Gly	Ala	50	55	60	
Asp	Tyr	Thr	Ala	Val	Ala	Glu	Ser	Leu	Lys	Gln	Val	Phe	Gly	Ile	Gln	65	70	75	80
Asn	Phe	Ser	Pro	Val	Tyr	Lys	Val	Glu	Lys	Ser	Val	Glu	Val	Leu	Lys	85	90	95	
Ser	Ala	Val	Gln	Glu	Ile	Met	Gln	Asp	Ile	Tyr	Lys	Glu	Gly	Met	Thr	100	105	110	
Phe	Lys	Ile	Ser	Ser	Lys	Arg	Ser	Asp	His	Thr	Phe	Glu	Leu	Asp	Ser	115	120	125	
Arg	Glu	Leu	Asn	Gln	Thr	Leu	Gly	Arg	Ala	Val	Phe	Glu	Ala	Ile	Pro	130	135	140	
Asn	Val	Gln	Ala	Gln	Met	Lys	Ser	Pro	Asp	Ile	Asn	Leu	Gln	Val	Glu	145	150	155	160
Ile	Arg	Glu	Glu	Ala	Ala	Tyr	Leu	Ser	Tyr	Glu	Thr	Val	Arg	Gly	Ala	165	170	175	
Gly	Gly	Leu	Pro	Val	Gly	Thr	Ser	Gly	Lys	Gly	Met	Leu	Met	Leu	Ser	180	185	190	
Gly	Gly	Ile	Asp	Ser	Pro	Val	Ala	Gly	Tyr	Leu	Ala	Leu	Lys	Arg	Gly	195	200	205	
Val	Asp	Ile	Glu	Ala	Val	His	Phe	Ala	Ser	Pro	Pro	Tyr	Thr	Ser	Pro	210	215	220	
Gly	Ala	Leu	Lys	Lys	Ala	Gln	Asp	Leu	Thr	Arg	Lys	Leu	Thr	Lys	Phe	225	230	235	240
Gly	Gly	Asn	Ile	Gln	Phe	Ile	Glu	Val	Pro	Phe	Thr	Glu	Ile	Gln	Glu	245	250	255	
Glu	Ile	Lys	Ala	Lys	Ala	Pro	Glu	Ala	Tyr	Leu	Met	Thr	Leu	Thr	Arg	260	265	270	
Arg	Phe	Met	Met	Arg	Ile	Thr	Asp	Arg	Ile	Arg	Glu	Val	Arg	Asn	Gly	275	280	285	
Leu	Val	Ile	Ile	Asn	Gly	Glu	Ser	Leu	Gly	Gln	Val	Ala	Ser	Gln	Thr	290	295	300	
Leu	Glu	Ser	Met	Lys	Ala	Ile	Asn	Ala	Val	Thr	Asn	Thr	Pro	Ile	Ile	305	310	315	320
Arg	Pro	Val	Val	Thr	Met	Asp	Lys	Leu	Glu	Ile	Ile	Asp	Ile	Ala	Gln	325	330	335	
Glu	Ile	Asp	Thr	Phe	Asp	Ile	Ser	Ile	Gln	Pro	Phe	Glu	Asp	Cys	Cys				

				340					345					350					
Thr	Ile	Phe	Ala	Pro	Asp	Arg	Pro	Lys	Thr	Asn	Pro	Lys	Ile	Lys	Asn				
		355						360				365							
Ala	Glu	Gln	Tyr	Glu	Ala	Arg	Met	Asp	Val	Glu	Gly	Leu	Val	Glu	Arg				
	370					375					380								
Ala	Val	Ala	Gly	Ile	Met	Ile	Thr	Glu	Ile	Thr	Pro	Gln	Ala	Glu	Lys				
385					390					395					400				
Asp	Glu	Val	Asp	Asp	Leu	Ile	Asp	Asn	Leu	Leu									
				405					410										

(2) INFORMATION FOR SEQ ID NO:4870:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 166 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...166

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4870:

Gly	Gly	Lys	Ile	Met	Lys	Tyr	Asp	Leu	Tyr	Asp	Asn	Cys	Ile	Glu	Leu				
1				5				10					15						
Leu	Lys	Glu	Arg	Glu	Val	Thr	Ile	Glu	Asp	Met	Ala	Ala	Leu	Val	Ile				
		20						25					30						
Phe	Ser	Gln	Gln	Lys	Tyr	Tyr	Pro	Glu	Leu	Thr	Leu	Asp	Asp	Ala	Ser				
		35				40					45								
Tyr	Ala	Ile	Gln	Arg	Val	Leu	Lys	Lys	Arg	Glu	Val	Gln	Asn	Val	Ile				
	50					55				60									
Met	Thr	Gly	Ile	Glu	Leu	Asp	Lys	Leu	Ala	Glu	Ala	Gln	Lys	Leu	Ser				
65				70				75					80						
Pro	Glu	Phe	Gln	Lys	Ile	Met	Glu	Lys	Asp	Asn	Pro	Leu	Tyr	Gly	Ile				
			85					90					95						
Asp	Glu	Val	Ile	Val	Leu	Ser	Ile	Leu	Asn	Leu	Tyr	Gly	Ser	Ile	Ala				
		100						105				110							
Phe	Thr	Asn	Tyr	Gly	Tyr	Leu	Asp	Lys	Leu	Lys	Pro	Leu	Ile	Leu	Glu				
		115				120					125								
Arg	Leu	Asn	Glu	Asn	His	Glu	Gly	Val	Cys	Asn	Val	Phe	Leu	Asp	Asp				
	130					135					140								
Ile	Val	Gly	Ala	Ile	Ala	Ala	Ala	Ala	Cys	Ser	Lys	Ile	Ala	His	Asn				
145				150				155							160				
His	Ala	Ser	Asp	Glu	Ile														
				165															

(2) INFORMATION FOR SEQ ID NO:4871:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...73

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4871:

Arg	Leu	Lys	Met	Ser	Lys	Gln	Lys	Lys	Phe	Glu	Glu	Asn	Leu	Ala	Glu
1				5					10					15	
Leu	Glu	Thr	Ile	Val	Gln	Ser	Leu	Glu	Asn	Gly	Glu	Ile	Ala	Leu	Glu
			20					25					30		
Asp	Ala	Ile	Thr	Ala	Phe	Gln	Lys	Gly	Met	Val	Leu	Ser	Lys	Glu	Leu
		35					40					45			
Gln	Ala	Thr	Leu	Asp	Lys	Ala	Glu	Lys	Thr	Leu	Val	Lys	Val	Met	Gln
	50					55					60				
Glu	Asp	Gly	Thr	Glu	Ser	Asp	Phe	Glu							
65					70										

(2) INFORMATION FOR SEQ ID NO:4872:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 596 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...596

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4872:

Cys	Gln	Lys	Ile	Gln	Gly	Ile	Arg	Ala	Cys	Lys	Arg	Cys	Leu	Thr	Leu
1				5				10					15		
Arg	Met	Asn	Gly	Gly	Phe	Gln	Met	Lys	Glu	Phe	Tyr	Lys	Lys	Arg	Phe
			20					25					30		
Ala	Leu	Thr	Asp	Gly	Gly	Ala	Arg	Asn	Leu	Ser	Lys	Ala	Thr	Leu	Ala
		35					40					45			
Ser	Phe	Phe	Val	Tyr	Cys	Ile	Asn	Met	Leu	Pro	Ala	Ile	Leu	Leu	Met
	50					55					60				
Ile	Phe	Ala	Gln	Glu	Val	Leu	Glu	Asn	Met	Gly	Lys	Ser	Asn	Gly	Phe
65					70					75					80

Tyr	Ile	Val	Phe	Ser	Val	Leu	Ile	Leu	Ile	Ala	Met	Tyr	Ile	Leu	Leu
				85					90					95	
Ser	Ile	Glu	Tyr	Asp	Lys	Leu	Tyr	Asn	Thr	Thr	Tyr	Gln	Glu	Ser	Ala
			100					105					110		
Asp	Leu	Arg	Ile	Arg	Thr	Ala	Glu	Asn	Leu	Ser	Lys	Leu	Pro	Leu	Ser
		115					120					125			
Tyr	Phe	Ser	Lys	His	Asp	Ile	Ser	Asp	Ile	Ser	Gln	Thr	Ile	Met	Ala
	130					135					140				
Asp	Ile	Glu	Gly	Ile	Glu	His	Ala	Met	Ser	His	Ser	Ile	Pro	Lys	Val
145					150					155					160
Gly	Gly	Met	Val	Leu	Phe	Phe	Pro	Leu	Ile	Ser	Val	Met	Met	Leu	Ala
				165					170					175	
Gly	Asn	Val	Lys	Met	Gly	Leu	Ala	Val	Ile	Ile	Pro	Ser	Ile	Leu	Ser
			180					185					190		
Phe	Ile	Phe	Ile	Pro	Leu	Ser	Lys	Lys	Tyr	Gln	Val	Asn	Gly	Gln	Asn
		195					200					205			
Arg	Tyr	Tyr	Asp	Val	Leu	Arg	Lys	Asn	Ser	Glu	Ser	Phe	Gln	Glu	Asn
	210					215					220				
Ile	Glu	Met	Gln	Met	Glu	Ile	Lys	Ala	Tyr	Asn	Leu	Ser	Lys	Asp	Ile
225					230					235					240
Lys	Asp	Asp	Leu	Tyr	Lys	Lys	Met	Glu	Asp	Ser	Glu	Lys	Val	His	Leu
			245						250					255	
Lys	Ala	Glu	Val	Thr	Thr	Ile	Leu	Thr	Leu	Ser	Ile	Ser	Ser	Ile	Phe
			260					265					270		
Ser	Phe	Ile	Ser	Leu	Ala	Val	Val	Ile	Phe	Val	Gly	Val	Asn	Leu	Ile
		275					280					285			
Ile	Asn	Lys	Glu	Ile	Asn	Ser	Leu	Tyr	Leu	Ile	Gly	Tyr	Leu	Leu	Ala
	290					295					300				
Ala	Met	Lys	Ile	Lys	Asp	Ser	Leu	Asp	Ala	Ser	Lys	Glu	Gly	Leu	Met
305					310					315					320
Glu	Ile	Phe	Tyr	Leu	Ser	Pro	Lys	Ile	Glu	Arg	Leu	Lys	Glu	Ile	Gln
			325						330					335	
Asn	Gln	Asp	Leu	Gln	Glu	Gly	Asp	Asp	Tyr	Ser	Leu	Lys	Lys	Phe	Asp
			340					345					350		
Ile	Asp	Leu	Lys	Asp	Val	Glu	Phe	Ala	Tyr	Asn	Lys	Asp	Glu	Lys	Val
	355					360						365			
Leu	Asn	Gly	Val	Ser	Phe	Lys	Ala	Lys	Gln	Gly	Glu	Val	Thr	Ala	Leu
	370					375					380				
Val	Gly	Ala	Ser	Gly	Cys	Gly	Lys	Thr	Thr	Ile	Leu	Lys	Leu	Ile	Ser
385					390					395					400
Arg	Leu	Tyr	Asp	Tyr	Asp	Lys	Gly	Gln	Ile	Leu	Ile	Asp	Gly	Lys	Asp
			405						410					415	
Ile	Lys	Glu	Ile	Ser	Thr	Glu	Ser	Leu	Phe	Asp	Lys	Val	Ser	Ile	Val
			420					425					430		
Phe	Gln	Asp	Val	Val	Leu	Phe	Asn	Gln	Ser	Val	Met	Glu	Asn	Ile	Arg
		435					440					445			
Ile	Gly	Lys	Gln	Asp	Ala	Ser	Asp	Glu	Glu	Val	Lys	Arg	Ala	Ala	Lys
	450					455					460				
Leu	Ala	Asn	Cys	Thr	Asp	Phe	Ile	Glu	Lys	Met	Asp	Lys	Gly	Phe	Asp
465					470					475					480
Thr	Val	Ile	Gly	Glu	Asn	Gly	Ala	Glu	Leu	Ser	Gly	Gly	Glu	Arg	Gln
			485					490						495	
Arg	Leu	Ser	Ile	Ala	Arg	Ala	Phe	Leu	Lys	Asp	Ala	Pro	Ile	Leu	Ile
			500					505					510		
Leu	Asp	Glu	Ile	Thr	Ala	Ser	Leu	Asp	Val	Asn	Asn	Glu	Lys	Lys	Ile
	515						520					525			
Gln	Glu	Ser	Leu	Asn	Asn	Leu	Val	Lys	Asp	Lys	Thr	Val	Val	Ile	Ile

530		535		540											
Ser	His	Arg	Met	Lys	Ser	Ile	Glu	Asn	Ala	Asp	Lys	Ile	Val	Val	Leu
545					550					555					560
Gln	Asn	Gly	Arg	Val	Glu	Ser	Glu	Gly	Lys	His	Glu	Glu	Leu	Leu	Gln
				565						570					575
Lys	Ser	Lys	Ile	Tyr	Lys	Asn	Leu	Ile	Glu	Lys	Thr	Lys	Met	Ala	Glu
				580					585					590	
Glu	Phe	Ile	Tyr												
				595											

(2) INFORMATION FOR SEQ ID NO:4873:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 86 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...86
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4873:

Val	Lys	Lys	Met	Phe	Lys	Asp	Phe	Ile	Gln	Ser	Ile	Tyr	Glu	Lys	Val
1			5						10					15	
Tyr	Ile	Ile	Asn	Phe	Glu	Lys	Cys	Ser	Gln	Ile	Pro	Cys	Leu	Thr	Ser
			20					25					30		
Glu	Glu	Leu	Lys	Ser	Leu	Gly	Lys	Trp	Tyr	Val	Ser	Thr	Gly	Lys	Glu
			35				40					45			
Trp	Ile	Cys	His	Ser	Asp	Ala	Asp	Leu	Glu	Glu	Phe	Lys	Asn	Leu	Phe
			50			55					60				
Leu	Asn	Phe	Ile	Asn	Pro	Glu	Glu	Trp	Asp	Thr	Ile	Ser	Phe	Asp	Ser
65					70				75						80
Asp	Phe	Met	Pro	Phe	Gln										
					85										

(2) INFORMATION FOR SEQ ID NO:4874:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 294 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4874:

Glu	Lys	Lys	Met	Arg	Asn	Val	Arg	Val	Ala	Thr	Ile	Gln	Met	Gln	Cys
1			5					10					15		
Ala	Lys	Asp	Val	Ala	Thr	Asn	Ile	Gln	Thr	Ala	Glu	Arg	Leu	Val	Arg
		20					25					30			
Gln	Ala	Ala	Glu	Gln	Gly	Ala	Gln	Ile	Ile	Leu	Leu	Pro	Glu	Leu	Phe
		35				40						45			
Glu	His	Pro	Tyr	Phe	Cys	Gln	Glu	Arg	Gln	Tyr	Asp	Tyr	Tyr	Gln	Tyr
	50				55					60					
Ala	Gln	Ser	Val	Ala	Glu	Asn	Thr	Ala	Ile	Gln	His	Phe	Lys	Val	Ile
65					70					75					80
Ala	Lys	Glu	Leu	Gln	Val	Val	Leu	Pro	Ile	Ser	Phe	Tyr	Glu	Lys	Asp
			85					90						95	
Gly	Asn	Val	Leu	Tyr	Asn	Ser	Ile	Ala	Val	Ile	Asp	Ala	Asp	Gly	Glu
		100						105					110		
Val	Leu	Gly	Val	Tyr	Arg	Lys	Thr	His	Ile	Pro	Asp	Asp	His	Tyr	Tyr
	115					120						125			
Gln	Glu	Lys	Phe	Tyr	Phe	Thr	Pro	Gly	Asn	Thr	Gly	Phe	Lys	Val	Trp
	130					135					140				
Asn	Thr	Arg	Tyr	Ala	Lys	Ile	Gly	Ile	Gly	Ile	Cys	Trp	Asp	Gln	Trp
145					150					155					160
Phe	Pro	Glu	Thr	Ala	Arg	Cys	Leu	Ala	Leu	Asn	Gly	Ala	Glu	Leu	Leu
			165					170						175	
Phe	Tyr	Pro	Thr	Ala	Ile	Gly	Ser	Glu	Pro	Ile	Leu	Asp	Thr	Asp	Ser
		180						185					190		
Cys	Gly	His	Trp	Gln	Arg	Thr	Met	Gln	Gly	His	Ala	Ala	Ala	Asn	Ile
	195						200					205			
Val	Pro	Val	Ile	Ala	Ala	Asn	Arg	Tyr	Gly	Leu	Glu	Glu	Val	Thr	Pro
	210					215					220				
Ser	Glu	Glu	Asn	Gly	Gly	Gln	Ser	Ser	Ser	Leu	Asp	Phe	Tyr	Gly	Ser
225				230						235					240
Ser	Phe	Met	Thr	Asp	Glu	Thr	Gly	Ala	Ile	Leu	Glu	Arg	Ala	Glu	Arg
			245					250						255	
Gln	Glu	Glu	Ala	Val	Leu	Leu	Ala	Thr	Tyr	Asp	Leu	Asp	Lys	Gly	Ala
		260					265						270		
Ser	Glu	Arg	Leu	Asn	Trp	Gly	Leu	Phe	Arg	Asp	Arg	Arg	Pro	Glu	Met
	275						280					285			
Tyr	Arg	Gln	Ile	Thr	Asp										
290															

(2) INFORMATION FOR SEQ ID NO:4875:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 255 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4875:

```
Asn Arg Lys Ile Asp Thr Met Thr Lys Ile Lys Ile Val Thr Asp Ser
1          5          10          15
Ser Val Thr Ile Glu Pro Glu Leu Val Lys Gln Leu Asp Ile Thr Ile
          20          25          30
Val Pro Leu Ser Val Met Ile Asp Asn Val Val Tyr Ser Asp Ala Asp
          35          40          45
Leu Lys Glu Glu Gly Lys Phe Leu Gln Leu Met Gln Glu Ser Lys Asn
          50          55          60
Leu Pro Lys Thr Ser Gln Pro Pro Val Gly Val Phe Ala Glu Ile Phe
65          70          75          80
Glu Asp Leu Cys Lys Asp Gly Gly Gln Ile Leu Ala Ile His Met Ser
          85          90          95
His Ala Leu Ser Gly Thr Val Glu Ala Ala Arg Gln Gly Ala Ser Leu
          100         105         110
Ser Thr Ala Asp Val Thr Val Val Asp Ser Ser Phe Thr Asp Gln Ala
          115         120         125
Leu Lys Phe Gln Val Val Glu Ala Ala Lys Leu Ala Gln Glu Gly Lys
          130         135         140
Asp Met Glu Ala Ile Leu Ser His Val Glu Glu Val Lys Asn His Thr
145         150         155         160
Glu Leu Tyr Ile Gly Val Ser Thr Leu Glu Asn Leu Val Lys Gly Gly
          165         170         175
Arg Ile Ser Arg Val Thr Gly Leu Leu Ser Ser Leu Leu Asn Ile Arg
          180         185         190
Val Val Met Gln Met Lys Asp His Glu Leu Gln Pro Met Val Lys Gly
          195         200         205
Arg Gly Thr Lys Thr Phe Lys Lys Trp Leu Asp Glu Leu Ile Thr Ser
          210         215         220
Leu Ser Glu Arg Ala Val Ala Glu Ile Gly Ile Ser Tyr Ser Gly Ser
225         230         235         240
Asp Arg Leu Gly Lys Arg Asp Glu Arg Lys Leu Thr Ser Leu Cys
          245         250         255
```

(2) INFORMATION FOR SEQ ID NO:4876:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 192 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...192

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4876:

Arg	Gly	Lys	Met	Ser	Thr	Leu	Ala	Lys	Ile	Glu	Ala	Leu	Leu	Phe	Val
1			5					10						15	
Ala	Gly	Glu	Asp	Gly	Ile	Arg	Val	Arg	Gln	Leu	Ala	Glu	Leu	Leu	Ser
		20						25					30		
Leu	Pro	Pro	Thr	Gly	Ile	Gln	Gln	Ser	Leu	Gly	Lys	Leu	Ala	Gln	Lys
		35				40						45			
Tyr	Glu	Lys	Asp	Pro	Asp	Ser	Ser	Leu	Ala	Leu	Ile	Glu	Thr	Ser	Gly
	50					55					60				
Ala	Tyr	Arg	Leu	Val	Thr	Lys	Pro	Gln	Phe	Ala	Glu	Ile	Leu	Lys	Glu
65					70				75						80
Tyr	Ser	Lys	Ala	Pro	Ile	Asn	Gln	Ser	Leu	Ser	Arg	Ala	Ala	Leu	Glu
			85					90						95	
Thr	Leu	Ser	Ile	Ile	Ala	Tyr	Lys	Gln	Pro	Ile	Thr	Arg	Ile	Glu	Ile
			100					105					110		
Asp	Ala	Ile	Arg	Gly	Val	Asn	Ser	Ser	Gly	Ala	Leu	Ala	Lys	Leu	Gln
	115						120					125			
Ala	Phe	Asp	Leu	Ile	Lys	Glu	Asp	Gly	Lys	Lys	Glu	Val	Leu	Gly	Arg
	130					135					140				
Pro	Asn	Leu	Tyr	Val	Thr	Asp	Tyr	Phe	Leu	Asp	Tyr	Met	Gly	Ile	
145					150				155					160	
Asn	His	Leu	Glu	Glu	Leu	Pro	Val	Ile	Asp	Glu	Leu	Glu	Ile	Gln	Ala
			165					170					175		
Gln	Glu	Ser	Gln	Leu	Phe	Gly	Glu	Arg	Ile	Glu	Glu	Asp	Glu	Asn	Gln
			180					185					190		

(2) INFORMATION FOR SEQ ID NO:4877:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 264 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...264

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4877:

Phe	Met	Lys	Ile	Pro	Leu	Leu	Thr	Phe	Ala	Arg	His	Lys	Phe	Val	Tyr
1				5				10						15	
Val	Leu	Leu	Thr	Leu	Leu	Phe	Leu	Ala	Leu	Val	Tyr	Arg	Asp	Val	Leu
			20					25					30		
Met	Thr	Tyr	Phe	Phe	Phe	Asp	Ile	His	Ala	Pro	Asp	Leu	Ala	Lys	Phe
		35				40						45			
Asp	Gly	Gln	Ala	Ile	Lys	Asn	Asp	Leu	Leu	Lys	Ser	Ala	Leu	Asp	Phe

50		55		60											
Arg	Ile	Leu	Gln	Phe	Asn	Leu	Gly	Phe	Tyr	Gln	Ser	Phe	Ile	Ile	Pro
65					70					75					80
Ile	Ile	Ile	Val	Leu	Leu	Gly	Phe	Gln	Tyr	Ile	Glu	Leu	Lys	Asn	Lys
				85					90					95	
Val	Leu	Arg	Leu	Ser	Ile	Gly	Arg	Glu	Val	Ser	Tyr	Gln	Gly	Leu	Lys
			100					105					110		
Arg	Lys	Leu	Thr	Leu	Gln	Val	Ala	Ser	Ile	Pro	Cys	Leu	Ile	Tyr	Leu
		115					120					125			
Val	Thr	Val	Leu	Ile	Ile	Ala	Ile	Ile	Thr	Tyr	Phe	Leu	Gly	Thr	Phe
	130					135					140				
Ser	Pro	Leu	Gly	Trp	Asn	Ser	Leu	Phe	Ser	Asp	Gly	Ser	Gly	Leu	Gln
145					150					155					160
Arg	Leu	Leu	Asp	Gly	Glu	Ile	Lys	Ser	Tyr	Leu	Phe	Phe	Thr	Cys	Val
			165						170					175	
Leu	Leu	Ile	Gly	Ile	Phe	Ile	Asn	Ala	Ile	Tyr	Phe	Leu	Gln	Ile	Val
		180					185						190		
Asp	Tyr	Val	Gly	Asn	Val	Thr	Arg	Ser	Ala	Ile	Thr	Tyr	Leu	Met	Phe
	195						200					205			
Leu	Trp	Leu	Gly	Ser	Met	Leu	Leu	Tyr	Ser	Ala	Leu	Pro	Tyr	Tyr	Met
	210					215					220				
Val	Pro	Met	Thr	Ser	Leu	Met	Gln	Ala	Ser	Tyr	Gly	Asp	Val	Ser	Leu
225					230					235					240
Met	Lys	Leu	Phe	Thr	Pro	Tyr	Ile	Leu	Tyr	Ile	Val	Pro	Tyr	Met	Val
				245					250					255	
Leu	Glu	Lys	Tyr	Glu	Asp	Asn	Val								
		260													

(2) INFORMATION FOR SEQ ID NO:4878:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 240 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...240

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4878:

Thr	Met	Lys	Ile	Asp	Ile	Leu	Thr	Leu	Phe	Pro	Glu	Met	Phe	Ser	Pro
1				5					10					15	
Leu	Glu	His	Ser	Ile	Val	Gly	Lys	Ala	Arg	Glu	Lys	Gly	Leu	Leu	Asp
			20					25					30		
Ile	Gln	Tyr	His	Asn	Phe	Arg	Glu	Asn	Ala	Glu	Lys	Ala	Arg	His	Val
	35					40					45				
Asp	Asp	Glu	Pro	Tyr	Gly	Gly	Gly	Gln	Gly	Met	Leu	Leu	Arg	Ala	Gln
50					55					60					
Pro	Ile	Phe	Asp	Ser	Phe	Asp	Ala	Ile	Glu	Lys	Lys	Asn	Pro	Arg	Val

65		70		75		80
Ile	Leu	Leu	Asp	Pro	Ala	Glu
		85		90		95
Asp	Leu	Ala	Gln	Glu	Glu	Leu
		100		105		110
Gly	Tyr	Asp	Glu	Arg	Ile	Lys
		115		120		125
Gly	Asp	Tyr	Val	Leu	Thr	Gly
		130		135		140
Asp	Ala	Thr	Val	Arg	Leu	Ile
		145		150		155
His	Gln	Asp	Asp	Ser	Phe	Ser
		165		170		175
Thr	Arg	Pro	Tyr	Asp	Tyr	Arg
		180		185		190
Ser	Gly	His	His	Glu	Lys	Ile
		195		200		205
Lys	Lys	Thr	Tyr	Glu	Arg	Arg
		210		215		220
Thr	Val	Glu	Glu	Glu	Lys	Met
		225		230		235
						240

(2) INFORMATION FOR SEQ ID NO:4879:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...74

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4879:

Lys	Met	Lys	Ile	Met	Leu	Leu	Asn	Ile	His	Glu	Arg	Ser	Thr	Ile	Ile
1				5					10					15	
Leu	Ser	Arg	Gly	Lys	Lys	Phe	Ile	Arg	Phe	Leu	Thr	Cys	Phe	Lys	Gly
			20					25					30		
Asp	Lys	Met	Glu	Asn	Leu	Leu	Asp	Val	Ile	Glu	Gln	Phe	Leu	Ser	Leu
		35					40					45			
Ser	Asp	Glu	Lys	Leu	Glu	Glu	Leu	Ala	Asp	Lys	Asn	Gln	Leu	Leu	Arg
	50					55					60				
Leu	Gln	Glu	Glu	Lys	Glu	Arg	Lys	Asn	Ala						
65					70										

(2) INFORMATION FOR SEQ ID NO:4880:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 266 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...266

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4880:

Glu	Met	Lys	Ile	Gly	Phe	Ile	Gly	Leu	Gly	Asn	Met	Gly	Ala	Ser	Leu	1	5	10	15
Ala	Lys	Ser	Val	Leu	Gln	Thr	Arg	Thr	Ser	Asp	Glu	Ile	Leu	Leu	Ala	20	25	30	
Asn	Arg	Ser	Gln	Ala	Lys	Val	Asp	Ala	Phe	Ile	Ala	Asp	Phe	Gly	Gly	35	40	45	
Gln	Ala	Ser	Ser	Asn	Glu	Lys	Met	Phe	Ala	Glu	Ala	Asp	Val	Ile	Phe	50	55	60	
Leu	Gly	Val	Lys	Pro	Ala	Gln	Phe	Ser	Glu	Leu	Leu	Ser	Gln	Tyr	Gln	65	70	75	80
Thr	Ile	Leu	Glu	Lys	Arg	Glu	Ser	Leu	Leu	Leu	Ile	Ser	Met	Ala	Ala	85	90	95	
Gly	Leu	Thr	Leu	Glu	Lys	Leu	Ala	Ser	Leu	Ile	Pro	Ser	Gln	His	Arg	100	105	110	
Ile	Ile	Arg	Met	Met	Pro	Asn	Thr	Pro	Ala	Ser	Ile	Gly	Gln	Gly	Val	115	120	125	
Ile	Ser	Tyr	Ala	Leu	Ser	Pro	Asn	Cys	Arg	Ala	Glu	Asp	Ser	Glu	Ile	130	135	140	
Phe	Cys	Gln	Leu	Leu	Ala	Lys	Ala	Gly	Leu	Leu	Val	Glu	Leu	Gly	Glu	145	150	155	160
Ser	Leu	Ile	Asn	Ala	Ala	Thr	Gly	Leu	Ala	Gly	Cys	Gly	Pro	Ala	Phe	165	170	175	
Val	Tyr	Leu	Phe	Ile	Glu	Ala	Leu	Ala	Asp	Ala	Gly	Val	Gln	Thr	Gly	180	185	190	
Leu	Pro	Arg	Glu	Thr	Ala	Leu	Lys	Met	Ala	Ala	Gln	Thr	Val	Val	Gly	195	200	205	
Ala	Gly	Gln	Leu	Val	Leu	Glu	Ser	Gln	Gln	His	Pro	Gly	Val	Leu	Lys	210	215	220	
Asp	Gln	Val	Cys	Ser	Pro	Gly	Gly	Ser	Thr	Ile	Ala	Gly	Val	Ala	Ser	225	230	235	240
Leu	Glu	Ala	His	Ala	Phe	Arg	Gly	Thr	Val	Met	Glu	Ala	Val	His	Gln	245	250	255	
Ala	Tyr	Lys	Arg	Thr	Gln	Glu	Leu	Gly	Lys							260	265		

(2) INFORMATION FOR SEQ ID NO:4881:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 65 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4881:

Leu	Asp	Glu	Ile	Gly	Phe	Gln	Gly	Ala	Ser	Ala	Pro	Ser	Arg	Lys	Val
1				5				10						15	
Leu	Leu	Ala	Ser	Gly	Thr	Thr	Lys	Ser	Val	Ser	Thr	Ser	Ser	Leu	Met
			20					25					30		
Pro	Lys	Pro	Ser	His	Ser	Leu	Gln	Glu	Pro	Lys	Gly	Ala	Leu	Lys	Glu
			35				40					45			
Lys	Arg	Arg	Gly	Ser	Asn	Ser	Gly	Thr	Val	Lys	Pro	Gln	Thr	Gly	Gln
	50					55					60				
Ala															
65															

(2) INFORMATION FOR SEQ ID NO:4882:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 179 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...179

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4882:

Lys	Val	Glu	Ile	Met	Ser	Tyr	Phe	Lys	Lys	Tyr	Lys	Phe	Asp	Lys	Ser
1				5				10						15	
Gln	Phe	Lys	Leu	Gly	Met	Arg	Thr	Phe	Lys	Thr	Gly	Ile	Ala	Val	Phe
			20					25					30		
Leu	Val	Leu	Leu	Ile	Phe	Gly	Phe	Phe	Gly	Trp	Lys	Gly	Leu	Gln	Ile
			35				40					45			
Gly	Ala	Leu	Thr	Ala	Val	Phe	Ser	Leu	Arg	Glu	Ser	Phe	Asp	Glu	Ser
			50				55				60				
Val	His	Phe	Gly	Thr	Ser	Arg	Ile	Leu	Gly	Asn	Ser	Ile	Gly	Gly	Leu
65					70				75					80	
Tyr	Ala	Leu	Val	Phe	Phe	Leu	Leu	Asn	Thr	Phe	Phe	His	Glu	Ala	Phe

				85					90				95			
Trp	Val	Thr	Leu	Val	Val	Val	Pro	Ile	Cys	Thr	Met	Leu	Thr	Ile	Met	
			100					105					110			
Thr	Asn	Val	Ala	Met	Asn	Asn	Lys	Ala	Gly	Val	Ile	Gly	Gly	Val	Ala	
		115					120					125				
Ala	Met	Leu	Ile	Ile	Thr	Leu	Ser	Ile	Pro	Ser	Gly	Glu	Thr	Ile	Leu	
	130					135					140					
Tyr	Val	Phe	Val	Arg	Val	Leu	Glu	Thr	Phe	Met	Gly	Val	Phe	Val	Ala	
145				150						155					160	
Ile	Ile	Val	Asn	Tyr	Asp	Ile	Asp	Arg	Ile	Arg	Leu	Phe	Leu	Glu	Lys	
			165					170						175		
Lys	Glu	Lys														

(2) INFORMATION FOR SEQ ID NO:4883:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1967 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...1967

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4883:

Ile	Lys	Glu	Ile	Lys	Val	Phe	Lys	Lys	Asp	Arg	Phe	Ser	Ile	Arg	Lys	
1				5					10					15		
Ile	Lys	Gly	Val	Val	Gly	Ser	Val	Phe	Leu	Gly	Ser	Leu	Leu	Met	Ala	
		20						25				30				
Pro	Ser	Val	Val	Asp	Ala	Ala	Thr	Tyr	His	Tyr	Val	Asn	Lys	Glu	Ile	
		35				40					45					
Ile	Ser	Gln	Glu	Ala	Lys	Asp	Leu	Ile	Gln	Thr	Gly	Lys	Pro	Asp	Arg	
	50				55						60					
Asn	Glu	Val	Val	Tyr	Gly	Leu	Val	Tyr	Gln	Lys	Asp	Gln	Leu	Pro	Gln	
65				70					75					80		
Thr	Gly	Thr	Glu	Ala	Ser	Val	Leu	Thr	Ala	Phe	Gly	Leu	Leu	Thr	Val	
			85					90						95		
Gly	Ser	Leu	Leu	Leu	Ile	Tyr	Lys	Arg	Lys	Lys	Ile	Ala	Ser	Val	Phe	
		100					105					110				
Leu	Val	Gly	Ala	Met	Gly	Leu	Val	Val	Leu	Pro	Ser	Ala	Gly	Ala	Val	
		115				120					125					
Asp	Pro	Val	Ala	Thr	Leu	Ala	Leu	Ala	Ser	Arg	Glu	Gly	Val	Val	Glu	
	130				135					140						
Met	Glu	Gly	Tyr	Arg	Tyr	Val	Gly	Tyr	Leu	Ser	Gly	Asp	Ile	Leu	Lys	
145				150				155						160		
Thr	Leu	Gly	Leu	Asp	Thr	Val	Leu	Glu	Lys	Thr	Ser	Ala	Lys	Pro	Gly	
			165					170						175		
Glu	Val	Thr	Val	Val	Glu	Val	Glu	Thr	Pro	Gln	Ser	Thr	Thr	Asn	Gln	

			180					185				190				
Glu	Gln	Ala	Arg	Thr	Glu	Asn	Gln	Val	Val	Glu	Thr	Glu	Glu	Ala	Pro	
		195					200					205				
Lys	Thr	Glu	Glu	Ser	Pro	Lys	Glu	Glu	Pro	Lys	Ser	Glu	Ile	Lys	Pro	
	210					215					220					
Thr	Asp	Asp	Thr	Leu	Pro	Lys	Val	Glu	Lys	Gly	Lys	Lys	Ile	Xaa	Xaa	
225					230					235					240	
Thr	Ala	Pro	Val	Glu	Glu	Val	Gly	Gly	Glu	Val	Glu	Ser	Lys	Pro	Glu	
			245						250					255		
Glu	Lys	Val	Ala	Val	Lys	Pro	Glu	Ser	Gln	Pro	Ser	Asp	Lys	Pro	Ala	
		260						265					270			
Glu	Glu	Ser	Lys	Val	Glu	Pro	Pro	Val	Glu	Gln	Ala	Lys	Gly	Pro	Glu	
	275						280					285				
Gln	Pro	Val	Gln	Pro	Thr	Gln	Ala	Glu	Gln	Pro	Arg	Ile	Pro	Lys	Asp	
	290					295					300					
Ser	Ser	Gln	Pro	Glu	Asp	Pro	Lys	Glu	Asp	Arg	Gly	Ala	Glu	Asp	Thr	
305					310					315					320	
Pro	Lys	Gln	Glu	Asp	Thr	Gln	Pro	Glu	Val	Val	Glu	Thr	Lys	Asp	Glu	
			325						330					335		
Ala	Ala	Asn	Gln	Pro	Val	Glu	Glu	Pro	Lys	Val	Glu	Thr	Pro	Ala	Val	
		340						345					350			
Glu	Lys	Gln	Thr	Glu	Pro	Lys	Val	Glu	Gln	Val	Gly	Glu	Pro	Val	Glu	
	355						360				365					
Pro	Ser	Glu	Asp	Glu	Lys	Ala	Pro	Val	Ser	Pro	Glu	Lys	Gln	Pro	Glu	
	370					375					380					
Ala	Pro	Glu	Glu	Lys	Ala	Val	Glu	Glu	Thr	Pro	Lys	Pro	Glu	Asp	Lys	
385					390					395					400	
Ile	Lys	Gly	Ile	Gly	Thr	Lys	Glu	Pro	Val	Asp	Lys	Ser	Glu	Leu	Asn	
			405					410						415		
Asn	Gln	Ile	Asp	Lys	Ala	Ser	Ser	Val	Ser	Pro	Thr	Asp	Tyr	Ser	Thr	
		420						425					430			
Ala	Ser	Tyr	Asn	Ala	Leu	Gly	Pro	Val	Leu	Glu	Thr	Ala	Lys	Gly	Val	
	435						440					445				
Tyr	Ala	Ser	Glu	Pro	Val	Lys	Gln	Pro	Glu	Val	Asn	Ser	Glu	Thr	Asn	
	450					455					460					
Lys	Leu	Lys	Thr	Ala	Ile	Asp	Ala	Leu	Asn	Val	Asp	Lys	Ser	Glu	Leu	
465					470					475					480	
Gln	Glu	Gln	Leu	Arg	Val	Ala	Glu	Gln	Lys	Gln	Gln	Ala	Asp	Tyr	Ser	
			485						490					495		
Ala	Lys	Thr	Trp	Arg	Glu	Phe	Lys	Ile	Ala	Glu	Leu	Gln	Ala	Lys	Glu	
		500						505					510			
Ile	Asn	Asn	Gln	Thr	Thr	Pro	Leu	Pro	Lys	Gln	Ser	Glu	Ile	Asp	Ala	
		515					520					525				
Ala	Thr	Lys	Ala	Leu	Gln	Asp	Ala	Leu	Gln	Ala	Leu	Ala	Val	Asp	Lys	
	530					535						540				
Thr	Val	Leu	Gln	Asn	Ala	Ile	Asn	Thr	Ala	Asn	Ser	Lys	Arg	Glu	Glu	
545					550					555					560	
Glu	Tyr	Thr	Ala	Gln	Thr	Trp	Lys	Ala	Leu	Glu	Asp	Ala	Leu	Thr	Ala	
			565					570						575		
Val	Asn	Pro	Val	Asn	Glu	Asp	Glu	Thr	Ala	Thr	Gln	Ser	Lys	Val	Asp	
		580						585					590			
Glu	Ala	Thr	Arg	Asn	Leu	Glu	Glu	Ala	Ile	Asn	Asn	Leu	Val	Leu	Leu	
	595					600						605				
Thr	Glu	Lys	Pro	Val	Leu	Thr	Phe	Ile	Glu	Thr	Asp	Lys	Lys	Ala	Leu	
	610					615					620					
Glu	Arg	Glu	Val	Val	Ala	Lys	Tyr	Ser	Leu	Glu	Asn	Gln	Asn	Lys	Thr	
625					630					635					640	

Lys	Ile	Lys	Ser	Ile	Thr	Ala	Thr	Leu	Lys	Lys	Gly	Glu	Thr	Val	Val
				645					650					655	
Ser	Thr	Val	Glu	Leu	Ile	Gly	Asp	Asp	Val	Thr	Asn	Glu	Thr	Ile	Thr
			660					665						670	
Ser	Ala	Phe	Lys	Asn	Leu	Glu	Tyr	Tyr	Lys	Glu	Tyr	Thr	Leu	Ser	Thr
		675						680						685	
Thr	Met	Val	Tyr	Asp	Arg	Gly	Asp	Gly	Asp	Val	Thr	Glu	Ile	Leu	Asp
	690					695					700				
Asn	Gln	Pro	Ile	Gln	Leu	Asp	Leu	Lys	Lys	Val	Glu	Leu	Lys	Asn	Ile
705					710					715					720
Lys	Arg	Thr	Asp	Leu	Ile	Lys	Tyr	Glu	Asn	Gly	Lys	Glu	Thr	Asn	Glu
				725					730						735
Ser	Leu	Ile	Thr	Thr	Val	Pro	Asp	Asp	Lys	Arg	Asn	Tyr	Tyr	Leu	Lys
			740					745						750	
Ile	Thr	Ser	Lys	Asn	Gln	Lys	Thr	Thr	Leu	Leu	Ala	Val	Lys	Asn	Ile
		755						760					765		
Glu	Glu	Thr	Thr	Val	Asn	Gly	Thr	Pro	Val	Tyr	Lys	Val	Thr	Ala	Ile
	770					775					780				
Ala	Asp	Asn	Leu	Val	Ser	Arg	Thr	Ala	Asp	Asn	Lys	Phe	Glu	Glu	Glu
785					790					795					800
Tyr	Val	His	Tyr	Ile	Glu	Lys	Pro	Lys	Val	His	Glu	Asp	Asn	Val	Tyr
			805						810					815	
Tyr	Asn	Phe	Lys	Glu	Leu	Val	Glu	Ala	Ile	Gln	Asn	Asp	Pro	Ser	Lys
		820						825					830		
Glu	Tyr	Arg	Leu	Gly	Gln	Ser	Met	Ser	Ala	Arg	Asn	Val	Val	Pro	Asn
		835					840					845			
Gly	Lys	Ser	Tyr	Ile	Thr	Lys	Glu	Phe	Thr	Gly	Lys	Leu	Leu	Ser	Ser
	850					855					860				
Glu	Gly	Lys	Gln	Phe	Ala	Ile	Thr	Glu	Leu	Glu	His	Pro	Leu	Phe	Asn
865					870					875					880
Val	Ile	Thr	Asn	Ala	Thr	Ile	Asn	Asn	Val	Asn	Phe	Glu	Asn	Val	Glu
			885						890					895	
Ile	Glu	Arg	Ser	Gly	Gln	Asp	Asn	Ile	Ala	Ser	Leu	Ala	Asn	Thr	Met
			900					905						910	
Lys	Gly	Ser	Ser	Val	Ile	Thr	Asn	Val	Lys	Ile	Thr	Gly	Thr	Leu	Ser
		915					920						925		
Gly	Arg	Asn	Asn	Val	Ala	Gly	Phe	Val	Asn	Asn	Met	Asn	Asp	Gly	Thr
	930					935					940				
Arg	Ile	Glu	Asn	Val	Ala	Phe	Phe	Gly	Lys	Leu	His	Ser	Thr	Ser	Gly
945					950					955					960
Asn	Gly	Ser	His	Thr	Gly	Gly	Ile	Ala	Gly	Thr	Asn	Tyr	Arg	Gly	Ile
			965						970					975	
Val	Arg	Lys	Ala	Tyr	Val	Asp	Ala	Thr	Ile	Thr	Gly	Asn	Lys	Thr	Arg
		980						985					990		
Ala	Ser	Leu	Leu	Val	Pro	Lys	Val	Asp	Tyr	Gly	Leu	Thr	Leu	Asp	His
		995					1000						1005		
Leu	Ile	Gly	Thr	Lys	Ala	Leu	Leu	Thr	Glu	Ser	Val	Val	Lys	Gly	Lys
	1010					1015					1020				
Ile	Asp	Val	Ser	Asn	Pro	Val	Glu	Val	Gly	Ala	Ile	Ala	Ser	Lys	Thr
1025					1030					1035					1040
Trp	Pro	Val	Gly	Thr	Val	Ser	Asn	Ser	Val	Ser	Tyr	Ala	Lys	Ile	Ile
			1045						1050					1055	
Arg	Gly	Glu	Glu	Leu	Phe	Gly	Ser	Asn	Asp	Val	Asp	Asp	Ser	Asp	Tyr
			1060					1065					1070		
Ala	Ser	Ala	His	Ile	Lys	Asp	Leu	Tyr	Ala	Val	Glu	Gly	Tyr	Ser	Ser
		1075					1080					1085			
Gly	Asn	Arg	Ser	Phe	Arg	Lys	Ser	Lys	Thr	Phe	Thr	Lys	Leu	Thr	Lys

1090	1095	1100
Glu Gln Ala Asp Ala Lys Val Thr Thr Phe Asn Ile Thr Ala Asp Lys		
1105	1110	1115
Leu Glu Ser Asp Leu Ser Pro Leu Ala Lys Leu Asn Glu Glu Lys Ala		1120
	1125	1130
Tyr Ser Ser Ile Gln Asp Tyr Asn Ala Glu Tyr Asn Gln Ala Tyr Lys		1135
	1140	1145
Asn Leu Glu Lys Leu Ile Pro Phe Tyr Asn Lys Asp Tyr Ile Val Tyr		1150
	1155	1160
Gln Gly Asn Lys Leu Asn Lys Glu His His Leu Asn Thr Lys Glu Val		1165
	1170	1175
Leu Ser Val Thr Ala Met Asn Asn Asn Glu Phe Ile Thr Asn Leu Asp		1180
1185	1190	1195
Glu Ala Asn Lys Ile Ile Val His Tyr Ala Asp Gly Thr Lys Asp Tyr		1200
	1205	1210
Phe Asn Leu Ser Ser Ser Ser Glu Gly Leu Ser Asn Val Lys Glu Tyr		1215
	1220	1225
Thr Ile Thr Asp Leu Gly Ile Lys Tyr Thr Pro Asn Ile Val Gln Lys		1230
	1235	1240
Asp Asn Thr Thr Leu Val Asn Asp Ile Lys Ser Ile Leu Glu Ser Val		1245
	1250	1255
Glu Leu Gln Ser Gln Thr Met Tyr Gln His Leu Asn Arg Leu Gly Asp		1260
1265	1270	1275
Tyr Arg Val Asn Ala Ile Lys Asp Leu Tyr Leu Glu Glu Ser Phe Thr		1280
	1285	1290
Asp Val Lys Glu Asn Leu Thr Asn Leu Ile Thr Lys Leu Val Gln Asn		1295
	1300	1305
Glu Glu His Gln Leu Asn Asp Ser Pro Ala Ala Arg Gln Met Ile Arg		1310
	1315	1320
Asp Lys Val Glu Lys Asn Lys Ala Ala Leu Leu Leu Gly Leu Thr Tyr		1325
	1330	1335
Leu Asn Arg Tyr Tyr Gly Val Lys Phe Gly Asp Val Asn Ile Lys Glu		1340
1345	1350	1355
Leu Met Leu Phe Lys Pro Asp Phe Tyr Gly Glu Lys Val Ser Val Leu		1360
	1365	1370
Asp Arg Leu Ile Glu Ile Gly Ser Lys Glu Asn Asn Ile Lys Gly Ser		1375
	1380	1385
Arg Thr Phe Asp Ala Phe Gly Gln Val Leu Ala Lys Tyr Thr Lys Ser		1390
	1395	1400
Gly Asn Leu Asp Ala Phe Leu Asn Tyr Asn Arg Gln Leu Phe Thr Asn		1405
	1410	1415
Ile Asp Asn Met Asn Asp Trp Phe Ile Asp Ala Thr Glu Asp His Val		1420
1425	1430	1435
Tyr Ile Ala Glu Arg Ala Ser Glu Val Glu Glu Ile Lys Asn Ser Lys		1440
	1445	1450
His Arg Ala Phe Asp Asn Leu Lys Arg Ser His Leu Arg Asn Thr Ile		1455
	1460	1465
Leu Pro Leu Leu Asn Ile Asp Lys Ala His Leu Tyr Leu Ile Ser Asn		1470
	1475	1480
Tyr Asn Ala Ile Ala Phe Gly Ser Ala Glu Arg Leu Gly Lys Lys Ser		1485
	1490	1495
Leu Glu Asp Ile Lys Asp Ile Val Asn Lys Ala Ala Asp Gly Tyr Arg		1500
1505	1510	1515
Asn Tyr Tyr Asp Phe Trp Tyr Arg Leu Ala Ser Asp Asn Val Lys Gln		1520
	1525	1530
Arg Leu Leu Arg Asp Ala Val Ile Pro Ile Trp Glu Gly Tyr Asn Ala		1535
	1540	1545
		1550

Pro	Gly	Gly	Trp	Val	Glu	Lys	Tyr	Gly	Arg	Tyr	Asn	Thr	Asp	Lys	Val	1555	1560	1565
Tyr	Thr	Pro	Leu	Arg	Glu	Phe	Phe	Gly	Pro	Met	Asp	Lys	Tyr	Tyr	Asn	1570	1575	1580
Tyr	Asn	Gly	Thr	Gly	Ala	Tyr	Ala	Ala	Ile	Tyr	Pro	Asn	Ser	Asp	Asp	1585	1590	1595
Ile	Arg	Thr	Asp	Val	Lys	Tyr	Val	His	Leu	Glu	Met	Val	Gly	Glu	Tyr	1605	1610	1615
Gly	Ile	Ser	Val	Tyr	Thr	His	Glu	Thr	Thr	His	Val	Asn	Asp	Arg	Ala	1620	1625	1630
Ile	Tyr	Leu	Gly	Gly	Phe	Gly	His	Arg	Glu	Gly	Thr	Asp	Ala	Glu	Ala	1635	1640	1645
Tyr	Ala	Gln	Gly	Met	Leu	Gln	Thr	Pro	Val	Thr	Gly	Ser	Gly	Phe	Asp	1650	1655	1660
Glu	Phe	Gly	Ser	Leu	Gly	Ile	Asn	Met	Val	Phe	Lys	Arg	Lys	Asn	Asp	1665	1670	1675
Gly	Asn	Gln	Trp	Tyr	Ile	Thr	Asp	Pro	Lys	Thr	Leu	Lys	Thr	Arg	Glu	1685	1690	1695
Asp	Ile	Asn	Arg	Tyr	Met	Lys	Gly	Tyr	Asn	Asp	Thr	Leu	Thr	Leu	Leu	1700	1705	1710
Asp	Glu	Ile	Glu	Ala	Glu	Ser	Val	Ile	Ser	Gln	Gln	Asn	Lys	Asp	Leu	1715	1720	1725
Asn	Ser	Ala	Trp	Phe	Lys	Lys	Ile	Asp	Arg	Glu	Tyr	Arg	Asp	Asn	Asn	1730	1735	1740
Lys	Leu	Asn	Gln	Trp	Asp	Lys	Ile	Arg	Asn	Leu	Ser	Gln	Glu	Glu	Lys	1745	1750	1755
Asn	Glu	Leu	Asn	Ile	Gln	Ser	Val	Asn	Asp	Leu	Val	Asp	Gln	Gln	Leu	1765	1770	1775
Met	Thr	Asn	Arg	Asn	Pro	Gly	Asn	Gly	Ile	Tyr	Lys	Pro	Glu	Ala	Ile	1780	1785	1790
Ser	Tyr	Asn	Asp	Gln	Ser	Pro	Tyr	Val	Gly	Val	Arg	Met	Met	Thr	Gly	1795	1800	1805
Ile	Tyr	Gly	Gly	Asn	Thr	Ser	Lys	Gly	Ala	Pro	Gly	Ala	Val	Ser	Phe	1810	1815	1820
Lys	His	Asn	Ala	Phe	Arg	Leu	Trp	Gly	Tyr	Tyr	Gly	Tyr	Glu	Asn	Gly	1825	1830	1835
Phe	Leu	Gly	Tyr	Ala	Ser	Asn	Lys	Tyr	Lys	Gln	Gln	Ser	Lys	Thr	Asp	1845	1850	1855
Gly	Glu	Ser	Val	Leu	Ser	Asp	Glu	Tyr	Ile	Ile	Lys	Lys	Ile	Ser	Asn	1860	1865	1870
Asn	Thr	Phe	Asn	Thr	Ile	Glu	Glu	Phe	Lys	Lys	Ala	Tyr	Phe	Lys	Glu	1875	1880	1885
Val	Lys	Asp	Lys	Ala	Thr	Lys	Gly	Leu	Thr	Thr	Phe	Glu	Val	Asn	Gly	1890	1895	1900
Ser	Ser	Val	Ser	Ser	Tyr	Asp	Asp	Leu	Leu	Thr	Leu	Phe	Lys	Glu	Ala	1905	1910	1915
Val	Lys	Lys	Asp	Ala	Glu	Thr	Leu	Lys	Gln	Glu	Ala	Asn	Gly	Asn	Lys	1925	1930	1935
Thr	Val	Ser	Met	Asn	Asn	Thr	Val	Lys	Leu	Lys	Glu	Ala	Val	Tyr	Lys	1940	1945	1950
Lys	Leu	Leu	Gln	Gln	Thr	Asp	Ser	Phe	Lys	Thr	Ser	Ile	Phe	Lys		1955	1960	1965

(2) INFORMATION FOR SEQ ID NO:4884:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 471 amino acids

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(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
      (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
      (A) NAME/KEY: misc_feature
      (B) LOCATION 1...471
```

Glu 1	Lys	Glu	Met	Ser 5	Ser	Gly	Lys	Ile	Ala 10	Gln	Val	Ile	Gly	Pro 15	Val
Val	Asp	Val	Leu 20	Phe	Ala	Ala	Gly	Glu 25	Lys	Leu	Pro	Glu	Ile 30	Asn	Asn
Ala	Leu	Val	Val 35	Tyr	Lys	Asn	Asp 40	Glu	Arg	Lys	Thr	Lys 45	Ile	Val	Leu
Glu	Val	Ala	Leu 50	Glu	Leu	Gly	Asp 55	Gly	Met	Val	Arg	Thr 60	Ile	Ala	Met
Glu 65	Ser	Thr	Asp	Gly	Leu	Thr	Arg	Gly	Met	Glu	Val	Leu	Asp	Thr	Gly
Arg	Pro	Ile	Ser 85	Val	Pro	Val	Gly	Lys	Glu 90	Thr	Leu	Gly	Arg	Val	Phe
Asn	Val	Leu	Gly 100	Asp	Thr	Ile	Asp	Leu	Glu	Ala	Pro	Phe	Thr	Glu	Asp
Ala	Glu	Arg	Gln 115	Pro	Ile	His	Lys	Lys	Ala	Pro	Thr	Phe	Asp	Glu	Leu
Ser	Thr	Ser	Ser 130	Glu	Ile	Leu	Glu	Thr	Gly	Ile	Lys	Val	Ile	Asp	Leu
Leu 145	Ala	Pro	Tyr	Leu	Lys	Gly	Gly	Lys	Val	Gly	Leu	Phe	Gly	Gly	Ala
Gly	Val	Gly	Lys 165	Thr	Val	Leu	Ile	Gln	Glu	Leu	Ile	His	Asn	Ile	Ala
Gln	Glu	His	Gly 180	Gly	Ile	Ser	Val	Phe	Ala	Gly	Val	Gly	Glu	Arg	Thr
Arg	Glu	Gly	Asn 195	Asp	Leu	Tyr	Trp	Glu	Met	Lys	Glu	Ser	Gly	Val	Ile
Glu	Lys	Thr	Ala 210	Met	Val	Phe	Gly	Gln	Met	Asn	Glu	Pro	Pro	Gly	Ala
Arg 225	Met	Arg	Val	Ala	Leu	Thr	Gly	Leu	Thr	Ile	Ala	Glu	Tyr	Phe	Arg
Asp	Val	Glu	Gly 245	Gln	Asp	Val	Leu	Leu	Phe	Ile	Asp	Asn	Ile	Phe	Arg
Phe	Thr	Gln	Ala 260	Gly	Ser	Glu	Val	Ser	Ala	Leu	Leu	Gly	Arg	Met	Pro
Ser	Ala	Val	Gly 275	Tyr	Gln	Pro	Thr	Leu	Ala	Thr	Glu	Met	Gly	Gln	Leu
Gln	Glu	Arg	Ile 290	Thr	Ser	Thr	Lys	Lys	Gly	Ser	Val	Thr	Ser	Ile	Gln
Ala 305	Ile	Tyr	Val	Pro	Ala	Asp	Asp	Tyr	Thr	Asp	Pro	Ala	Pro	Ala	Thr
Ala	Phe	Ala	His 310	Leu	Asp	Ser	Thr	Thr	Asn	Leu	Glu	Arg	Lys	Leu	Val

				325					330					335			
Gln	Leu	Gly	Ile	Tyr	Pro	Ala	Val	Asp	Pro	Leu	Ala	Ser	Ser	Ser	Arg		
				340					345					350			
Ala	Leu	Ala	Pro	Glu	Ile	Val	Gly	Glu	Glu	His	Tyr	Ala	Val	Ala	Ala		
				355					360					365			
Glu	Val	Lys	Arg	Val	Leu	Gln	Arg	Tyr	His	Glu	Leu	Gln	Asp	Ile	Ile		
				370					375					380			
Ala	Ile	Leu	Gly	Met	Asp	Glu	Leu	Ser	Asp	Glu	Glu	Lys	Thr	Leu	Val		
					390									395			400
Ala	Arg	Ala	Arg	Arg	Ile	Gln	Phe	Phe	Leu	Ser	Gln	Asn	Phe	Asn	Val		
					405					410				415			
Ala	Glu	Gln	Phe	Thr	Gly	Gln	Pro	Gly	Ser	Tyr	Val	Pro	Val	Ala	Glu		
				420					425					430			
Thr	Val	Arg	Gly	Phe	Lys	Glu	Ile	Leu	Asp	Gly	Lys	Tyr	Asp	His	Leu		
				435					440					445			
Pro	Glu	Asp	Ala	Phe	Arg	Gly	Val	Gly	Ser	Ile	Glu	Asp	Val	Ile	Ala		
				450										460			
Lys	Ala	Glu	Lys	Met	Gly	Phe											
				465													470

(2) INFORMATION FOR SEQ ID NO:4885:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4885:

Asn	Glu	Glu	Met	Asp	Met	Thr	Lys	Ile	Ala	Leu	Leu	Ser	Asp	Ile	His
1			5						10					15	
Gly	Asn	Thr	Thr	Ala	Leu	Glu	Ala	Val	Leu	Ala	Asp	Ala	Gln	Gln	Leu
			20					25					30		
Gly	Val	Asp	Glu	Tyr	Trp	Leu	Leu	Gly	Asp	Ile	Leu	Met	Pro	Gly	Thr
		35				40						45			
Gly	Arg	Arg	Arg	Ile	Leu	Asp	Leu	Leu	Asp	Gln	Leu	Pro	Ile	Thr	Ala
	50				55					60					
Arg	Val	Leu	Gly	Asn	Trp	Glu	Asp	Ser	Leu	Trp	His	Gly	Val	Arg	Lys
65				70				75						80	
Glu	Leu	Asp	Ser	Thr	Arg	Pro	Ser	Gln	Arg	Tyr	Leu	Leu	Arg	Gln	Cys
			85					90						95	
Gln	Tyr	Val	Leu	Glu	Glu	Ile	Ser	Leu	Glu	Glu	Ile	Glu	Val	Leu	His
			100					105					110		
Asn	Gln	Pro	Leu	Gln	Ile	His	Arg	Gln	Phe	Gly	Asp	Leu	Thr	Val	Gly
		115				120						125			
Ile	Ser	His	His	Leu	Pro	Asp	Lys	Asn	Trp	Gly	Arg	Glu	Leu	Ile	His

130		135		140											
Thr	Gly	Lys	Gln	Glu	Glu	Phe	Asp	Arg	Leu	Val	Thr	His	Pro	Pro	Cys
145		150								155					160
Asp	Ile	Ala	Val	Tyr	Gly	His	Ile	His	Gln	Gln	Leu	Leu	Arg	Tyr	Gly
		165							170						175
Thr	Gly	Gly	Gln	Leu	Ile	Val	Asn	Pro	Gly	Ser	Ile	Gly	Gln	Pro	Phe
		180						185						190	
Phe	Leu	Asp	Ala	Gln	Leu	Arg	Lys	Asp	Leu	Arg	Ala	Gln	Tyr	Met	Ile
		195					200					205			
Leu	Glu	Phe	Asp	Asp	Lys	Gly	Leu	Val	Asp	Met	Asp	Phe	Arg	Arg	Val
	210					215					220				
Asp	Tyr	Asp	Val	Ala	Ala	Glu	Leu	Gln	Leu	Ala	Lys	Asp	Leu	Arg	Leu
225					230					235					240
Pro	Tyr	Phe	Glu	Val	Tyr	Tyr	Glu	Ser	Leu	Val	Asn	Gly	Ile	His	His
		245							250					255	
Thr	His	His	Gln	Glu	Phe	Leu	Arg	Glu	Leu	Ala	Gln	Lys	Glu	Gly	Cys
		260					265						270		
Asp	Arg	Glu	Leu	Asp	Asp	Trp	Leu	Lys	Ser	Gly	Asn	Asp			
	275					280					285				

(2) INFORMATION FOR SEQ ID NO:4886:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 153 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...153

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4886:

Lys	Gly	Glu	Ile	Met	Gly	Lys	Pro	Met	Leu	Val	Phe	Lys	Arg	Phe	Gly
1			5						10					15	
His	Gln	Ile	His	Leu	Met	Val	Gln	Lys	Glu	Ala	Lys	Arg	Cys	Gly	Ile
		20					25						30		
Glu	Phe	Met	Gly	Gly	Pro	Gln	Gly	Gln	Val	Val	His	Phe	Leu	Asp	Asn
	35					40					45				
Arg	Glu	Lys	Asn	Gln	Asp	Leu	Val	Leu	Ile	Lys	Asp	Ile	Asp	Gln	Glu
	50				55				60						
Leu	Asn	Ile	Thr	Lys	Ser	Val	Ala	Ser	Asn	Leu	Val	Lys	Arg	Ile	Val
65			70					75						80	
Gln	Asn	Cys	Leu	Val	Glu	Leu	Glu	Ala	Ser	Pro	Val	Asp	Lys	Arg	Ala
		85					90						95		
Lys	Phe	Val	Arg	Leu	Thr	Asp	Lys	Ala	Arg	Ser	Gln	Met	Gln	Gln	Val
		100					105					110			
Lys	Ala	Phe	Phe	Glu	Arg	Ile	Asp	Lys	Gln	Leu	Met	Glu	Asp	Ile	Asp
	115					120					125				
Glu	Asp	Glu	Leu	Leu	Ile	Phe	Glu	Lys	Val	Leu	Gly	Gln	Leu	Gln	Ala

130		135	140
Lys Tyr Gln Gly Asn Arg	Arg Arg Glu		
145	150		

(2) INFORMATION FOR SEQ ID NO:4887:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 326 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...326

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4887:

Asp	Leu	Trp	Ile	Ile	Leu	Asn	Ser	Glu	Glu	Thr	Cys	His	Tyr	Trp	Lys
1			5					10						15	
Arg	Pro	Arg	Gln	Thr	Gly	Gly	Arg	Gly	Val	Val	Ser	Thr	Cys	Ser	Tyr
			20					25					30		
Glu	Ala	Arg	Ala	Phe	Gly	Val	His	Ser	Ala	Met	Ser	Ser	Lys	Glu	Ala
			35				40					45			
Tyr	Glu	Arg	Cys	Pro	Gln	Ala	Val	Phe	Ile	Ser	Gly	Asn	Tyr	Glu	Lys
			50			55				60					
Tyr	Lys	Ser	Val	Gly	Leu	Arg	Ile	Arg	Ala	Ile	Phe	Lys	Arg	Tyr	Thr
65					70				75					80	
Asp	Leu	Ile	Glu	Pro	Met	Ser	Ile	Asp	Glu	Ala	Tyr	Leu	Asp	Val	Thr
			85					90					95		
Glu	Asn	Lys	Leu	Gly	Ile	Lys	Ser	Ala	Val	Lys	Ile	Ala	Arg	Leu	Ile
			100				105						110		
Gln	Lys	Asp	Ile	Trp	Lys	Glu	Leu	His	Leu	Thr	Ala	Ser	Ala	Gly	Val
		115				120						125			
Ser	Tyr	Asn	Lys	Phe	Leu	Ala	Lys	Met	Ala	Ser	Asp	Tyr	Gln	Lys	Pro
		130				135					140				
His	Gly	Leu	Thr	Val	Ile	Leu	Pro	Glu	Gln	Ala	Glu	Asp	Phe	Leu	Lys
145					150				155					160	
Gln	Met	Asp	Ile	Ser	Lys	Phe	His	Gly	Val	Gly	Lys	Lys	Thr	Val	Glu
			165					170						175	
Arg	Leu	His	Gln	Met	Gly	Val	Phe	Thr	Gly	Ala	Asp	Leu	Leu	Glu	Val
			180					185					190		
Pro	Glu	Val	Thr	Leu	Ile	Asp	Arg	Phe	Gly	Arg	Leu	Gly	Tyr	Asp	Leu
		195				200						205			
Tyr	Arg	Lys	Ala	Arg	Gly	Ile	His	Asn	Ser	Pro	Val	Lys	Ser	Asn	Arg
		210				215					220				
Ile	Arg	Lys	Ser	Ile	Gly	Lys	Glu	Lys	Thr	Tyr	Gly	Lys	Ile	Leu	Arg
225					230				235					240	
Ala	Glu	Glu	Asp	Ile	Lys	Lys	Glu	Leu	Thr	Leu	Leu	Ser	Glu	Lys	Val
			245					250					255		
Ala	Leu	Asn	Leu	His	Gln	Gln	Glu	Lys	Ala	Gly	Lys	Ile	Val	Ile	Leu

	260		265		270										
Lys	Ile	Arg	Tyr	Glu	Asp	Phe	Ser	Thr	Leu	Thr	Lys	Arg	Lys	Ser	Leu
	275		280		285										
Ala	Gln	Lys	Thr	Gln	Asp	Ala	Ser	Gln	Ile	Ser	Gln	Ile	Ala	Leu	Gln
	290		295		300										
Leu	Tyr	Glu	Glu	Leu	Ser	Glu	Lys	Glu	Arg	Gly	Val	Arg	Leu	Leu	Gly
305				310					315						320
Ile	Thr	Leu	Thr	Gly	Phe										
				325											

(2) INFORMATION FOR SEQ ID NO:4888:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 73 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...73
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4888:

Arg	Lys	Trp	Ile	Trp	Pro	Pro	Gln	Ala	Gly	Gln	Val	Tyr	Ala	Cys	Phe
1			5				10							15	
Ser	Ser	Leu	Ser	Ser	Asn	Thr	Phe	Thr	Asn	Ser	Pro	Leu	Val	Ser	Leu
		20					25						30		
Ala	Thr	Asn	Met	Asn	Ser	Leu	Leu	Phe	Tyr	Ile	Ile	Arg	Lys	Lys	Glu
		35				40						45			
Lys	Arg	Ser	Gly	Lys	Phe	Leu	Ile	Phe	Met	Cys	Val	Tyr	Leu	Ile	Phe
50						55					60				
Leu	Ala	Ser	Lys	Val	Ala	Lys	Arg	Ser							
65					70										

(2) INFORMATION FOR SEQ ID NO:4889:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 118 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4889:

```

Thr Pro Trp Ile Arg Leu Arg Ser Cys Arg Pro Thr Pro Leu Pro Pro
1          5          10          15
Phe Arg Arg Cys Ala Arg Ser Arg Ser Pro Ser Asn Arg Pro Cys Pro
          20          25          30
Arg Thr Asp Arg Arg Arg Pro Gly His Arg Ser Thr Arg Ala Thr Lys
          35          40          45
Arg Gln Arg Pro Lys Ser Pro Pro Arg Thr Ala Thr Arg Arg Pro Arg
          50          55          60
Arg Leu Ser Pro Thr Ser Pro Arg Arg Leu Pro Pro Thr Gly Arg Arg
65          70          75          80
Pro Ile Gly Lys Pro Pro Cys Gln Leu Pro Arg Lys Gln Arg Gln Arg
          85          90          95
Gln Arg Gln Arg Gln Arg Gln Arg Gln Arg Gln Arg Gln Arg Gln Gln
          100          105          110
Cys Cys Arg Pro Asp Arg
          115

```

(2) INFORMATION FOR SEQ ID NO:4890:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 119 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...119

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4890:

```

Arg Thr Trp Ile Ser Thr Ala Gly Trp Leu Ser Ala Ala Val Glu Lys
1          5          10          15
Thr Cys Asp Leu Asp Val Gly Ile Val Val Leu Arg Ser Ile Ser Phe
          20          25          30
Val Asn Thr Pro Pro Ile Val Ser Ile Pro Ser Asp Asn Gly Val Thr
          35          40          45
Ser Arg Arg Thr Thr Ser Leu Thr Ser Pro Val Ile Thr Pro Pro Trp
          50          55          60
Ile Ala Ala Pro Ile Ala Thr Thr Ser Ser Gly Phe Thr Asp Leu Phe
65          70          75          80
Gly Ser Leu Pro Val Ser Ala Leu Thr Ala Ser Thr Thr Ala Gly Ile
          85          90          95
Arg Val Glu Pro Pro Thr Arg Ile Thr Ser Ser Ile Ser Asp Lys Leu
          100          105          110
Lys Pro Ala Ser Glu Arg Ala

```

(2) INFORMATION FOR SEQ ID NO:4891:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 93 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4891:

```

Leu Glu Trp Ile Ser Thr Ser Ala Leu Phe Thr Leu Ala Ser Lys Val
1          5          10          15
Thr Ile Pro Leu Pro Pro Glu Ile Ser Ser Cys Ser Lys Ala Phe
          20          25          30
Leu Val Pro Cys Ser Gln Thr Asn Lys Ser Ala Pro Trp Ser Leu Ser
          35          40          45
Ala Cys Phe Ser Lys Tyr Leu Ser Arg Ser Val Glu Ala Asp Ser Ser
          50          55          60
Ala Pro Ser Met Ile Lys Leu Ile Leu Thr Gly Lys Ser Ser Trp Cys
65          70          75          80
Cys Ile Tyr Phe Leu Lys Ala Leu Lys Arg Ala Val Ile
          85          90

```

(2) INFORMATION FOR SEQ ID NO:4892:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 292 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...292

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4892:

```

Arg Trp Trp Ile Arg Ile Leu Arg Ile Leu Ser Val Ala Ser Thr Glu
1          5          10          15

```

Arg	Ser	Ser	Arg	Met	Ile	Lys	Leu	Trp	Arg	Arg	Tyr	Lys	Pro	Phe	Ile
			20					25					30		
Asn	Ala	Gly	Val	Gln	Glu	Leu	Ile	Thr	Tyr	Arg	Val	Asn	Phe	Ile	Leu
	35						40					45			
Tyr	Arg	Ile	Gly	Asp	Val	Met	Gly	Ala	Phe	Val	Ala	Phe	Tyr	Leu	Trp
	50					55					60				
Lys	Ala	Val	Phe	Asp	Ser	Ser	Gln	Glu	Ser	Leu	Ile	Gln	Gly	Phe	Ser
65					70					75					80
Met	Ala	Asp	Ile	Thr	Leu	Tyr	Ile	Ile	Met	Ser	Phe	Val	Thr	Asn	Leu
			85						90					95	
Leu	Thr	Arg	Ser	Asp	Ser	Ser	Phe	Met	Ile	Gly	Glu	Glu	Val	Lys	Asp
			100					105					110		
Gly	Ser	Ile	Ile	Met	Arg	Leu	Leu	Arg	Pro	Val	His	Phe	Ala	Ala	Ser
	115						120					125			
Tyr	Leu	Phe	Thr	Glu	Leu	Gly	Ser	Lys	Trp	Leu	Ile	Phe	Ile	Ser	Val
	130					135					140				
Gly	Leu	Pro	Phe	Leu	Ser	Val	Ile	Val	Leu	Met	Lys	Ile	Ile	Ser	Gly
145					150					155					160
Gln	Gly	Ile	Val	Glu	Val	Leu	Gly	Leu	Thr	Val	Leu	Tyr	Leu	Phe	Ser
			165						170					175	
Leu	Thr	Leu	Ala	Tyr	Leu	Ile	Asn	Phe	Phe	Phe	Asn	Ile	Cys	Phe	Gly
		180						185					190		
Phe	Ser	Ala	Phe	Val	Phe	Lys	Asn	Leu	Trp	Gly	Ser	Asn	Leu	Leu	Lys
	195						200					205			
Thr	Ser	Ile	Val	Ala	Phe	Met	Ser	Gly	Ser	Leu	Ile	Pro	Leu	Ala	Phe
	210					215					220				
Phe	Pro	Lys	Val	Val	Ser	Asp	Ile	Leu	Ser	Phe	Leu	Pro	Phe	Ser	Ser
225					230					235					240
Leu	Ile	Tyr	Thr	Pro	Val	Met	Ile	Ile	Val	Gly	Lys	Tyr	Asp	Ala	Ser
			245						250					255	
Gln	Ile	Leu	Gln	Ala	Leu	Leu	Leu	Gln	Phe	Phe	Trp	Leu	Leu	Val	Met
		260						265					270		
Val	Gly	Leu	Ser	Gln	Leu	Ile	Trp	Lys	Arg	Val	Gln	Ser	Phe	Ile	Thr
	275						280					285			
Ile	Gln	Gly	Gly												
	290														

(2) INFORMATION FOR SEQ ID NO:4893:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 67 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...67

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4893:

Ala	Cys	Arg	Ile	Ala	Gln	Leu	Arg	Ser	Thr	Asn	Ser	Cys	Asn	Ser	Ile
1				5					10					15	
Ile	Ser	Ile	Leu	Ile	Lys	Lys	Cys	Asp	Ile	Leu	Glu	Arg	Thr	Ser	Gln
			20					25					30		
Arg	Gly	Ser	Thr	Phe	Ile	Tyr	Val	Pro	Gln	Lys	Arg	Gly	Thr	Pro	Leu
		35					40					45			
Ile	Gly	Ser	Asn	Val	Ala	Thr	Val	Leu	Cys	Phe	His	Lys	Lys	Leu	Lys
	50					55					60				
Ser	Ser	Ile													
65															

(2) INFORMATION FOR SEQ ID NO:4894:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 70 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4894:

Lys	Thr	Arg	Ile	Leu	Tyr	Ser	Met	Lys	Ile	Lys	Glu	Gln	Thr	Arg	Lys
1				5					10					15	
Leu	Ala	Ala	Gly	Cys	Ser	Lys	His	Cys	Phe	Glu	Val	Val	Asp	Arg	Thr
			20					25					30		
Asp	Glu	Val	Ser	Ser	Lys	His	Gly	Phe	Glu	Val	Val	Asp	Glu	Thr	Asp
		35					40					45			
Glu	Val	Ser	Asn	His	Thr	Tyr	Gly	Lys	Val	Lys	Leu	Thr	Trp	Phe	Glu
	50					55					60				
Asp	Ile	Leu	Glu	Glu	Tyr										
65					70										

(2) INFORMATION FOR SEQ ID NO:4895:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 346 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...346

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4895:

Cys	Trp	Arg	Ile	Tyr	Lys	Met	Lys	Leu	Phe	Lys	Lys	Met	Met	Gln	Val
1			5					10						15	
Val	Leu	Ala	Thr	Phe	Phe	Phe	Gly	Leu	Leu	Gly	Thr	Ser	Thr	Val	Cys
		20					25					30			
Ala	Asp	Asp	Ser	Glu	Gly	Trp	Gln	Phe	Val	Gln	Lys	Asn	Gly	Arg	Thr
		35				40						45			
Tyr	Tyr	Lys	Lys	Gly	Asp	Leu	Lys	Glu	Thr	Tyr	Trp	Arg	Val	Ile	Asp
	50				55					60					
Gly	Lys	Tyr	Tyr	Tyr	Phe	Asp	Pro	Leu	Ser	Gly	Glu	Met	Val	Val	Gly
65				70					75					80	
Trp	Gln	Tyr	Ile	Pro	Ala	Pro	His	Lys	Gly	Val	Thr	Ile	Gly	Pro	Ser
			85				90						95		
Pro	Arg	Gln	Glu	Ile	Ala	Phe	Arg	Pro	Asp	Trp	Phe	Tyr	Phe	Gly	Gln
		100					105						110		
Asp	Gly	Val	Leu	Gln	Glu	Phe	Val	Gly	Lys	Gln	Val	Leu	Glu	Ala	Lys
	115						120				125				
Thr	Ala	Thr	Asn	Thr	Asn	Lys	His	His	Gly	Glu	Glu	Tyr	Asp	Ser	Pro
	130					135				140					
Ala	Glu	Lys	Arg	Val	Tyr	Tyr	Phe	Glu	Asp	Gln	Arg	Ser	Tyr	His	Thr
145				150					155					160	
Leu	Lys	Thr	Gly	Trp	Val	Tyr	Asp	Asp	Gly	Asp	Trp	Tyr	Tyr	Leu	Gln
			165					170						175	
Lys	Asp	Gly	Gly	Phe	Asp	Ser	Arg	Ile	Asn	Arg	Leu	Thr	Val	Gly	Glu
		180					185					190			
Leu	Ala	Arg	Gly	Trp	Val	Lys	Asp	Tyr	Pro	Leu	Thr	Tyr	Asp	Glu	Glu
	195					200					205				
Lys	Leu	Lys	Pro	Ala	Pro	Trp	Tyr	Tyr	Leu	Asp	Pro	Ala	Thr	Gly	Ile
	210				215					220					
Met	Gln	Thr	Gly	Trp	Gln	His	Leu	Gly	Asn	Lys	Trp	Tyr	Tyr	Leu	Arg
225					230				235					240	
Ser	Ser	Gly	Ala	Met	Ala	Thr	Gly	Trp	Tyr	Gln	Asp	Gly	Ser	Thr	Trp
			245					250					255		
Tyr	Tyr	Leu	Asp	Ala	Glu	Asn	Gly	Asp	Met	Lys	Thr	Gly	Trp	Gln	Asn
		260					265					270			
Leu	Gly	Asn	Lys	Trp	Tyr	Tyr	Leu	Arg	Ser	Ser	Gly	Ala	Met	Ala	Thr
	275					280					285				
Gly	Trp	Tyr	Gln	Glu	Gly	Ser	Thr	Trp	Tyr	Tyr	Leu	Asn	Ala	Ser	Asn
	290					295				300					
Gly	Asp	Met	Lys	Thr	Gly	Trp	Phe	Gln	Val	Asn	Gly	Asn	Trp	Tyr	Tyr
305					310				315					320	
Ala	Tyr	Asp	Ser	Gly	Ala	Leu	Ala	Val	Asn	Thr	Thr	Val	Gly	Gly	Tyr
			325					330					335		
Tyr	Leu	Asn	Tyr	Asn	Gly	Glu	Trp	Val	Lys						
		340					345								

(2) INFORMATION FOR SEQ ID NO:4896:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 218 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...218
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4896:

```

Lys Glu Gly Met Thr Ser Met Arg Lys Lys Thr Ile Gly Glu Val Leu
1      5      10      15
Arg Leu Asp Arg Ile Asn Gln Gly Leu Ser Leu Asp Glu Leu Gln Lys
20      25      30
Lys Thr Glu Ile Gln Leu Asp Met Leu Glu Ala Met Glu Ala Asp Asp
35      40      45
Phe Asp Gln Leu Pro Ser Pro Phe Tyr Thr Arg Ser Phe Leu Lys Lys
50      55      60
Tyr Ala Trp Ala Val Glu Leu Asp Asp Gln Ile Val Leu Asp Ala Tyr
65      70      75      80
Asp Ser Gly Ser Met Ile Thr Tyr Glu Glu Val Asp Val Asp Glu Asp
85      90      95
Glu Leu Thr Gly Arg Arg Arg Ser Asn Lys Lys Lys Lys Lys Lys Thr
100     105     110
Ser Phe Leu Pro Leu Phe Tyr Phe Ile Leu Phe Ala Leu Ser Ile Leu
115     120     125
Ile Phe Val Thr Tyr Tyr Val Trp Asn Tyr Ile Gln Thr Gln Pro Glu
130     135     140
Glu Pro Ser Leu Ser Asn Tyr Ser Val Val Gln Ser Thr Ser Ser Thr
145     150     155     160
Ser Ser Val Pro His Ser Ser Ser Ser Ser Ser Ser Ser Ile Glu Ser
165     170     175
Ala Ile Ser Val Ser Gly Glu Gly Asn His Val Glu Ile Ala Tyr Lys
180     185     190
Thr Ser Lys Glu Thr Val Lys Leu Gln Leu Ala Val Ser Asp Val Ser
195     200     205
Lys Leu Gly Gln Cys Phe Arg Lys Arg Thr
210     215

```

(2) INFORMATION FOR SEQ ID NO:4897:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 246 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4897:

Ser	Arg	Gly	Ile	Met	Glu	Leu	Phe	Lys	Thr	Trp	Lys	Lys	Asn	Met	Val
1				5					10					15	
Leu	Tyr	Gly	Leu	Lys	Ser	Gln	Ile	Gly	Thr	Val	Tyr	Arg	Asn	Asn	Asp
			20					25					30		
Arg	Thr	Thr	Ser	Phe	Tyr	Asp	Val	Gly	Asn	Phe	Leu	Tyr	Leu	Ala	Gly
		35					40					45			
Glu	Leu	Asp	Ser	Arg	Phe	Trp	Glu	Asp	Phe	Val	Arg	Lys	Tyr	Gly	Leu
	50					55				60					
Asp	Tyr	Lys	Ile	Ile	Ile	Ser	Glu	Asn	Thr	Asn	Trp	Gln	Asp	Phe	Leu
65					70					75					80
His	Arg	Lys	Val	Gly	Leu	Asn	Ser	Phe	Thr	Arg	Tyr	Ser	Phe	Lys	Asp
			85						90					95	
Lys	Ala	Asn	Phe	Gln	Val	Glu	Phe	Leu	Asn	Asn	Leu	Val	Thr	His	Leu
		100						105					110		
Glu	Glu	Gly	Tyr	Asn	Ile	Val	Pro	Ile	Asp	Asn	His	Ile	Tyr	Asn	Cys
	115					120						125			
Phe	Ser	Thr	Glu	Glu	Trp	Ser	Gln	Asp	Leu	Gln	Gly	Asp	Phe	Glu	Ser
	130					135					140				
Tyr	Gln	Asp	Phe	Val	Leu	Lys	Gly	Gly	Phe	Gly	Phe	Val	Ile	Leu	Lys
145					150					155					160
Asn	Asn	Glu	Leu	Ile	Ala	Gly	Ile	Ser	Ser	Gly	Leu	Val	Tyr	Arg	Lys
			165						170						175
Ala	Val	Glu	Val	Glu	Val	Ala	Thr	Arg	Pro	Asn	Glu	Gln	Gly	Asn	Gly
		180						185					190		
Phe	Ala	Lys	Lys	Leu	Gly	Ala	Ala	Met	Ile	Leu	Glu	Ser	Leu	Asn	Arg
	195						200					205			
Asp	Met	Phe	Pro	Leu	Trp	Asp	Ala	His	Asn	Glu	Ala	Ser	Lys	Lys	Val
	210					215					220				
Ala	Glu	Phe	Leu	Gly	Tyr	Glu	Leu	Ser	Glu	Pro	Tyr	Glu	Ala	Phe	Glu
225					230					235					240
Leu	Glu	Glu	Ile	Leu	Ile										
				245											

(2) INFORMATION FOR SEQ ID NO:4898:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 483 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...483

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4898:

Asn	Val	Gly	Ile	Ile	Ile	Lys	Leu	Ile	Lys	Asp	Glu	Glu	Arg	Arg	Lys
1			5					10					15		
Met	Glu	Ala	Val	Leu	Ala	Ile	Asp	Leu	Gly	Ala	Thr	Ser	Gly	Arg	Ala
		20					25						30		
Ile	Val	Gly	Tyr	Leu	Ser	Glu	Asn	Lys	Leu	Val	Met	Glu	Glu	Ile	Asn
		35					40					45			
Arg	Phe	Ser	Asn	Leu	Pro	Ile	Arg	Val	Lys	Gly	His	Leu	Ser	Trp	Asp
	50					55					60				
Ile	Asp	Phe	Leu	Leu	Ala	Lys	Ile	Leu	Glu	Ser	Ile	Arg	Leu	Ala	Asn
65					70				75						80
Thr	Ser	Tyr	Lys	Ile	Leu	Ser	Ile	Gly	Ile	Asp	Thr	Trp	Gly	Val	Asp
			85						90					95	
Phe	Gly	Leu	Ile	Asp	Asn	Glu	Gly	Lys	Leu	Leu	Leu	Gln	Pro	Val	His
		100						105					110		
Tyr	Arg	Asp	Glu	Arg	Thr	Lys	Gly	Val	Leu	Lys	Glu	Ile	Ser	Glu	Met
		115					120					125			
Thr	Glu	Leu	Glu	Lys	Leu	Tyr	Ser	Glu	Thr	Gly	Asn	Gln	Ile	Met	Glu
	130					135					140				
Ile	Asn	Thr	Leu	Phe	Gln	Leu	Phe	Lys	Ala	Arg	Gln	Glu	Ser	Pro	Asp
145					150					155					160
Ser	Phe	Tyr	Lys	Thr	Asn	Lys	Ile	Leu	Leu	Met	Pro	Asp	Leu	Phe	Asn
			165						170					175	
Tyr	Leu	Leu	Thr	Gly	Lys	Phe	Ala	Thr	Glu	Lys	Ser	Ile	Ala	Ser	Thr
		180						185					190		
Thr	Gln	Leu	Phe	Asp	Pro	Arg	Ser	Gln	Asn	Trp	Asn	Gln	Asn	Ile	Leu
	195						200					205			
Lys	Leu	Phe	Glu	Leu	Asp	Ser	Ser	Leu	Leu	Pro	Glu	Ile	Val	Ser	Glu
	210					215					220				
Gly	Asn	Val	Leu	Gly	Arg	Ile	Lys	Glu	Glu	Tyr	Gly	Leu	Gly	Asp	Ile
225					230					235					240
Pro	Val	Val	Asn	Val	Cys	Ser	His	Asp	Thr	Ala	Ser	Ala	Ile	Val	Ser
			245						250					255	
Val	Pro	Lys	Thr	Glu	Gly	Ser	Leu	Phe	Ile	Ser	Ser	Gly	Thr	Trp	Ser
		260						265					270		
Leu	Val	Gly	Val	Glu	Leu	Thr	Ser	Pro	Ile	Leu	Thr	Thr	Glu	Ser	Phe
		275					280					285			
Ser	Tyr	Gly	Phe	Thr	Asn	Glu	Val	Gly	Lys	Asp	Gly	Val	Ile	Thr	Phe
	290				295					300					
Leu	Lys	Asn	Cys	Thr	Gly	Leu	Trp	Ile	Ile	Glu	Glu	Leu	Arg	Arg	Ser
305					310					315					320
Phe	Glu	Arg	Arg	Gly	Lys	Ala	Tyr	Ser	Phe	Asp	Asp	Ile	Arg	Thr	Met
			325						330					335	
Val	Glu	Lys	Glu	Lys	Glu	Asn	Leu	Pro	Leu	Ile	Asp	Thr	Glu	Ser	Thr
		340					345						350		
Glu	Phe	Ala	Thr	Glu	Ser	Asp	Met	His	Lys	Thr	Leu	Thr	Glu	Tyr	Leu
	355						360					365			
Ala	Tyr	His	His	Glu	Thr	Arg	Glu	Trp	Thr	Asp	Gly	Gln	Leu	Phe	Lys
	370					375					380				
Ile	Val	Tyr	Glu	Ser	Leu	Ala	Glu	Thr	Tyr	Arg	Lys	Ala	Ile	Glu	Leu
385					390					395					400
Leu	Glu	Glu	Leu	Thr	His	Lys	Val	Tyr	Lys	Arg	Ile	Tyr	Val	Ile	Gly
			405						410					415	
Gly	Gly	Ala	Arg	Ala	Ser	Tyr	Phe	Asn	Gln	Met	Ile	Ala	Asp	Arg	Thr
		420						425				430			
Gly	Lys	Glu	Val	Leu	Thr	Gly	Ser	Thr	Glu	Gly	Thr	Ala	Val	Gly	Asn

	435		440		445										
Ile	Val	Val	Gln	Leu	Leu	Ser	Gln	Gly	Lys	Ile	Asn	Glu	Asp	Thr	Glu
	450					455					460				
Leu	Lys	Asp	Ile	Met	Thr	Asn	Ile	Ala	Asp	Thr	Gln	Tyr	Tyr	Tyr	Pro
465					470					475					480
Gln	Leu	Ser													

(2) INFORMATION FOR SEQ ID NO:4899:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 65 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...65
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4899:

Glu	Lys	Gly	Ile	Lys	Ile	Met	Arg	Gly	Arg	Lys	Arg	Arg	Arg	Asn	Leu
1				5				10						15	
Asp	Tyr	Val	Leu	Val	Gln	Ala	Glu	Ala	Thr	Ala	Ile	Val	Arg	Cys	Val
			20					25					30		
Gly	Ser	Gly	Ile	Ser	Lys	Glu	Phe	Pro	Lys	Lys	Arg	Glu	Val	Ile	Arg
			35				40					45			
Pro	Gln	Pro	Ala	Lys	Gly	Ser	Tyr	Ala	Arg	Ala	Asp	Lys	Thr	Ser	Trp
50					55						60				
Gly															
65															

(2) INFORMATION FOR SEQ ID NO:4900:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 250 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...250

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4900:

Met	Lys	Val	Leu	Ile	Leu	Glu	Asp	Val	Ile	Glu	His	Gln	Val	Arg	Leu
1			5						10					15	
Glu	Arg	Ile	Leu	Asp	Glu	Ile	Ser	Lys	Glu	Ser	Asn	Ile	Pro	Ile	Ser
		20						25					30		
Tyr	Lys	Thr	Thr	Gly	Lys	Val	Arg	Glu	Phe	Glu	Glu	Tyr	Ile	Glu	Asn
		35					40					45			
Asp	Glu	Val	Asn	Gln	Leu	Tyr	Phe	Leu	Asp	Ile	Asp	Ile	His	Gly	Ile
	50					55					60				
Glu	Lys	Lys	Gly	Phe	Glu	Val	Ala	Gln	Leu	Ile	Arg	His	Tyr	Asn	Pro
65					70					75					80
Tyr	Ala	Ile	Ile	Val	Phe	Ile	Thr	Ser	Arg	Ser	Glu	Phe	Ala	Thr	Leu
			85						90					95	
Thr	Tyr	Lys	Tyr	Gln	Val	Ser	Ala	Leu	Asp	Phe	Val	Asp	Lys	Asp	Ile
		100						105					110		
Asn	Asp	Glu	Met	Phe	Lys	Lys	Arg	Ile	Glu	Gln	Asn	Ile	Phe	Tyr	Thr
		115					120					125			
Lys	Ser	Met	Leu	Leu	Glu	Asn	Glu	Asp	Val	Val	Asp	Tyr	Phe	Asp	Tyr
	130					135					140				
Asn	Tyr	Lys	Gly	Asn	Asp	Leu	Lys	Ile	Pro	Tyr	His	Asp	Ile	Leu	Tyr
145					150					155					160
Ile	Glu	Thr	Thr	Gly	Val	Ser	His	Lys	Leu	Arg	Ile	Ile	Gly	Lys	Asn
			165						170					175	
Phe	Ala	Lys	Glu	Phe	Tyr	Gly	Thr	Met	Thr	Asp	Ile	Gln	Glu	Lys	Asp
		180						185					190		
Lys	His	Thr	Gln	Arg	Phe	Tyr	Ser	Pro	His	Lys	Ser	Phe	Leu	Val	Asn
		195					200					205			
Ile	Gly	Asn	Ile	Arg	Glu	Ile	Asp	Arg	Lys	Asn	Leu	Glu	Ile	Val	Phe
	210					215					220				
Tyr	Glu	Asp	His	Arg	Cys	Pro	Ile	Ser	Arg	Leu	Lys	Ile	Arg	Lys	Leu
225					230					235					240
Lys	Asp	Ile	Leu	Glu	Lys	Lys	Ser	Gln	Lys						
			245						250						

(2) INFORMATION FOR SEQ ID NO:4901:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 364 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...364

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4901:

Tyr	Thr	Tyr	Leu	Trp	Arg	Lys	Tyr	Met	Lys	Arg	Glu	Ile	Leu	Leu	Glu
1			5					10					15		

Arg	Ile	Asp	Lys	Leu	Lys	Gln	Leu	Met	Pro	Trp	Tyr	Val	Leu	Glu	Tyr	20	25	30
Tyr	Gln	Ser	Lys	Leu	Ala	Val	Pro	Tyr	Ser	Phe	Thr	Thr	Leu	Tyr	Glu	35	40	45
Tyr	Leu	Lys	Glu	Tyr	Asp	Arg	Phe	Phe	Ser	Trp	Val	Leu	Glu	Ser	Gly	50	55	60
Ile	Ser	Asn	Ala	Asp	Lys	Ile	Ser	Asp	Ile	Pro	Leu	Ser	Val	Leu	Glu	65	70	75
Asn	Met	Ser	Lys	Lys	Asp	Met	Glu	Ser	Phe	Ile	Leu	Tyr	Leu	Arg	Glu	85	90	95
Arg	Pro	Leu	Leu	Asn	Ala	Asn	Thr	Thr	Lys	Gln	Gly	Val	Ser	Gln	Thr	100	105	110
Thr	Ile	Asn	Arg	Thr	Leu	Ser	Ala	Leu	Ser	Ser	Leu	Tyr	Lys	Tyr	Leu	115	120	125
Thr	Glu	Glu	Val	Glu	Asn	Asp	Gln	Gly	Glu	Pro	Tyr	Phe	Tyr	Arg	Asn	130	135	140
Val	Met	Lys	Lys	Val	Ser	Thr	Lys	Lys	Lys	Lys	Glu	Thr	Leu	Ala	Ala	145	150	155
Arg	Ala	Glu	Asn	Ile	Lys	Gln	Lys	Leu	Phe	Leu	Gly	Asp	Glu	Thr	Glu	165	170	175
Gly	Phe	Leu	Thr	Tyr	Ile	Asp	Gln	Glu	His	Pro	Gln	Gln	Leu	Ser	Asn	180	185	190
Arg	Ala	Leu	Ser	Ser	Phe	Asn	Lys	Asn	Lys	Glu	Arg	Asp	Leu	Ala	Ile	195	200	205
Ile	Ala	Leu	Leu	Leu	Ala	Ser	Gly	Val	Arg	Leu	Ser	Glu	Ala	Val	Asn	210	215	220
Leu	Asp	Leu	Arg	Asp	Leu	Asn	Leu	Lys	Met	Met	Val	Ile	Asn	Val	Thr	225	230	235
Arg	Lys	Gly	Gly	Lys	Arg	Asp	Ser	Val	Asn	Val	Ala	Ala	Phe	Ala	Lys	245	250	255
Pro	Tyr	Leu	Glu	Asn	Tyr	Leu	Ala	Ile	Arg	Asn	Gln	Arg	Tyr	Lys	Thr	260	265	270
Glu	Lys	Thr	Asp	Thr	Ala	Leu	Phe	Leu	Thr	Leu	Tyr	Arg	Gly	Val	Pro	275	280	285
Asn	Arg	Ile	Asp	Ala	Ser	Ser	Val	Glu	Lys	Met	Val	Ala	Lys	Tyr	Ser	290	295	300
Glu	Asp	Phe	Lys	Val	Arg	Val	Thr	Pro	His	Lys	Leu	Arg	His	Thr	Leu	305	310	315
Ala	Thr	Arg	Leu	Tyr	Asp	Ala	Thr	Lys	Ser	Gln	Val	Leu	Val	Ser	His	325	330	335
Gln	Leu	Gly	His	Ala	Ser	Thr	Gln	Val	Thr	Asp	Leu	Tyr	Thr	His	Ile	340	345	350
Val	Asn	Asp	Glu	Gln	Lys	Asn	Ala	Leu	Asp	Ser	Leu					355	360	

(2) INFORMATION FOR SEQ ID NO:4902:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 401 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...401

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4902:

Asn	Asp	Tyr	Leu	Ser	Phe	Gln	Ser	Ile	Phe	Val	Asn	Arg	Ile	Ser	Phe
1				5					10					15	
Leu	Leu	Tyr	Ala	Leu	Ser	Ser	Pro	Leu	Phe	Lys	Val	Tyr	Phe	Phe	Gly
			20					25					30		
Gly	Ser	Glu	Met	Ser	Asp	Ser	Lys	Tyr	Met	Lys	Leu	Ala	Ile	Lys	Leu
		35					40					45			
Ala	Gln	Lys	Gly	Ala	Gly	Tyr	Val	Asn	Pro	Asn	Pro	Met	Val	Gly	Ala
	50					55				60					
Ile	Ile	Val	Lys	Asp	Asn	His	Ile	Ile	Gly	Gln	Gly	Tyr	His	Glu	Phe
65					70					75				80	
Phe	Gly	Gly	Pro	His	Ala	Glu	Arg	Asn	Ala	Leu	Lys	Asn	Cys	Arg	Lys
				85					90					95	
Ser	Pro	Val	Gly	Ala	Thr	Leu	Tyr	Val	Thr	Leu	Glu	Pro	Cys	Cys	His
			100					105					110		
Phe	Gly	Lys	Thr	Pro	Pro	Cys	Ile	Asp	Ala	Ile	Ile	Asp	Ser	Gly	Ile
		115					120					125			
Thr	Arg	Val	Val	Ile	Gly	Ser	Leu	Asp	Cys	Asn	Pro	Ile	Val	Ser	Gly
	130					135					140				
Lys	Gly	Val	Lys	Ile	Leu	Glu	Glu	Asn	Asn	Leu	Gln	Val	Thr	Val	Gly
145					150					155					160
Ile	Leu	Glu	Asn	Glu	Cys	Leu	Asn	Leu	Ile	Lys	Ser	Phe	Arg	Lys	Tyr
			165					170						175	
Ile	Thr	Gln	His	Val	Pro	Tyr	Val	Phe	Met	Lys	Tyr	Ala	Met	Ser	Met
			180					185					190		
Asp	Gly	Lys	Ile	Ala	Thr	Lys	Thr	Asn	Gln	Ser	Lys	Trp	Ile	Thr	Glu
		195				200						205			
Glu	Glu	Ala	Arg	Lys	His	Val	His	Gln	Leu	Arg	His	His	Val	Ser	Ala
	210					215					220				
Ile	Met	Val	Gly	Val	Asn	Thr	Val	Ile	Gln	Asp	Asp	Pro	Leu	Leu	Thr
225					230					235					240
Cys	Arg	Leu	Glu	Glu	Gly	Lys	Asn	Pro	Ile	Arg	Ile	Ile	Cys	Asp	Thr
			245					250					255		
His	Leu	Arg	Thr	Pro	Leu	Thr	Ser	Lys	Ile	Val	Lys	Thr	Ala	Asn	Asp
			260					265					270		
Ile	Lys	Thr	Tyr	Ile	Ala	Thr	Ser	Glu	Asp	Lys	Asn	Lys	Met	Lys	
		275					280				285				
Leu	Tyr	Gln	Asn	His	Gly	Cys	Glu	Ile	Leu	Ser	Ile	Lys	Lys	Lys	Gly
	290					295					300				
Asn	His	Ile	Asp	Leu	Ser	Ser	Leu	Met	Gln	His	Leu	Gly	Asn	Met	Gln
305					310					315					320
Ile	Asp	Ser	Leu	Val	Leu	Glu	Gly	Gly	Ser	Leu	Met	Asn	Trp	Ser	Ala
			325					330					335		
Leu	Glu	Gln	Gln	Ile	Val	Asp	Glu	Leu	Lys	Ile	Tyr	Ile	Ala	Pro	Lys
		340						345					350		
Ile	Phe	Gly	Gly	Ser	Ala	Lys	Phe	Pro	Val	Gly	Gly	Glu	Gly	Ile	Ser
		355					360					365			
Leu	Pro	Asn	Asp	Ala	Ile	Arg	Leu	Lys	Pro	Tyr	Ala	Phe	Ser	Gln	Ile
	370					375					380				

Gly Asn Asp Tyr Leu Ile Glu Ser Glu Val Ile Tyr Pro Cys Ser Gln
 385 390 395 400
 Glu

(2) INFORMATION FOR SEQ ID NO:4903:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4903:

Trp	Ser	Tyr	Leu	Lys	Lys	Asp	Val	Lys	Gln	Pro	Leu	Ala	Val	Asn	Gln
1				5					10					15	
Leu	Gln	Leu	Ser	Ala	Ala	Phe	Thr	Pro	Gly	Phe	Glu	Ser	Ala	Phe	His
			20					25					30		
Val	Asn	Met	Glu	Asp	Ser	Gln	Ala	Ala	Met	Arg	Asp	Gly	Ser	Ile	Phe
		35					40					45			
Glu	Tyr	Cys	Lys	Leu	His	Asp	Val	Val	Ile	Gln	Ala	Trp	Ser	Val	Leu
		50				55					60				
Gln	Phe	Gly	Tyr	Phe	Lys	Gly	Asn	Phe	Val	Gly	Asn	Glu	Lys	Phe	Gln
65					70				75					80	
Ala	Leu	Asn	Gln	Val	Leu	Asp	Arg	Leu	Ala	Ile	Lys	Tyr	Gly	Val	Thr
				85					90					95	
Ser	Ser	Thr	Ile	Ala	Ile	Ser	Trp	Ile	Leu	Arg	Tyr	Pro	Ala	Lys	Met
			100					105					110		
Gln	Ala	Val	Val	Gly	Thr	Thr	Asn	Pro	Lys	His	Leu	Arg	Glu	Val	Ser
		115					120					125			
Gln	Ala	Gln	Thr	Leu	Ala										
130															

(2) INFORMATION FOR SEQ ID NO:4904:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

Pro	Arg	Val	Ile	Gly	Val	Lys	Asn	Ser	Ser	Met	Pro	Val	Gln	Asp	Ile
130						135					140				
Gln	Thr	Phe	Val	Ser	Leu	Gly	Gly	Glu	Asp	His	Ile	Val	Phe	Asn	Gly
145					150					155					160
Pro	Asp	Glu	Gln	Phe	Leu	Gly	Gly	Arg	Leu	Met	Gly	Ala	Arg	Ala	Gly
				165					170					175	
Ile	Gly	Gly	Thr	Tyr	Gly	Ala	Met	Pro	Glu	Leu	Phe	Leu	Lys	Leu	Asn
			180					185					190		
Gln	Leu	Ile	Ala	Asp	Lys	Asp	Leu	Glu	Thr	Ala	Arg	Glu	Leu	Gln	Tyr
	195						200					205			
Ala	Ile	Asn	Ala	Ile	Ile	Gly	Lys	Leu	Thr	Ser	Val	His	Gly	Asn	Met
	210					215						220			
Tyr	Gly	Val	Ile	Lys	Glu	Val	Leu	Lys	Ile	Asn	Glu	Gly	Leu	Thr	Ile
225					230					235					240
Gly	Ser	Val	Arg	Ser	Pro	Leu	Thr	Pro	Val	Thr	Glu	Glu	Asp	Arg	Pro
				245					250					255	
Val	Val	Glu	Glu	Ala	Ala	Ala	Leu	Ile	Arg	Glu	Thr	Lys	Glu	Arg	Phe
			260					265					270		

Leu

(2) INFORMATION FOR SEQ ID NO:4906:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 480 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...480

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4906:

Ile	Arg	Tyr	Phe	Ser	Arg	Arg	Ile	Arg	Phe	Leu	Trp	Lys	Leu	Trp	Glu
1				5					10					15	
Lys	Glu	Lys	Ile	Gly	Trp	Gly	Ile	Glu	Met	Asn	Gly	Lys	Leu	Val	Lys
			20					25					30		
Pro	Ser	Leu	Ala	Ile	Val	Gln	Ser	Phe	Leu	Val	Ile	Leu	Leu	Ala	Tyr
		35					40					45			
Leu	Leu	Ser	Thr	Val	Arg	Glu	Thr	Glu	Ile	Val	Ser	Thr	Thr	Ala	Ile
	50					55				60					
Val	Leu	Tyr	Ile	Leu	His	Tyr	Phe	Ala	Phe	Tyr	Ile	Ser	Asp	Tyr	Gly
65					70					75					80
Gln	Asp	Phe	Phe	Lys	Arg	Gly	Tyr	Leu	Ile	Glu	Leu	Val	Gln	Thr	Leu
				85					90					95	
Lys	Tyr	Ile	Leu	Phe	Phe	Ala	Leu	Ala	Ile	Ser	Ile	Ser	Asn	Phe	Phe
			100					105					110		
Leu	Glu	Asp	Arg	Phe	Ser	Ile	Ser	Arg	Arg	Gly	Met	Ile	Tyr	Phe	Leu
		115						120					125		

Leu	Leu	His	Val	Leu	Leu	Val	Tyr	Val	Leu	Asn	Arg	Phe	Ile	Lys	Trp
130						135					140				
Tyr	Trp	Lys	Arg	Ala	Tyr	Pro	Asn	Phe	Lys	Gly	Ser	Lys	Lys	Ile	Leu
145					150					155					160
Leu	Leu	Thr	Ala	Thr	Ser	Arg	Val	Glu	Lys	Val	Leu	Asp	Arg	Leu	Ile
				165						170					175
Glu	Ser	Asp	Asp	Val	Val	Gly	Glu	Leu	Val	Ala	Val	Ser	Val	Leu	Asp
			180					185						190	
Lys	Pro	Asp	Phe	Gln	His	Asp	Tyr	Leu	Lys	Val	Val	Ala	Glu	Gly	Glu
		195					200						205		
Ile	Val	Asn	Phe	Ala	Thr	His	Glu	Val	Val	Asp	Glu	Val	Phe	Ile	Asn
	210					215					220				
Leu	Pro	Ser	Glu	Lys	Tyr	Asn	Ile	Gly	Glu	Leu	Val	Ser	Gln	Phe	Glu
225					230					235					240
Thr	Met	Gly	Val	Asp	Val	Thr	Val	Asn	Leu	Asn	Ala	Phe	Asp	Cys	Ile
				245					250					255	
Leu	Ala	His	Asn	Lys	Gln	Ile	Cys	Glu	Met	Ala	Gly	Leu	Asn	Val	Val
			260					265					270		
Thr	Phe	Ser	Thr	Thr	Phe	Tyr	Lys	Thr	Ser	His	Val	Ile	Ala	Lys	Arg
		275					280					285			
Val	Ile	Asp	Ile	Ile	Gly	Ser	Leu	Val	Gly	Leu	Ile	Leu	Cys	Gly	Leu
	290				295						300				
Val	Ser	Ile	Val	Leu	Val	Pro	Leu	Ile	Arg	Lys	Asp	Gly	Gly	Ser	Ala
305					310					315					320
Ile	Phe	Ala	Gln	Thr	Arg	Ile	Gly	Lys	Asn	Gly	Arg	His	Phe	Thr	Phe
				325					330					335	
Tyr	Lys	Phe	Arg	Ser	Met	Cys	Val	Asp	Ala	Glu	Glu	Lys	Lys	Arg	Glu
			340					345					350		
Leu	Met	Glu	Gln	Asn	Thr	Met	Gln	Gly	Gly	Met	Phe	Lys	Val	Asp	Glu
	355						360					365			
Asp	Pro	Arg	Ile	Thr	Lys	Ile	Gly	His	Phe	Ile	Arg	Lys	Thr	Ser	Leu
	370					375					380				
Asp	Glu	Leu	Pro	Gln	Phe	Tyr	Asn	Val	Leu	Lys	Gly	Asp	Met	Ser	Leu
385					390					395					400
Val	Gly	Thr	Arg	Pro	Pro	Thr	Val	Asp	Glu	Tyr	Glu	His	Tyr	Thr	Pro
				405					410					415	
Glu	Gln	Lys	Arg	Arg	Leu	Ser	Phe	Lys	Pro	Gly	Ile	Thr	Gly	Leu	Trp
			420					425					430		
Gln	Val	Ser	Gly	Arg	Ser	Glu	Ile	Lys	Asn	Phe	Asp	Glu	Val	Val	Lys
	435						440					445			
Leu	Asp	Val	Ala	Tyr	Ile	Asp	Gly	Trp	Thr	Ile	Trp	Lys	Asp	Ile	Glu
450						455					460				
Ile	Leu	Leu	Lys	Thr	Val	Lys	Val	Val	Leu	Met	Lys	Asp	Gly	Ala	Lys
465					470					475					480

(2) INFORMATION FOR SEQ ID NO:4907:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 71 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...71

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4907:

```
Arg Met Tyr Phe Val Ile Ala Glu Phe Asn Ala Asn Trp Phe Thr His
1           5           10           15
Arg Asn Ser Lys Arg Ser Tyr Phe Leu His His Ile Lys Phe Lys Phe
          20           25           30
Phe Tyr Asn Leu Thr Ser Thr Tyr Gln Lys His Ala Arg Asn Ile Phe
          35           40           45
Thr Asp Phe Asp Leu Ser His Asn Ile Phe Tyr His Leu Thr Ser Leu
          50           55           60
Tyr Leu Trp Leu Ser Tyr Tyr
65           70
```

(2) INFORMATION FOR SEQ ID NO:4908:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4908:

```
Glu Thr His Phe Ile Ser Leu Phe Phe Val Thr Thr Val Asp Gly Asn
1           5           10           15
Leu Arg Gly Tyr Pro Thr Thr Lys Val Lys Ile Cys Lys Ala Ser Lys
          20           25           30
Asp Phe Leu Glu Asn Pro Ser Leu Leu Phe Gly Val Lys Ile Asp Gln
          35           40           45
Ala Asn Thr Val Phe Gln Val Thr Lys Thr Ser Leu Tyr Ala Pro Ser
          50           55           60
Thr Gly Val Glu Ile Phe
65           70
```

(2) INFORMATION FOR SEQ ID NO:4909:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 70 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4909:

Glu	Thr	His	Phe	Ile	Ser	Leu	Phe	Phe	Val	Thr	Thr	Val	Asp	Gly	Asn
1				5					10					15	
Leu	Arg	Gly	Tyr	Pro	Thr	Thr	Lys	Val	Lys	Ile	Cys	Lys	Ala	Ser	Lys
		20					25						30		
Asp	Phe	Leu	Glu	Asn	Pro	Ser	Leu	Leu	Phe	Gly	Val	Lys	Ile	Asp	Gln
		35					40					45			
Ala	Asn	Thr	Val	Phe	Gln	Val	Thr	Lys	Thr	Ser	Leu	Tyr	Ala	Pro	Ser
	50					55					60				
Thr	Gly	Val	Glu	Ile	Phe										
65					70										

(2) INFORMATION FOR SEQ ID NO:4910:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 70 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...70

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4910:

Glu	Thr	His	Phe	Ile	Ser	Leu	Phe	Phe	Val	Thr	Thr	Val	Asp	Gly	Asn
1				5					10					15	
Leu	Arg	Gly	Tyr	Pro	Thr	Thr	Lys	Val	Lys	Ile	Cys	Lys	Ala	Ser	Lys
		20					25						30		
Asp	Phe	Leu	Glu	Asn	Pro	Ser	Leu	Leu	Phe	Gly	Val	Lys	Ile	Asp	Gln
		35					40					45			
Ala	Asn	Thr	Val	Phe	Gln	Val	Thr	Lys	Thr	Ser	Leu	Tyr	Ala	Pro	Ser
	50					55					60				
Thr	Gly	Val	Glu	Ile	Phe										
65					70										

(2) INFORMATION FOR SEQ ID NO:4911:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 302 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...302
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4911:

Gln	Thr	His	Leu	Lys	Gly	Lys	Asp	Ser	Lys	Met	Gln	Gly	Gln	Ile	Ile	1	5	10	15
Lys	Ala	Leu	Ala	Gly	Phe	Tyr	Tyr	Val	Glu	Ser	Asp	Gly	Gln	Val	Tyr	20	25	30	
Gln	Thr	Arg	Ala	Arg	Gly	Asn	Phe	Arg	Lys	Lys	Gly	His	Thr	Pro	Tyr	35	40	45	
Val	Gly	Asp	Trp	Val	Asp	Phe	Ser	Ala	Glu	Glu	Asn	Ser	Glu	Gly	Tyr	50	55	60	
Ile	Leu	Lys	Ile	His	Glu	Arg	Lys	Asn	Ser	Leu	Val	Arg	Pro	Pro	Ile	65	70	75	80
Val	Asn	Ile	Asp	Gln	Ala	Val	Val	Ile	Met	Ser	Val	Lys	Glu	Pro	Asp	85	90	95	
Phe	Asn	Ser	Asn	Leu	Leu	Asp	Arg	Phe	Leu	Val	Leu	Leu	Glu	His	Lys	100	105	110	
Gly	Ile	His	Pro	Ile	Val	Tyr	Ile	Ser	Lys	Met	Asp	Leu	Leu	Glu	Asp	115	120	125	
Arg	Gly	Glu	Leu	Asp	Phe	Tyr	Gln	Gln	Thr	Tyr	Gly	Asp	Ile	Gly	Tyr	130	135	140	
Asp	Phe	Val	Thr	Ser	Lys	Glu	Glu	Leu	Leu	Ser	Leu	Leu	Thr	Gly	Lys	145	150	155	160
Val	Thr	Val	Phe	Met	Gly	Gln	Thr	Gly	Val	Gly	Lys	Ser	Thr	Leu	Leu	165	170	175	
Asn	Lys	Ile	Ala	Pro	Asp	Leu	Asn	Leu	Glu	Thr	Gly	Glu	Ile	Ser	Asp	180	185	190	
Ser	Leu	Gly	Arg	Gly	Arg	His	Thr	Thr	Arg	Ala	Val	Ser	Phe	Tyr	Asn	195	200	205	
Leu	Asn	Gly	Gly	Lys	Ile	Ala	Asp	Thr	Pro	Gly	Phe	Ser	Ser	Leu	Asp	210	215	220	
Tyr	Glu	Val	Ser	Arg	Ala	Glu	Asp	Leu	Asn	Gln	Ala	Phe	Pro	Glu	Ile	225	230	235	240
Ala	Thr	Val	Ser	Arg	Asp	Cys	Lys	Phe	Arg	Thr	Cys	Thr	His	Thr	His	245	250	255	
Glu	Pro	Ser	Cys	Ala	Val	Lys	Pro	Ala	Val	Glu	Glu	Gly	Val	Ile	Ala	260	265	270	
Thr	Phe	Arg	Phe	Asp	Asn	Tyr	Leu	Gln	Phe	Leu	Ser	Glu	Ile	Glu	Asn	275	280	285	
Arg	Arg	Glu	Thr	Tyr	Lys	Lys	Val	Ser	Lys	Lys	Ile	Pro	Lys			290	295	300	

(2) INFORMATION FOR SEQ ID NO:4912:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 69 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...69
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4912:

Lys	Tyr	Asn	Leu	Tyr	Ser	Leu	Lys	Ile	Ser	Ser	Asn	His	Val	Ser	Phe
1				5				10					15		
Ala	Leu	Leu	Tyr	Ile	Trp	Leu	Leu	Thr	Ser	Ser	Val	Leu	Ser	Thr	Thr
			20					25					30		
Ser	Lys	Gln	Cys	Phe	Glu	Leu	Thr	Ser	Ser	Val	Leu	Ser	Thr	Thr	Ser
		35					40					45			
Lys	Gln	Cys	Phe	Glu	Leu	Thr	Ala	Ala	Ser	Phe	Leu	Val	Cys	Ser	Leu
		50				55						60			
Ile	Phe	Ile	Glu	Tyr											
65															

(2) INFORMATION FOR SEQ ID NO:4913:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 275 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...275
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4913:

Pro	Ser	Asn	Phe	Leu	Glu	Glu	Met	Met	Lys	Leu	Leu	Phe	Ile	Leu	Ile
1				5					10					15	
Ser	Met	Val	Leu	Val	Ser	Leu	Tyr	Met	Val	Ile	Thr	Ser	Val	Asp	His
			20					25					30		
Arg	Glu	Glu	Ile	Leu	Phe	Gly	Asn	Tyr	Pro	Ser	Val	Asp	Val	Thr	Gly

		35					40					45			
Met	Met	Ile	Asn	Gln	Pro	Val	Ala	Ser	Arg	Glu	Glu	Val	Thr	Glu	Ala
	50						55				60				
Leu	Ser	His	Leu	Ala	Val	Glu	His	Asn	Ser	Leu	Ile	Ala	Arg	Arg	Ile
65					70					75					80
Val	Glu	Pro	Asn	Glu	Ala	Gly	Glu	Thr	Arg	Phe	Thr	Tyr	Ala	Thr	Tyr
			85						90					95	
Gly	Glu	Gly	Lys	Leu	Pro	Glu	Gly	Leu	Thr	Ile	Ser	Ser	Lys	Glu	Ser
			100					105					110		
Ala	Glu	Thr	Ser	Asp	Leu	Leu	Gly	Ser	Tyr	Leu	Ile	Val	Ser	Gly	Ser
		115					120					125			
Leu	Asp	Gly	Val	Ser	Leu	Gln	Thr	Thr	Leu	Lys	Glu	Leu	Gly	Tyr	Gln
	130					135					140				
Gly	Phe	Val	Ser	Asn	Gly	Glu	Asp	Pro	Phe	Ser	Ile	Val	Leu	Leu	Leu
145					150					155					160
Thr	Ala	Thr	Pro	Met	Val	Leu	Leu	Ser	Leu	Ala	Ile	Phe	Leu	Leu	Thr
				165					170					175	
Phe	Met	Ser	Leu	Thr	Leu	Ile	Tyr	Arg	Ile	Lys	Ser	Leu	Arg	Gln	Ala
			180					185					190		
Gly	Ile	Arg	Leu	Ile	Xaa	Gly	Glu	Ser	Leu	Phe	Gly	Val	Ala	Leu	Arg
	195					200						205			
Pro	Val	Leu	Glu	Asp	Val	Arg	Gln	Leu	Ile	Cys	Ser	Val	Leu	Val	Ser
	210					215					220				
Ser	Leu	Leu	Gly	Leu	Gly	Ile	Leu	Trp	Tyr	Gln	Gly	Ala	Leu	Phe	Met
225					230					235					240
Ala	Thr	Val	Gln	Leu	Val	Ile	Ile	Ala	Leu	Leu	Leu	Tyr	Gly	Leu	His
				245					250					255	
Leu	Gly	Arg	Asp	Phe	Tyr	Leu	Thr	Lys	Cys	Arg	Leu	Ser	Thr	Trp	Phe
			260					265						270	
Thr	Gly	Lys													
		275													

(2) INFORMATION FOR SEQ ID NO:4914:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 210 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...210

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4914:

Phe	Ser	Asn	Phe	Cys	Gly	Asp	Lys	Gly	Pro	Ile	Val	Ser	Asp	Asp	Val
1				5					10					15	
Tyr	Phe	Ala	Ser	Thr	Leu	Arg	Arg	Gly	Val	Pro	Ala	Ala	Glu	Ala	Gly
		20						25				30			
Met	Asp	Arg	Val	Gln	Ala	Asp	Tyr	Thr	Gly	Met	Leu	Gly	Thr	Val	Met

35	40	45																	
Asn	Ala	Leu	Val	Met	Ala	Asp	Ser	Leu	Gln	Gln	Val	Gly	Val	Asp	Thr				
50	55	60																	
Arg	Val	Gln	Thr	Ala	Ile	Ala	Met	Gln	Gln	Val	Ala	Glu	Pro	Tyr	Val				
65	70	75	80																
Arg	Gly	Arg	Ala	Leu	Arg	His	Leu	Glu	Lys	Gly	Arg	Ile	Val	Ile	Phe				
85	90	95																	
Gly	Ala	Gly	Ile	Gly	Ser	Pro	Tyr	Phe	Ser	Thr	Asp	Thr	Thr	Ala	Ala				
100	105	110																	
Leu	Arg	Ala	Ala	Glu	Ile	Glu	Ala	Asp	Ala	Ile	Leu	Met	Ala	Lys	Asn				
115	120	125																	
Gly	Val	Asp	Gly	Val	Tyr	Asn	Ala	Asp	Pro	Lys	Lys	Asp	Lys	Thr	Ala				
130	135	140																	
Val	Lys	Phe	Glu	Glu	Leu	Thr	His	Arg	Asp	Val	Ile	Asn	Lys	Gly	Leu				
145	150	155	160																
Arg	Ile	Met	Asp	Ser	Thr	Ala	Ser	Thr	Leu	Ser	Met	Asp	Asn	Asp	Ile				
165	170	175																	
Asp	Leu	Val	Val	Phe	Asn	Met	Asn	Gln	Ser	Gly	Asn	Ile	Lys	Arg	Val				
180	185	190																	
Val	Phe	Gly	Glu	Asn	Ile	Gly	Thr	Thr	Val	Ser	Asn	Asn	Ile	Glu	Glu				
195	200	205																	
Lys	Glu																		
210																			

(2) INFORMATION FOR SEQ ID NO:4915:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 219 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4915:

Met	Lys	Asn	Phe	Thr	Asn	Ile	Lys	Phe	Lys	Glu	Asn	Gly	Glu	Phe	Asn				
1	5	10	15																
His	Phe	Pro	Gly	Asn	Thr	Val	Val	Ala	Asn	Leu	Tyr	Thr	Lys	Gln	Asp				
20	25	30																	
Leu	Met	Glu	Val	Val	Asp	Ile	Ile	Gln	Ser	Arg	Tyr	Arg	Glu	Leu	Pro				
35	40	45																	
Phe	Ile	Asp	Lys	Phe	Thr	Leu	Thr	Pro	Arg	Asn	Ser	Ile	His	Met	Thr				
50	55	60																	
Val	Ile	Glu	Leu	Leu	Cys	His	Glu	Asn	Arg	Glu	Thr	Glu	Phe	Trp	Ser				
65	70	75	80																
Ser	Asn	Leu	Pro	Leu	Asp	Thr	Pro	Leu	Gln	Glu	Ile	His	Asp	Tyr	Phe				
85	90	95																	
Ala	Lys	Gln	Leu	Glu	Ile	Phe	Pro	Leu	Leu	Asp	Glu	Glu	Ile	His	Met				

				100					105					110					
Arg	Ile	Thr	Glu	Met	Gly	Lys	Gln	Asn	Ile	Leu	Val	Glu	Pro	Ala	Asp				
				115				120					125						
Glu	Ala	Ser	Ala	Lys	Arg	Leu	Glu	Glu	Ile	Arg	Thr	Tyr	Val	Ser	Glu				
				130				135				140							
Lys	Ala	Gly	Val	Cys	Phe	Pro	Asn	His	Asp	Arg	Tyr	Gln	Phe	His	Ile				
145					150					155					160				
Ser	Ile	Gly	Tyr	Leu	Arg	Ile	Pro	Leu	Thr	Glu	Glu	Glu	Glu	Glu	Glu				
				165					170						175				
Phe	Thr	Lys	Val	Arg	Ala	Glu	Leu	Thr	Glu	Ile	Leu	Leu	Glu	Lys	Ile				
				180				185					190						
Pro	Thr	Ile	Thr	Val	Asn	Arg	Ile	Asp	Tyr	Thr	Val	Phe	Glu	Asp	Met				
				195				200					205						
Arg	Gln	Phe	Val	Pro	Tyr	His	Glu	Lys	Phe	Lys									
				210				215											

(2) INFORMATION FOR SEQ ID NO:4916:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 336 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4916:

Ile	His	Phe	Val	Thr	Asn	Leu	Met	Arg	Asn	Phe	Pro	Val	Val	Ser	Asp				
1				5				10						15					
Gly	Pro	Phe	Thr	Pro	Glu	Asp	Tyr	Val	Gly	Arg	Ile	Asn	Tyr	Glu	Leu				
			20					25					30						
Ala	Asn	Asp	Phe	Gly	Asn	Leu	Leu	Asn	Arg	Thr	Phe	Ser	Met	Ile	Asn				
		35				40						45							
Lys	Tyr	Phe	Asp	Gly	Gln	Ile	Pro	Ala	Tyr	Val	Glu	Gly	Val	Thr	Glu				
	50					55				60									
Phe	Asp	His	Val	Leu	Ala	Glu	Val	Ala	Glu	Gln	Ser	Ile	Ala	Asp	Phe				
65				70				75						80					
His	Thr	His	Met	Glu	Ala	Val	Asp	Tyr	Pro	Arg	Ala	Leu	Glu	Ala	Val				
			85					90						95					
Trp	Thr	Leu	Ile	Ser	Arg	Thr	Asn	Lys	Tyr	Ile	Asp	Glu	Thr	Ala	Pro				
			100					105					110						
Trp	Val	Leu	Ala	Lys	Asp	Glu	Ala	Leu	Arg	Asp	Gln	Leu	Ala	Ser	Val				
			115					120					125						
Met	Ser	His	Leu	Ala	Ala	Ser	Ile	Arg	Val	Val	Ala	His	Leu	Ile	Glu				
		130				135					140								
Pro	Phe	Met	Met	Glu	Thr	Ser	Arg	Ala	Val	Leu	Thr	Gln	Leu	Gly	Leu				
145					150					155					160				

Glu	Glu	Val	Ser	Ser	Leu	Glu	Asn	Leu	Ser	Leu	Ala	Asp	Phe	Pro	Ala
				165					170					175	
Asp	Val	Thr	Val	Val	Ala	Lys	Gly	Thr	Pro	Ile	Phe	Pro	Arg	Leu	Asn
			180					185					190		
Met	Glu	Glu	Glu	Ile	Ala	Tyr	Ile	Lys	Glu	Gln	Met	Glu	Gly	Asn	Lys
		195					200					205			
Pro	Ala	Val	Glu	Lys	Glu	Trp	Asn	Pro	Asp	Glu	Val	Glu	Leu	Lys	Leu
	210					215					220				
Asn	Lys	Asp	Glu	Ile	Lys	Phe	Glu	Asp	Phe	Asp	Lys	Val	Glu	Ile	Arg
225					230					235					240
Val	Ala	Glu	Val	Lys	Glu	Val	Ser	Lys	Val	Glu	Gly	Ser	Asp	Lys	Leu
				245					250					255	
Leu	Gln	Phe	Cys	Leu	Asp	Ala	Gly	Asp	Gly	Glu	Asp	Arg	Gln	Ile	Leu
			260					265					270		
Ser	Gly	Ile	Ala	Lys	Tyr	Tyr	Pro	Asn	Glu	Gln	Glu	Leu	Val	Gly	Lys
	275						280					285			
Lys	Val	Gln	Ile	Val	Ala	Asn	Leu	Lys	Pro	Arg	Lys	Met	Met	Lys	Lys
	290					295					300				
Tyr	Val	Ser	Gln	Gly	Met	Ile	Leu	Ser	Ala	Glu	His	Asp	Gly	Lys	Leu
305					310					315					320
Thr	Leu	Leu	Thr	Val	Asp	Pro	Ala	Val	Pro	Asn	Gly	Ser	Val	Ile	Gly
				325					330					335	

(2) INFORMATION FOR SEQ ID NO:4917:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 304 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4917:

Pro	Asn	Leu	Val	Lys	Glu	Gly	Arg	Arg	Arg	Met	Val	Lys	Glu	Arg	Asn
1				5					10					15	
Leu	Thr	Arg	Trp	Ile	Phe	Val	Leu	Pro	Ala	Met	Ile	Ile	Val	Gly	Leu
			20					25					30		
Leu	Phe	Val	Tyr	Pro	Phe	Phe	Ser	Ser	Ile	Phe	Tyr	Ser	Phe	Thr	Asn
		35					40					45			
Lys	His	Leu	Ile	Met	Pro	Asn	Tyr	Lys	Phe	Val	Gly	Leu	Ala	Asn	Tyr
	50					55					60				
Lys	Ala	Val	Leu	Ser	Asp	Pro	Asn	Phe	Phe	Asn	Ala	Phe	Phe	Asn	Ser
65					70					75					80
Ile	Lys	Trp	Thr	Val	Phe	Ser	Leu	Val	Gly	Gln	Val	Leu	Val	Gly	Phe
			85						90					95	
Val	Leu	Ala	Leu	Ala	Leu	His	Arg	Val	Arg	His	Phe	Lys	Lys	Leu	Tyr
			100					105					110		

Arg	Thr	Leu	Leu	Ile	Val	Pro	Trp	Ala	Phe	Pro	Thr	Ile	Val	Ile	Ala
		115					120					125			
Phe	Ser	Trp	Gln	Trp	Ile	Leu	Asn	Gly	Val	Tyr	Gly	Tyr	Leu	Pro	Asn
	130					135					140				
Leu	Ile	Val	Lys	Leu	Gly	Leu	Met	Glu	His	Thr	Pro	Ala	Phe	Leu	Thr
145					150					155					160
Asp	Ser	Thr	Trp	Ala	Phe	Leu	Cys	Leu	Val	Phe	Ile	Asn	Ile	Trp	Phe
				165					170					175	
Gly	Ala	Pro	Met	Ile	Met	Val	Asn	Val	Leu	Ser	Ala	Leu	Gln	Thr	Val
			180					185					190		
Pro	Glu	Glu	Gln	Phe	Glu	Ala	Ala	Lys	Ile	Asp	Gly	Ala	Ser	Ser	Trp
		195					200					205			
Gln	Val	Phe	Lys	Phe	Ile	Val	Phe	Pro	His	Ile	Lys	Val	Val	Val	Gly
	210					215					220				
Leu	Leu	Val	Val	Leu	Arg	Thr	Val	Trp	Ile	Phe	Asn	Asn	Phe	Asp	Ile
225					230					235					240
Ile	Tyr	Leu	Ile	Thr	Gly	Gly	Gly	Pro	Ala	Asn	Ala	Thr	Thr	Thr	Leu
				245					250					255	
Pro	Ile	Phe	Ala	Tyr	Asn	Leu	Gly	Trp	Gly	Thr	Lys	Leu	Leu	Gly	Arg
			260				265					270			
Ala	Ser	Ala	Val	Thr	Val	Leu	Leu	Phe	Ile	Phe	Leu	Val	Ala	Ile	Cys
		275					280					285			
Phe	Ile	Tyr	Phe	Ala	Ile	Ile	Ser	Lys	Trp	Glu	Lys	Glu	Gly	Arg	Lys
	290					295					300				

(2) INFORMATION FOR SEQ ID NO:4918:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 348 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...348

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4918:

Lys	Ser	Leu	Val	Asn	Ser	Ala	Lys	Leu	Leu	Thr	Thr	Leu	Met	Lys	Arg
1				5				10						15	
Thr	Trp	Arg	Asn	Ser	Phe	Val	Thr	Asn	Leu	Asn	Thr	Pro	Phe	Met	Ile
			20					25					30		
Gly	Asn	Val	Glu	Ile	Pro	Asn	Arg	Thr	Val	Leu	Ala	Pro	Met	Ala	Gly
		35				40						45			
Val	Thr	Asn	Ser	Ala	Phe	Arg	Thr	Ile	Ala	Lys	Glu	Leu	Gly	Ala	Gly
	50					55					60				
Leu	Val	Val	Met	Glu	Met	Val	Ser	Asp	Lys	Gly	Ile	Gln	Tyr	Asn	Asn
65					70					75				80	
Glu	Lys	Thr	Leu	His	Met	Leu	His	Ile	Asp	Glu	Gly	Glu	Asn	Pro	Val

			85					90				95			
Ser	Ile	Gln	Leu	Leu	Gly	Ser	Asp	Glu	Asp	Ser	Leu	Ala	Arg	Ala	Ala
			100					105					110		
Glu	Phe	Ile	Gln	Glu	Asn	Thr	Lys	Thr	Asp	Ile	Val	Asp	Ile	Asn	Met
		115					120					125			
Gly	Cys	Pro	Val	Asn	Lys	Ile	Val	Lys	Asn	Glu	Ala	Gly	Ala	Met	Trp
	130					135					140				
Leu	Lys	Asp	Pro	Asp	Lys	Ile	Tyr	Ser	Ile	Ile	Asn	Lys	Val	Gln	Ser
145					150					155					160
Val	Leu	Asp	Ile	Pro	Leu	Thr	Val	Lys	Met	Arg	Thr	Gly	Trp	Ala	Asp
				165					170					175	
Pro	Ser	Leu	Ala	Val	Glu	Asn	Ala	Leu	Ala	Ala	Glu	Ala	Ala	Gly	Val
		180					185						190		
Ser	Ala	Leu	Ala	Met	His	Gly	Arg	Thr	Arg	Glu	Gln	Met	Tyr	Thr	Gly
	195					200					205				
His	Ala	Asp	Leu	Glu	Thr	Leu	Tyr	Lys	Val	Ala	Gln	Ala	Leu	Thr	Lys
	210					215					220				
Ile	Pro	Phe	Ile	Ala	Asn	Gly	Asp	Ile	Arg	Thr	Val	Gln	Glu	Ala	Lys
225					230					235					240
Gln	Arg	Ile	Glu	Glu	Val	Gly	Ala	Asp	Ala	Val	Met	Ile	Gly	Arg	Ala
			245						250					255	
Ala	Met	Gly	Asn	Pro	Tyr	Leu	Phe	Asn	Gln	Ile	Asn	His	Tyr	Phe	Glu
		260					265					270			
Thr	Gly	Glu	Ile	Leu	Pro	Asp	Leu	Thr	Phe	Glu	Asp	Lys	Met	Lys	Ile
	275					280						285			
Ala	Tyr	Glu	His	Leu	Lys	Arg	Leu	Ile	Asn	Leu	Lys	Gly	Glu	Asn	Val
	290					295					300				
Ala	Val	Arg	Glu	Phe	Arg	Gly	Leu	Ala	Pro	His	Tyr	Leu	Arg	Gly	Thr
305					310					315					320
Ser	Gly	Ala	Ala	Lys	Leu	Arg	Gly	Ala	Ile	Ser	Gln	Ala	Ser	Thr	Leu
			325					330						335	
Ala	Glu	Ile	Glu	Ala	Leu	Leu	Gln	Leu	Glu	Lys	Val				
			340					345							

(2) INFORMATION FOR SEQ ID NO:4919:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 670 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...670
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4919:

Tyr	Pro	Leu	Val	Tyr	Gln	Tyr	Arg	Glu	Phe	Lys	Thr	Ser	Ile	Arg	His
1			5					10					15		
Ile	Arg	Lys	Arg	Asn	Lys	Met	Thr	Glu	Glu	Ile	Lys	Asn	Leu	Gln	Ala

Ile	Leu	Asn	Val	Glu	Lys	Ala	Ser	Met	Asp	Lys	Ile	Leu	Ala	Asn	Glu	485	490	495
Glu	Ile	Arg	Ser	Leu	Phe	Thr	Ala	Met	Gly	Thr	Gly	Phe	Gly	Ala	Glu	500	505	510
Phe	Asp	Val	Ser	Lys	Ala	Arg	Tyr	Gln	Lys	Leu	Val	Leu	Met	Thr	Asp	515	520	525
Ala	Asp	Val	Asp	Gly	Ala	His	Ile	Arg	Thr	Leu	Leu	Leu	Thr	Leu	Ile	530	535	540
Tyr	Arg	Tyr	Met	Lys	Pro	Ile	Leu	Glu	Ala	Gly	Tyr	Val	Tyr	Ile	Ala	545	550	555
Gln	Pro	Pro	Ile	Tyr	Gly	Val	Lys	Val	Gly	Ser	Glu	Ile	Lys	Glu	Tyr	565	570	575
Ile	Gln	Pro	Gly	Ala	Asp	Gln	Glu	Ile	Lys	Leu	Gln	Glu	Ala	Leu	Ala	580	585	590
Arg	Tyr	Ser	Glu	Gly	Arg	Thr	Lys	Pro	Thr	Ile	Gln	Arg	Tyr	Lys	Gly	595	600	605
Leu	Gly	Glu	Met	Asp	Asp	His	Gln	Leu	Trp	Glu	Thr	Thr	Met	Asp	Pro	610	615	620
Glu	His	Arg	Leu	Met	Ala	Arg	Val	Ser	Val	Asp	Asp	Ala	Ala	Glu	Ala	625	630	635
Asp	Lys	Ile	Phe	Asp	Met	Leu	Met	Gly	Asp	Arg	Val	Glu	Pro	Arg	Arg	645	650	655
Glu	Phe	Ile	Glu	Glu	Asn	Ala	Val	Tyr	Ser	Thr	Leu	Asp	Val			660	665	670

(2) INFORMATION FOR SEQ ID NO:4920:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 147 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...147
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4920:

Glu	Thr	Ile	Val	Tyr	Thr	Ile	Ile	Lys	Ser	Asn	Ile	Lys	Lys	Phe	Ser	1	5	10	15
Leu	Leu	Thr	Ile	Phe	Ile	Val	Ala	Gly	Gln	Leu	Leu	Leu	Ile	Tyr	Ala	20	25	30	
Ala	Thr	Ile	Asn	Ala	Leu	Val	Leu	Asn	Glu	Leu	Ile	Ala	Met	Asn	Leu	35	40	45	
Glu	Arg	Phe	Leu	Lys	Leu	Ser	Ile	Tyr	Gln	Met	Ile	Val	Trp	Cys	Gly	50	55	60	
Ile	Ile	Phe	Leu	Asp	Trp	Val	Val	Lys	Asn	Tyr	Gln	Val	Glu	Val	Ile	65	70	75	80
Arg	Lys	Phe	Asn	Leu	Lys	Ile	Arg	Asn	Arg	Val	Ala	Thr	Asp	Ile	Ser	85	90	95	

Asn	Ser	Thr	Tyr	Gln	Glu	Phe	His	Ser	Lys	Ser	Ser	Gly	Thr	Tyr	Leu
			100					105					110		
Ser	Trp	Leu	Asn	Asn	Asp	Val	His	Thr	Leu	Asn	Asp	Gln	Ala	Phe	Lys
		115					120					125			
Gln	Leu	Phe	Leu	Val	Ile	Lys	Gly	Asp	Phe	Trp	Tyr	Tyr	Ile	Cys	Ser
	130					135					140				
Cys	Asp	Ser													
145															

(2) INFORMATION FOR SEQ ID NO:4921:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 81 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...81

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4921:

Gly	Asp	Ile	Val	Gly	Ser	Gln	Asn	Gln	Tyr	Phe	Trp	Ile	Ile	Gly	Gly
1				5					10					15	
Ala	Thr	Asp	Leu	Tyr	Asn	Ser	Lys	Glu	Glu	Ile	Gly	Tyr	Ser	Val	Ser
			20					25					30		
Glu	Val	Val	His	Ile	Leu	Ser	Glu	Ser	Leu	Ser	Val	Asn	Cys	Lys	Glu
		35					40					45			
Ser	Lys	Thr	Leu	Lys	Gln	Ile	Phe	Glu	Thr	Ala	Leu	Leu	Glu	Val	Lys
	50				55					60					
Asp	Glu	Ile	Gly	Leu	Asn	Ser	Tyr	Lys	Leu	Thr	Glu	Tyr	Ser	Lys	Met
65					70				75					80	
Lys															

(2) INFORMATION FOR SEQ ID NO:4922:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 301 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...301

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4922:

Gln	Ser	Ile	Val	Lys	Lys	Lys	Arg	Ser	Phe	Ile	Met	Lys	Lys	Lys	Asn
1				5					10					15	
Gly	Lys	Ala	Lys	Lys	Trp	Gln	Leu	Tyr	Ala	Ala	Ile	Gly	Ala	Ala	Ser
			20					25					30		
Val	Val	Val	Leu	Gly	Ala	Gly	Gly	Ile	Leu	Leu	Phe	Arg	Gln	Pro	Ser
		35				40						45			
Gln	Thr	Ala	Leu	Lys	Asp	Glu	Pro	Thr	His	Leu	Val	Val	Ala	Asn	Glu
	50					55					60				
Gly	Ser	Val	Ala	Ser	Ser	Val	Leu	Leu	Ser	Gly	Thr	Val	Thr	Ala	Lys
65					70					75					80
Asn	Glu	Gln	Tyr	Val	Tyr	Phe	Asp	Ala	Ser	Lys	Gly	Asp	Leu	Asp	Glu
			85					90						95	
Ile	Leu	Val	Ser	Val	Gly	Asp	Lys	Val	Ser	Glu	Gly	Gln	Ala	Leu	Val
		100						105					110		
Lys	Tyr	Ser	Ser	Ser	Glu	Ala	Gln	Ala	Ala	Tyr	Asp	Ser	Ala	Ser	Arg
	115						120					125			
Ala	Val	Ala	Lys	Ala	Asp	Arg	His	Ile	Asn	Glu	Leu	Asn	Gln	Ala	Arg
	130					135					140				
Asn	Glu	Ala	Ala	Ser	Ala	Gln	Ala	Pro	Gln	Leu	Pro	Ala	Pro	Val	Gly
145					150					155					160
Gly	Glu	Asp	Ala	Thr	Val	Gln	Ser	Pro	Thr	Pro	Val	Ala	Gly	Asn	Ser
			165					170						175	
Val	Ala	Ser	Ile	Asp	Ala	Gln	Leu	Gly	Asp	Ala	Arg	Asp	Ala	Arg	Ala
		180						185					190		
Asp	Ala	Ala	Ala	Gln	Leu	Ser	Lys	Ala	Gln	Ser	Gln	Leu	Asp	Ala	Thr
	195						200					205			
Thr	Val	Leu	Ser	Thr	Leu	Glu	Gly	Thr	Val	Val	Glu	Val	Asn	Ser	Asn
	210					215					220				
Val	Ser	Lys	Ser	Pro	Thr	Gly	Ala	Ser	Gln	Val	Met	Val	His	Ile	Val
225					230					235					240
Ser	Asn	Glu	Asn	Leu	Gln	Val	Lys	Gly	Glu	Leu	Ser	Glu	Tyr	Asn	Leu
			245					250						255	
Xaa	Asn	Leu	Ser	Val	Gly	Gln	Glu	Val	Ser	Phe	Thr	Ser	Lys	Val	Tyr
		260						265					270		
Pro	Asp	Lys	Lys	Trp	Thr	Gly	Lys	Leu	Ser	Tyr	Ile	Ser	Asp	Cys	Pro
	275					280						285			
Lys	Asn	Asn	Gly	Glu	Ala	Ala	Ser	Pro	Ala	Ala	Ala	Glu			
	290					295					300				

(2) INFORMATION FOR SEQ ID NO:4923:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 305 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...305

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4923:

Glu	Val	Ile	Val	Met	Ile	Gln	Trp	Trp	Gln	Ile	Leu	Leu	Leu	Thr	Leu
1				5					10					15	
Tyr	Ser	Ala	Tyr	Gln	Ile	Cys	Asp	Glu	Leu	Thr	Ile	Val	Ser	Ser	Ala
			20					25					30		
Gly	Ser	Pro	Val	Phe	Ala	Gly	Phe	Ile	Thr	Gly	Leu	Ile	Met	Gly	Asp
		35				40						45			
Val	Thr	Thr	Gly	Leu	Leu	Ile	Gly	Gly	Asn	Leu	Gln	Leu	Phe	Val	Leu
	50					55					60				
Gly	Val	Gly	Thr	Phe	Gly	Gly	Ala	Ser	Arg	Ile	Asp	Ala	Thr	Ser	Gly
65					70					75					80
Ala	Val	Leu	Ala	Thr	Ala	Phe	Ser	Val	Ser	Gln	Gly	Ile	Asp	Ala	Pro
				85					90					95	
Leu	Ala	Ile	Thr	Thr	Ile	Ala	Val	Pro	Val	Ala	Ala	Leu	Leu	Thr	Tyr
			100					105					110		
Phe	Asp	Val	Leu	Gly	Arg	Met	Thr	Thr	Thr	Phe	Phe	Ala	His	Arg	Val
	115					120						125			
Asp	Ala	Ala	Ile	Glu	Arg	Phe	Asp	Tyr	Lys	Gly	Ile	Glu	Arg	Asn	Tyr
	130					135					140				
Leu	Leu	Gly	Ala	Ile	Pro	Trp	Ala	Leu	Ser	Arg	Ala	Leu	Pro	Val	Phe
145					150					155					160
Phe	Ala	Leu	Ala	Phe	Gly	Gly	Ala	Phe	Val	Gln	Ser	Val	Val	Asp	Phe
				165					170					175	
Val	Glu	Ala	Tyr	Lys	Trp	Val	Ala	Asp	Gly	Leu	Thr	Leu	Ala	Gly	Arg
			180					185					190		
Met	Leu	Pro	Gly	Leu	Gly	Phe	Ala	Ile	Leu	Leu	Arg	Tyr	Leu	Pro	Val
	195						200					205			
Lys	Arg	Asn	Leu	His	Tyr	Leu	Ala	Met	Gly	Phe	Gly	Leu	Thr	Ala	Met
	210					215					220				
Leu	Thr	Val	Leu	Tyr	Ser	Tyr	Val	Thr	Gly	Leu	Gly	Gly	Ala	Val	Ala
225					230					235					240
Gly	Ile	Val	Gly	Thr	Leu	Pro	Ala	Glu	Val	Ala	Glu	Lys	Ile	Gly	Phe
				245					250					255	
Val	Asn	Asn	Phe	Lys	Gly	Leu	Ser	Met	Ile	Gly	Ile	Ser	Ile	Val	Gly
		260						265					270		
Ile	Phe	Leu	Ala	Val	Leu	His	Phe	Lys	Asn	Ser	Gln	Lys	Val	Ala	Val
		275					280					285			
Ala	Ala	Pro	Ser	Thr	Pro	Ser	Glu	Ser	Gly	Glu	Ile	Glu	Asp	Asp	Glu
	290					295					300				
Phe															
305															

(2) INFORMATION FOR SEQ ID NO:4924:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

3811

His	Asn	Asp	Phe	Ser	Gln	Glu	His	Glu	Leu	Leu	Lys	Asp	Ile	Lys	Ile
50						55					60				
Gly	Asn	Thr	Leu	Phe	Lys	Lys	Gly	Glu	Leu	Pro	Ser	Asn	Phe	Asp	Ser
65					70					75					80
Val	Val	Lys	Val	Tyr	Phe	Glu	Ser	Val	Leu	Gly	Val	Ala	Phe	Ser	Ser
				85					90					95	
Gln	Ala	Met	Leu	Asp	Gly	Met	Glu	Thr	Phe	Phe	Ser	Glu	Arg	Ser	Tyr
			100					105					110		
Asn	Pro	Val	Ile	Glu	Tyr	Met	Glu	Lys	Ala	Ala	Glu	Lys	Trp	Asp	Gly
		115					120					125			
Arg	Lys	Arg	Ile	Asp	Arg	Met	Leu	Gln	Val	Tyr	Leu	Gly	Ala	Glu	Asp
	130					135					140				
Ile	Pro	Leu	Val	Ser	Lys	Ile	Ala	Gln	Met	Trp	Leu	Val	Gly	Ala	Val
145					150					155					160
Ala	Lys	Val	Tyr	Asp	Pro	Tyr	Val	Lys	Phe	Asp	Tyr	Val	Leu	Asp	Leu
				165					170					175	
Val	Gly	Gly	Gln	Gly	Val	Gly	Lys	Thr	Ser	Leu	Leu	Gln	Lys	Leu	Gly
			180					185					190		
Gly	Glu	Trp	Tyr	Thr	Asp	Ala	Val	Thr	Asp	Phe	Ser	Asn	Lys	Asp	Asn
		195					200					205			
Tyr	Asp	Ile	Met	Leu	Lys	Ser	Leu	Ile	Val	Asn	Asp	Asp	Glu	Met	Val
	210					215					220				
Ala	Ser	Asn	Arg	Met	Ser	Phe	Ala	Glu	Thr	Lys	Ala	Phe	Ile	Ser	Lys
225					230					235					240
Thr	Ser	Leu	Arg	Tyr	Arg	Lys	Pro	Tyr	Met	Lys	Arg	Thr	Glu	Glu	Phe
				245					250					255	
Ala	Lys	Asn	Phe	Ile	Leu	Ala	Arg	Thr	Thr	Asn	Gln	Thr	Glu	Tyr	Leu
			260					265					270		
Lys	Asp	Lys	Thr	Gly	Glu	Arg	Arg	Phe	Leu	Pro	Val	Met	Ala	Asp	Ser
	275						280					285			
Lys	Arg	Gln	Lys	Lys	His	Pro	Met	Glu	Ile	Glu	Pro	Glu	Thr	Ile	Glu
	290					295					300				
Gln	Ile	Trp	Gly	Glu	Ala	Val	Thr	Ile	Tyr	Arg	Ala	Gly	Ala	Asp	Leu
305					310					315					320
Met	Phe	Asp	Glu	Asn	Thr	Glu	Asp	Glu	Leu	Asn	Ile	Tyr	Arg	Glu	Gln
				325					330					335	
Phe	Met	Tyr	Arg	Asp	Glu	Val	Glu	Leu	Gln	Val	Leu	Glu	Tyr	Leu	Asp
			340					345					350		
Met	Pro	Val	Pro	Glu	Asn	Trp	Gln	Asn	Trp	Ser	Ile	Gln	Gln	Gln	His
	355						360					365			
Gln	Tyr	Thr	Ser	Lys	Tyr	Phe	Asp	Asn	Ser	Ser	Asp	Phe	Asp	Pro	Gly
	370					375					380				
Ser	Lys	Lys	Leu	Asp	Lys	Val	Ser	Thr	Arg	Glu	Met	Met	Tyr	Asn	Leu
385					390					395					400
Phe	Met	Arg	Asn	Ser	Asn	Asp	Arg	Lys	Leu	Ser	Thr	Lys	Ile	Asn	Met
			405						410					415	
Ile	Met	Asp	Asn	His	Pro	Asp	Trp	Lys	Lys	Ser	Val	Phe	Arg	Ala	Gly
			420					425				430			
Gly	Lys	Ser	Thr	Lys	Gly	Phe	Val	Arg	Val	Lys	Asp	Ser	Glu	Lys	Thr
		435					440					445			
Asn	Arg														
450															

(2) INFORMATION FOR SEQ ID NO:4926:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 132 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...132

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4926:

```
Ile Lys Ile Val Met Ile Glu Ile Lys Phe Asn Pro Val Ile Leu Asn
1      5      10      15
Asn Asn Ala Glu Thr Thr Pro Asn Lys Glu Met Thr Val Met Thr Gly
20      25      30
Ser Asn Thr Leu Asn Asp Leu Leu Thr Ala Gly Gly Ile Phe Ser Pro
35      40      45
Arg Phe Ile Cys Lys Ala Leu Thr Phe Asp Asn Ser Met Asn Asn Ser
50      55      60
Val Ala Ile Ile Ala Thr Ile Thr Pro Ala Asn Ile Ala Pro Val Pro
65      70      75      80
Val Leu Leu Asn Glu Arg Thr Pro Glu Met Phe Thr Ala Ser Phe Ala
85      90      95
Pro Ser Gly Thr Thr Glu Thr Val Phe Gly Ile Ile Thr Ile Lys Glu
100     105     110
Thr Asn Asp Ser Ile Asp Ala Ala Asn Gly Phe Ser Lys Ser Leu Phe
115     120     125
Leu Ala Lys Lys
130
```

(2) INFORMATION FOR SEQ ID NO:4927:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...66

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4927:

```
Thr Thr Val Val Asn Asn His Ile Leu Ile Leu Glu Val Glu Ser Gln
1      5      10      15
```

Phe	Phe	Val	Val	Gly	Glu	Asp	Thr	Glu	Lys	Gly	Ala	Thr	Arg	Thr	Glu
			20					25					30		
Asn	Gln	Phe	Asp	Thr	Phe	Phe	Asn	Gly	Leu	Val	Asn	Ser	Ser	Asp	Val
		35					40					45			
Ser	Leu	Trp	Asp	Phe	Leu	Gly	Phe	Ile	Glu	Glu	Gly	Ser	Ile	His	Ile
	50					55					60				
Gln	Gly														
65															

(2) INFORMATION FOR SEQ ID NO:4928:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 412 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...412

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4928:

Glu	Gly	Val	Val	Met	Lys	Val	Phe	Leu	Gln	Asn	Arg	Asp	Phe	Arg	Gln
1				5					10					15	
Leu	Thr	Ile	Asn	Gln	Trp	Ile	Ser	Thr	Leu	Gly	Asp	Thr	Ile	Phe	Tyr
			20					25					30		
Leu	Ala	Phe	Leu	Asn	Tyr	Val	Ala	Asp	Ala	Ser	Phe	Ala	Pro	Leu	Ala
		35					40					45			
Ile	Leu	Leu	Ile	Thr	Ile	Ser	Glu	Thr	Leu	Pro	Gln	Ile	Leu	Gln	Ile
	50					55					60				
Phe	Leu	Gly	Val	Leu	Ala	Asp	Phe	Gln	His	His	Arg	Val	Leu	Lys	Tyr
65					70					75					80
Thr	Val	Ile	Ser	Phe	Ala	Lys	Phe	Leu	Leu	Tyr	Ser	Ile	Val	Ser	Leu
				85					90					95	
Ser	Leu	Ser	Gly	Gln	Ser	Phe	Ser	Leu	Leu	Val	Ala	Phe	Ile	Cys	
			100					105				110			
Leu	Leu	Asn	Leu	Leu	Ser	Asp	Thr	Leu	Ser	Tyr	Phe	Ser	Gly	Ala	Met
		115					120					125			
Leu	Thr	Pro	Ile	Phe	Ile	Arg	Ile	Ile	Gly	Gln	Asp	His	Leu	Ala	Glu
	130					135					140				
Ala	Ile	Gly	Phe	Lys	Gln	Ser	Thr	Val	Ser	Leu	Val	Lys	Thr	Ile	Ser
145					150					155				160	
Asn	Ile	Leu	Gly	Gly	Val	Leu	Leu	Gly	Ile	Leu	Ser	Ile	Gln	Phe	Ile
			165					170					175		
Ser	Leu	Leu	Asn	Ala	Leu	Thr	Phe	Leu	Ile	Ala	Phe	Leu	Gly	Ile	Leu
			180					185					190		
Phe	Ile	Lys	Thr	Asp	Leu	Leu	Lys	Val	Glu	Lys	Thr	Ile	Ser	Tyr	Gln
	195					200						205			
Glu	Gly	Leu	Ser	Val	Lys	Ser	Phe	Cys	Gln	His	Leu	Leu	Gln	Ser	Ser

210		215		220	
Lys	Leu	Ile	Trp	Asn	Met
225		230		235	240
Ser	Thr	Ser	Gln	Ala	Val
		245		250	255
Phe	Leu	Arg	Asn	Gln	Pro
		260		265	270
Ala	Leu	Leu	Ser	Thr	Phe
		275		280	285
Val	Ser	Gly	Tyr	Leu	Gln
290		295		300	
Ala	Ser	Leu	Val	Ile	Gln
305		310		315	320
Arg	Phe	Asp	Trp	Ile	Leu
		325		330	335
Gly	Val	Leu	Ser	Pro	Arg
		340		345	350
Glu	Glu	Ser	Met	Gly	Ala
		355		360	365
Val	Leu	Pro	Ser	Leu	Phe
370		375		380	
Phe	Gly	Thr	Leu	Ala	Val
385		390		395	400
Ala	Phe	Val	Met	Leu	Leu
		405		410	

(2) INFORMATION FOR SEQ ID NO:4929:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 106 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...106

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4929:

Pro	Ser	Ser	Val	Arg	Asn	Ala	Ala	Ile	Pro	Ser	Leu	Ile	Ile	Ser	Ser
1			5					10				15			
Ser	Ser	Ala	Thr	Lys	Met	Phe	Ile	Ser	Leu	Pro	Phe	Tyr	Tyr	Gln	Asn
		20						25				30			
Ser	Ile	His	Leu	Phe	Pro	Ile	Cys	Tyr	Leu	Lys	Ile	Ser	Tyr	Gln	Pro
		35					40					45			
Ile	Ile	Tyr	Asp	Asn	Gly	Met	Asp	Phe	Ile	Tyr	Pro	Leu	Leu	Phe	Val
		50				55				60					
Asn	Asn	Asn	Val	Asn	Thr	Arg	Lys	Ser	Phe	Ile	Leu	Gln	Leu	Ile	Leu
65			70					75					80		
Phe	Glu	Asn	Leu	Phe	Lys	Pro	Arg	Gln	Leu	Tyr	Leu	Gln	Ser	Lys	Asn

	85	90	95
Ser Val Leu Ser Asn Leu Arg Leu Ala Ala			
	100	105	

(2) INFORMATION FOR SEQ ID NO:4930:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4930:

Leu	His	Ser	Val	Val	Lys	Ser	Leu	Pro	Ala	Gln	Thr	Ile	Gln	Ile	Gly
1				5				10						15	
Thr	Leu	Gly	Val	Asp	Phe	Ser	Arg	Leu	Ile	Pro	Gly	Ile	Leu	Ile	Ile
			20					25					30		
Ser	Met	Asn	Ser	Gly	Ala	Tyr	Val	Ser	Glu	Thr	Val	Arg	Ala	Gly	Ile
		35					40					45			
Asn	Ala	Val	Pro	Lys	Gly	Gln	Leu	Glu	Ala	Ala	Tyr	Ser	Leu	Gly	Ile
		50				55					60				
Arg	Pro	Lys	Asn	Ala	Met	Arg	Tyr	Val	Ile	Leu	Pro	Gln	Ala	Val	Lys
65					70					75					80
Asn	Ile	Leu	Pro	Ala	Leu	Gly	Asn	Glu	Phe	Ile	Thr	Ile	Ile	Lys	Asp
			85						90					95	
Ser	Ser	Leu	Leu	Ser	Ala	Ile	Gly	Val	Met	Glu	Leu	Trp	Asn	Gly	Ala
		100						105					110		
Thr	Thr	Val	Ser	Thr	Thr	Thr	Tyr	Leu	Pro	Leu	Thr	Pro	Leu	Leu	Phe
		115					120					125			
Ala	Ala	Phe	Tyr	Tyr	Leu	Ile	Met	Thr	Ser	Ile	Leu	Thr	Val	Ala	Leu
		130				135					140				
Lys	Ala	Phe	Glu	Lys	His	Met	Gly	Gln	Gly	Asp	Lys	Lys			
145					150					155					

(2) INFORMATION FOR SEQ ID NO:4931:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...68

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4931:

```
Ile Arg Ser Val Thr Ser Met Thr Arg Phe Ile Ser Cys Ser Ile Asn
1           5           10           15
Met Ile Val Ile Leu Asn Ser Ser Leu Ile Arg Arg Ile Asn Ser Val
          20           25           30
Asn Ser Ala Val Ser Cys Gly Phe Ile Pro Ala Ala Gly Ser Ser Lys
          35           40           45
Lys Arg Ile Leu Gly Ser Val Ala Arg Ala Arg Thr Ile Ser Lys Arg
          50           55           60
Arg Cys Cys Pro
65
```

(2) INFORMATION FOR SEQ ID NO:4932:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 82 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...82

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4932:

```
Thr Val Ser Val Gly Arg Met Thr Ala Pro Pro Phe Ser Asn Ser Cys
1           5           10           15
Leu Ile Leu Ser Ile Ile Asn His Asp His Pro Ile Leu Thr Lys Leu
          20           25           30
Val Phe Glu Cys Ser Asn Phe Phe Arg Lys Met Phe Ser Lys Lys
          35           40           45
Phe Gly Asn Thr Leu Thr Leu Leu Val Ser Asn Phe Lys Val Asn Leu
          50           55           60
Thr Thr Ile Leu Glu Ile Val Phe Cys Ile Phe Arg Asn Ser Thr Val
          65           70           75           80
Asn Ser
```

(2) INFORMATION FOR SEQ ID NO:4933:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...72

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4933:

Asn	Ile	Ser	Val	Lys	Ile	Arg	Ile	Met	Lys	Lys	Lys	Arg	Val	Ser	Arg
1				5					10					15	
Met	Lys	Lys	Asn	Arg	Gly	Ile	Gln	Lys	Leu	Ala	Ile	Leu	Val	Leu	Leu
			20					25					30		
Gly	Val	Phe	Met	Phe	Ser	Asn	Thr	Ile	Pro	Tyr	Gln	Gln	Phe	Ile	Gln
		35				40					45				
Lys	Asn	Arg	Gln	Leu	Glu	Ile	Arg	Val	Gln	Ser	Gln	Lys	Lys	Ser	Asn
	50					55					60				
Gly	Leu	Asp	Val	Gly	Lys	Ala	Asp								
65					70										

(2) INFORMATION FOR SEQ ID NO:4934:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 323 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...323

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4934:

Gly	Tyr	Asp	Leu	Cys	Ala	Thr	Ile	Leu	Arg	Tyr	Val	Ala	Pro	Asp	Lys
1				5				10						15	
Ala	Gly	Asn	Phe	Ala	Asn	Val	Ile	Leu	Gly	Phe	Asp	Asp	Phe	Asp	Ser
			20					25					30		
Tyr	Val	Gly	Asn	Ser	Pro	Lys	His	Gly	Ala	Ser	Val	Gly	Pro	Val	Ala
		35				40						45			
Gly	Arg	Ile	Ala	Gly	Ala	Thr	Phe	Glu	Leu	Asn	Gly	Lys	Thr	Tyr	Asp
	50					55					60				
Leu	Glu	Val	Asn	Asn	Ala	Ser	Asn	Cys	Asn	His	Ser	Gly	Ser	Thr	Gly
65				70					75					80	
Trp	Asp	Ser	Ser	Leu	Phe	Glu	Val	Glu	Glu	Val	Ser	Asp	His	Gly	Leu

				85					90					95					
Thr	Leu	Tyr	Thr	Glu	Arg	Thr	Asp	Gly	Thr	Gly	Gly	Phe	Pro	Gly	Asn				
			100					105					110						
Leu	Lys	Ile	Trp	Ile	Ser	Tyr	His	Leu	Glu	Glu	Thr	Gly	Ala	Tyr	Glu				
		115					120					125							
Ile	Ser	Tyr	Lys	Val	Thr	Thr	Asp	Gln	Asp	Thr	Leu	Val	Asn	Pro	Thr				
	130						135				140								
Asn	His	Ser	Tyr	Phe	Asn	Leu	Ser	Gly	Asp	Phe	Thr	Gln	Thr	Ile	Asp				
145					150					155					160				
Arg	His	Val	Phe	Gln	Leu	Asn	Thr	Glu	Gly	Ile	Tyr	Ser	Ile	Ala	Pro				
			165						170					175					
Asp	Gly	Val	Pro	Ala	Lys	Thr	Pro	Glu	Ala	Asn	Arg	Asp	Val	Val	Lys				
		180						185					190						
His	Val	Tyr	Asn	Gly	Thr	Leu	Leu	Lys	Asp	Ile	Phe	Ala	Glu	Glu	Asp				
	195						200				205								
Glu	Gln	Ile	Gln	Leu	Ala	Ser	Gly	Leu	Asp	His	Pro	Phe	Ala	Leu	Pro				
	210						215				220								
Ala	Gly	His	Asp	Asn	Ala	Gly	Phe	Leu	Tyr	Asp	Gln	Asn	Ser	Gly	Arg				
225					230					235					240				
Phe	Leu	Leu	Phe	Lys	Thr	Glu	Ala	Pro	Cys	Phe	Val	Val	Tyr	Thr	Ala				
			245						250					255					
Asn	Phe	Val	Asp	Glu	Ser	Val	Ile	Ile	Gly	Gly	Gln	Pro	Met	Leu	Gln				
		260						265						270					
His	Asn	Gly	Ile	Ala	Leu	Glu	Ala	Gln	Ala	Leu	Pro	Asp	Ala	Ile	His				
	275						280						285						
Ser	Asp	Leu	Lys	Gly	Gln	Val	Ile	Leu	Lys	Ala	Gly	Gln	Thr	Phe	Thr				
	290						295				300								
Ser	Lys	Thr	Arg	Tyr	Glu	Leu	Val	Val	Lys	Ser	Ser	Arg	His	Arg	Gly				
305					310					315					320				
Ile	Leu	Asn																	

(2) INFORMATION FOR SEQ ID NO:4935:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 74 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...74

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4935:

Ile	Phe	Pro	Val	Gln	Met	Phe	Gln	Val	Asn	Leu	Arg	Leu	Pro	Met	Ile
1			5					10					15		
Leu	Arg	Gln	Gln	Thr	Gly	Phe	Trp	Gln	Lys	Cys	Leu	Leu	Thr	Ser	Pro
		20						25				30			
Asn	Leu	Leu	Glu	Leu	Asn	Cys	His	Leu	Ile	Leu	Ile	Leu	Phe	Thr	Leu

	35		40		45
Ile	Lys	Arg	Gln	Leu	Phe
	50		55		60
Ala	Leu	Thr	Leu	Ser	Glu
65			70		

(2) INFORMATION FOR SEQ ID NO:4936:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...80
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4936:

Lys	Gln	Pro	Val	Val	Lys	Arg	Asp	Lys	Met	Ala	Lys	Ser	Asn	Phe	Glu
1			5					10					15		
Lys	Val	Glu	Ser	Val	Val	Gly	Trp	Val	Arg	Asp	Lys	Lys	Ile	Thr	Gly
		20				25						30			
Tyr	Arg	Ile	Ser	Lys	Glu	Thr	Asn	Ala	Arg	Glu	Met	Ser	Ile	Ile	Ala
	35					40					45				
Leu	Ala	Gln	Gly	Arg	Ala	Lys	Val	Lys	Asn	Ile	Ser	Phe	Glu	Thr	Ala
	50					55				60					
Leu	Gly	Leu	Ile	Asp	Phe	Tyr	Glu	Lys	Asn	Tyr	Glu	Lys	Phe	Glu	Asp
65				70				75						80	

(2) INFORMATION FOR SEQ ID NO:4937:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 119 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...119
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4937:

His	Lys	Pro	Val	Phe	Leu	Ile	Asn	Ser	Cys	Leu	Gly	Leu	Phe	Ser	Ala
1				5					10					15	
Thr	Tyr	Ser	Arg	Arg	His	Pro	Phe	Ser	Arg	Ser	Tyr	Gly	Val	Asn	Leu
			20					25					30		
Pro	Ser	Ser	Leu	Thr	Ala	Ile	Leu	Pro	Met	Val	Leu	Gly	Phe	Ser	Pro
		35					40					45			
His	Leu	Pro	Val	Ser	Val	Cys	Gly	Thr	Gly	Thr	Glu	Leu	Leu	Asp	Arg
	50					55					60				
Asp	Phe	Ser	Trp	Gln	His	Glu	Ile	Arg	Tyr	Phe	Gly	Ser	Lys	Leu	Pro
65					70					75					80
His	His	Tyr	Thr	Pro	Asp	Leu	Thr	Lys	Asp	Gly	Phe	Ser	Tyr	Leu	Ser
				85					90					95	
Ser	Ser	Val	Leu	Arg	Arg	Thr	Ser	Asn	Asn	Val	Arg	Ile	Ser	Tyr	Pro
			100					105					110		
Pro	Ala	Ser	Ser	His	Phe	Ser									
			115												

(2) INFORMATION FOR SEQ ID NO:4938:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 260 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...260

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4938:

Leu	Phe	Thr	Val	Glu	Leu	Arg	Lys	Met	Gln	Lys	Thr	Ile	Ser	Arg	Met
1				5					10					15	
Val	Val	Arg	Phe	Thr	Leu	Lys	Leu	Asp	Thr	Ser	Lys	Val	Lys	Val	Phe
			20					25					30		
Pro	Asn	Phe	Leu	Glu	Asn	Ile	Phe	Leu	Lys	Lys	Lys	Phe	Glu	His	Ser
		35					40					45			
Lys	Thr	Asn	Leu	Val	Lys	Ile	Gly	Trp	Ser	Trp	Leu	Met	Met	Asp	Arg
	50					55					60				
Ile	Arg	Gln	Glu	Leu	Glu	Lys	Gly	Gly	Ala	Val	Ile	Leu	Pro	Thr	Glu
65					70					75					80
Thr	Val	Tyr	Gly	Leu	Phe	Ala	Lys	Ala	Leu	Asp	Glu	Lys	Ala	Val	Asp
				85					90					95	
His	Val	Tyr	Gln	Leu	Lys	Arg	Arg	Pro	Arg	Asp	Lys	Ala	Leu	Asn	Leu
			100					105					110		
Asn	Val	Ala	Ser	Leu	Glu	Asp	Ile	Leu	His	Phe	Ser	Lys	Asn	Gln	Pro
		115					120					125			
Ala	Tyr	Leu	Gln	Lys	Leu	Val	Glu	Thr	Phe	Leu	Pro	Gly	Pro	Leu	Thr
	130					135					140				
Ile	Ile	Leu	Glu	Ala	Asn	Asp	Arg	Val	Pro	Tyr	Trp	Val	Asn	Ser	Asp
145					150					155					160

Leu	Ala	Thr	Ile	Gly	Phe	Arg	Met	Pro	Ser	His	Pro	Ile	Thr	Leu	Asp
				165					170					175	
Leu	Ile	Arg	Glu	Thr	Gly	Pro	Leu	Ile	Gly	Pro	Ser	Ala	Asn	Ile	Ser
			180					185					190		
Gly	Gln	Ala	Ser	Gly	Val	Thr	Phe	Glu	Gln	Ile	Leu	Lys	Asp	Phe	Asp
		195					200					205			
Gln	Glu	Val	Leu	Gly	Leu	Glu	Asp	Asp	Ala	Phe	Leu	Thr	Gly	Gln	Asp
	210					215					220				
Ser	Thr	Ile	Val	Asp	Leu	Ser	Gly	Asp	Lys	Val	Lys	Ile	Leu	Arg	Gln
225					230					235					240
Gly	Ala	Ile	Lys	Arg	Glu	Asp	Ile	Leu	Ala	Arg	Leu	Pro	Glu	Ile	Ser
				245					250					255	
Phe	Glu	Glu	Ala												
			260												

(2) INFORMATION FOR SEQ ID NO:4939:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 98 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...98
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4939:

Ala	Leu	Asp	Leu	Thr	Asn	Val	Gln	Leu	Tyr	Tyr	His	Ile	Ile	Ile	Pro
1				5					10					15	
Gln	Val	Leu	Arg	Arg	Leu	Leu	Pro	Gln	Ala	Ile	Asn	Leu	Val	Thr	Arg
			20					25					30		
Met	Ile	Lys	Thr	Thr	Ser	Leu	Val	Val	Leu	Ile	Gly	Val	Val	Glu	Val
		35				40						45			
Thr	Lys	Val	Gly	Gln	Gln	Ile	Ile	Asp	Ser	Asn	Arg	Leu	Thr	Ile	Pro
	50					55					60				
Thr	Ala	Ser	Phe	Trp	Ile	Tyr	Gly	Thr	Ile	Leu	Val	Leu	Tyr	Phe	Ala
65					70					75					80
Val	Cys	Tyr	Pro	Ile	Ser	Lys	Leu	Ser	Thr	His	Leu	Glu	Lys	His	Trp
				85					90					95	
Arg	Asn														

(2) INFORMATION FOR SEQ ID NO:4940:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 103 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...103
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4940:

Val	Cys	Thr	Val	Lys	Glu	Arg	Ile	Met	Pro	Val	Arg	Lys	Leu	Gln	Ser
1				5					10					15	
Tyr	Glu	Val	Asp	Tyr	Gln	Glu	Glu	Leu	Asn	Gln	Gln	Leu	Pro	His	Tyr
			20					25					30		
Gln	Ala	Tyr	Thr	Pro	Glu	Ala	Gln	Ser	Asp	Ala	Asn	Leu	Lys	Glu	Ile
			35				40					45			
Leu	Phe	Phe	Ile	Asn	Ile	Ala	Val	Phe	Cys	Ile	Cys	Ile	Ala	Ile	Phe
	50					55				60					
Ser	Phe	Ile	Phe	Leu	Ala	Leu	Lys	Leu	Ser	Thr	Ala	Leu	Ala	Phe	Ala
65					70					75				80	
Ala	Ala	Ile	Gly	Phe	Ser	Leu	Leu	Val	Leu	Lys	Val	Gln	Arg	Ser	Ile
			85					90						95	
Ile	Lys	Arg	Lys	Arg	Arg	Arg									
			100												

(2) INFORMATION FOR SEQ ID NO:4941:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 105 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...105
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4941:

Glu	Arg	Thr	Val	Gly	Phe	Ile	Ala	Ala	Met	Cys	Ile	Asp	Asn	Cys	Leu
1				5					10					15	
Ala	Ser	Ala	Ser	Ser	Pro	Pro	Ser	Thr	Thr	Glu	Ile	Thr	Pro	Ile	Arg
			20					25					30		
Pro	Pro	Leu	Cys	Trp	Tyr	Ala	Pro	Lys	Cys	Cys	Ala	Ser	Val	Phe	Ser
			35				40					45			
Ile	Asn	Ala	Lys	Arg	Arg	Asn	Glu	Ile	Phe	Ser	Pro	Ile	Val	Ala	Val
	50					55				60					
Ala	Asp	Thr	Tyr	Ala	Ala	Ser	Arg	Val	Ser	Pro	Glu	Gly	Ile	Ile	Lys

65		70		75		80									
Ala	Arg	Ala	Ser	Ser	Leu	Leu	Ala	Gly	Phe	Pro	Ser	Ala	Met	Thr	Leu
		85							90					95	
Ala	Val	Val	Phe	Thr	Asn	Ser	Thr	Asn							
		100						105							

(2) INFORMATION FOR SEQ ID NO:4942:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 285 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...285

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4942:

Arg	Pro	Thr	Val	Phe	Ala	Gly	Val	Ile	Leu	His	Val	Met	Leu	Gly	Ser
1				5				10					15		
Thr	Tyr	Ala	Trp	Ser	Val	Tyr	Arg	Asn	Pro	Ile	Ile	Glu	Lys	Thr	Gly
		20						25					30		
Trp	Asp	Gln	Ala	Ser	Val	Ala	Phe	Ala	Phe	Ser	Leu	Ala	Ile	Phe	Cys
		35					40					45			
Leu	Gly	Leu	Ser	Ala	Ala	Phe	Met	Gly	Arg	Leu	Val	Glu	Lys	Phe	Gly
	50					55				60					
Pro	Lys	Val	Met	Gly	Ser	Leu	Ser	Ala	Phe	Leu	Tyr	Ala	Gly	Gly	Asn
65					70				75						80
Ile	Leu	Thr	Gly	Phe	Ala	Ile	Asp	Arg	Gln	Glu	Leu	Trp	Leu	Leu	Tyr
			85					90					95		
Leu	Ala	Tyr	Gly	Ile	Leu	Gly	Gly	Leu	Gly	Leu	Gly	Ala	Gly	Tyr	Ile
		100					105						110		
Thr	Pro	Val	Ser	Thr	Ile	Ile	Lys	Trp	Phe	Pro	Asp	Lys	Arg	Gly	Leu
		115					120					125			
Ala	Thr	Gly	Leu	Ala	Ile	Met	Gly	Phe	Gly	Phe	Ala	Ser	Leu	Leu	Thr
	130					135					140				
Ser	Pro	Ile	Ala	Gln	His	Leu	Ile	Ala	Gly	Val	Trp	Ile	Val	Glu	Thr
145					150					155					160
Phe	Tyr	Ile	Leu	Gly	Ala	Ser	Tyr	Phe	Ile	Ile	Met	Leu	Leu	Ala	Ser
			165						170					175	
Gln	Phe	Ile	Lys	Arg	Pro	Asn	Glu	Gln	Glu	Leu	Ala	Ile	Leu	Ser	Ser
		180					185					190			
Ser	Gly	Lys	Glu	Lys	Thr	Ala	Ser	Leu	Thr	Gln	Gly	Met	Ala	Ala	Asn
		195					200					205			
Gln	Ala	Leu	Lys	Ser	Asn	Arg	Phe	Tyr	Met	Leu	Trp	Ile	Ile	Phe	Phe
	210					215					220				
Ile	Asn	Ile	Xaa	Cys	Gly	Leu	Gly	Leu	Ile	Ser	Ala	Ala	Ser	Pro	Met
225					230					235					240
Ala	Gln	Glu	Met	Ala	Gly	Leu	Ser	Thr	Ser	His	Ala	Ala	Val	Met	Val

				245					250					255					
Gly	Val	Leu	Gly	Ile	Phe	Asn	Gly	Phe	Gly	Arg	Leu	Leu	Trp	Ala	Ser				
			260					265					270						
Leu	Ser	Asp	Tyr	Ile	Gly	Pro	Pro	Leu	Thr	Phe	Asn	Ile							
		275				280						285							

(2) INFORMATION FOR SEQ ID NO:4943:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...85
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4943:

Phe	Leu	Ala	Val	Asn	Leu	Pro	Leu	Tyr	Thr	Phe	Leu	Ile	Ser	Pro	Val				
1				5				10				15							
Ser	Arg	Asn	Pro	Val	Leu	Ser	His	Leu	Val	His	Phe	Leu	Gly	Ser	Asn				
		20					25					30							
Leu	Glu	Phe	Asn	Arg	Pro	Phe	Trp	Ser	Ile	Asn	Ser	Arg	Met	Asp	Arg				
	35					40						45							
Leu	Ile	Thr	Ile	Gly	Leu	Ala	Val	Gly	Asn	Ile	Val	Phe	Glu	Ala	Thr				
	50				55					60									
Trp	His	Arg	Phe	Pro	Lys	Phe	Met	His	Val	Thr	Lys	His	Gly	Ile	Asn				
65				70				75					80						
Ile	Thr	Leu	Gly	Ile															
				85															

(2) INFORMATION FOR SEQ ID NO:4944:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 642 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...642

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4944:

Lys	Ala	Ala	Val	Leu	Ala	Lys	Ile	Gln	Glu	Gln	Gly	Lys	Leu	Thr	Lys	1	5	10	15
Glu	Leu	Glu	Glu	Ala	Ile	Leu	Val	Ala	Glu	Lys	Leu	Ala	Asp	Val	Glu	20	25	30	
Glu	Leu	Tyr	Leu	Pro	Tyr	Lys	Glu	Lys	Arg	Arg	Thr	Lys	Ala	Thr	Ile	35	40	45	
Ala	Arg	Glu	Ala	Gly	Leu	Phe	Pro	Leu	Ala	Arg	Leu	Ile	Leu	Gln	Asn	50	55	60	
Ile	Val	Asp	Leu	Glu	Lys	Glu	Ala	Glu	Lys	Phe	Val	Cys	Glu	Gly	Phe	65	70	75	80
Ala	Thr	Gly	Lys	Glu	Ala	Leu	Thr	Gly	Ala	Val	Asp	Ile	Leu	Val	Glu	85	90	95	
Ala	Leu	Ser	Glu	Asp	Val	Thr	Leu	Arg	Ser	Met	Thr	Tyr	Gln	Glu	Val	100	105	110	
Leu	Arg	His	Ser	Lys	Leu	Thr	Ser	Gln	Ala	Lys	Asp	Glu	Ser	Leu	Asp	115	120	125	
Glu	Lys	Gln	Val	Phe	Gln	Ile	Tyr	Tyr	Asp	Phe	Ser	Glu	Thr	Val	Gly	130	135	140	
Thr	Met	Gln	Gly	Tyr	Arg	Thr	Leu	Ala	Leu	Asn	Arg	Gly	Glu	Lys	Leu	145	150	155	160
Gly	Val	Leu	Lys	Ile	Gly	Phe	Glu	His	Ala	Thr	Asp	Arg	Ile	Leu	Ala	165	170	175	
Phe	Phe	Ala	Thr	Arg	Phe	Lys	Val	Lys	Asn	Ala	Tyr	Ile	Asp	Glu	Val	180	185	190	
Val	Gln	Gln	Ser	Val	Lys	Lys	Lys	Val	Leu	Pro	Ala	Ile	Glu	Arg	Arg	195	200	205	
Ile	Arg	Thr	Glu	Leu	Thr	Glu	Lys	Ala	Glu	Glu	Gly	Ala	Ile	Gln	Leu	210	215	220	
Phe	Ser	Asp	Asn	Leu	Arg	Asn	Leu	Leu	Leu	Val	Ala	Pro	Leu	Lys	Gly	225	230	235	240
Arg	Val	Val	Leu	Gly	Phe	Asp	Pro	Ala	Phe	Arg	Thr	Gly	Ala	Lys	Leu	245	250	255	
Ala	Val	Val	Asp	Ala	Thr	Gly	Lys	Met	Leu	Thr	Thr	Gln	Val	Ile	Tyr	260	265	270	
Pro	Val	Lys	Pro	Ala	Ser	Ala	Arg	Gln	Ile	Glu	Glu	Ala	Lys	Lys	Asp	275	280	285	
Leu	Ala	Asp	Leu	Ile	Gly	Gln	Tyr	Gly	Val	Glu	Ile	Ile	Ala	Ile	Gly	290	295	300	
Asn	Gly	Thr	Ala	Ser	Arg	Glu	Ser	Glu	Ala	Phe	Val	Ala	Glu	Val	Leu	305	310	315	320
Lys	Asp	Phe	Pro	Glu	Val	Ser	Tyr	Val	Ile	Val	Asn	Glu	Ser	Gly	Ala	325	330	335	
Ser	Val	Tyr	Ser	Ala	Ser	Glu	Leu	Ala	Arg	Gln	Glu	Phe	Pro	Asp	Leu	340	345	350	
Thr	Val	Glu	Lys	Arg	Ser	Ala	Ile	Ser	Ile	Ala	Arg	Arg	Leu	Gln	Asp	355	360	365	
Pro	Leu	Ala	Glu	Leu	Val	Lys	Ile	Asp	Pro	Lys	Ser	Ile	Gly	Val	Gly	370	375	380	
Gln	Tyr	Gln	His	Asp	Val	Ser	Gln	Lys	Lys	Leu	Ser	Glu	Ser	Leu	Asp	385	390	395	400
Phe	Val	Val	Asp	Thr	Val	Val	Asn	Gln	Val	Gly	Val	Asn	Val	Asn	Thr	405	410	415	
Ala	Ser	Pro	Ala	Leu	Leu	Ser	His	Val	Ala	Gly	Leu	Asn	Lys	Thr	Ile	420	425	430	
Ser	Glu	Asn	Ile	Val	Lys	Tyr	Arg	Glu	Glu	Glu	Gly	Lys	Ile	Thr	Ser				

[illegible]

(i) SEQUENCE CHARACTERISTICS:

(ii) MOLECULE TYPE: protein

(vi) ORIGINAL SOURCE:

(ix) FEATURE:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4945:

(2) INFORMATION FOR SEQ ID NO:4946:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 64 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...64

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4946:

Gln	Arg	Ala	Val	Phe	Leu	Ile	Asn	Ser	Cys	Leu	Gly	Leu	Phe	Thr	Ala
1				5					10					15	
Ala	Asp	Phe	Lys	Ser	Ala	Pro	Leu	Leu	Pro	Lys	Leu	Arg	Gly	His	Phe
			20					25					30		
Ala	Glu	Phe	Leu	Asn	Glu	Ser	Ser	Leu	Ala	His	Leu	Arg	Leu	Leu	Ala
			35				40					45			
Ser	Thr	Thr	Cys	Val	Cys	Leu	Arg	Tyr	Gly	Tyr	Ser	Met	Phe	Lys	Arg
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:4947:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 65 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...65

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4947:

Gln	Arg	Ala	Val	Phe	Leu	Ile	Asn	Ser	Cys	Leu	Gly	Leu	Phe	Thr	Ala
1				5					10					15	
Ala	Asp	Phe	Lys	Ser	Ala	Pro	Leu	Leu	Pro	Lys	Leu	Arg	Gly	His	Phe
			20					25					30		
Ala	Asp	Val	Pro	Tyr	Ile	Glu	Ser	Ser	Leu	Ala	His	Leu	Ser	Tyr	Ser
		35					40					45			

Pro Arg Leu Pro Val Ser Val Cys Gly Thr Gly Arg Val Cys Leu Ile
 50 55 60
 Arg
 65

(2) INFORMATION FOR SEQ ID NO:4948:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 73 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...73

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4948:

Asn Phe Tyr Val Lys Ser Leu Gly Ile Asn Phe Tyr Leu Phe Phe Pro
 1 5 10 15
 Thr His Leu Ser Thr Ile Leu Leu Arg Lys His Gly Leu Ile Ser Lys
 20 25 30
 Arg Thr Ser Lys Arg Tyr Tyr His Val Ala Ile Pro Phe Thr Arg Leu
 35 40 45
 Phe Cys Pro Ala Leu Val Ser Ile Asp Tyr Ile Arg Gly Glu Thr Phe
 50 55 60
 Phe Gly Ser Leu Ser Thr Val Val Gly
 65 70

(2) INFORMATION FOR SEQ ID NO:4949:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 329 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...329

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4949:

Ile Glu Asp Leu Lys Asn Gln Thr Tyr Pro Lys Glu Asn Ile Glu Ile

1				5				10					15			
Leu	Phe	Ile	Asn	Ala	Met	Ser	Thr	Asp	Gly	Thr	Thr	Ala	Ile	Ile	Gln	
			20					25					30			
Gln	Phe	Ile	Lys	Glu	Asp	Thr	Glu	Phe	Asn	Ser	Ile	Arg	Leu	Tyr	Asn	
		35					40					45				
Asn	Pro	Lys	Lys	Asn	Gln	Ala	Ser	Gly	Phe	Asn	Leu	Gly	Val	Lys	His	
	50				55						60					
Ser	Val	Gly	Asp	Leu	Ile	Leu	Lys	Ile	Asp	Ala	His	Ser	Lys	Val	Thr	
65				70					75						80	
Glu	Ser	Phe	Val	Met	Asn	Asn	Val	Ala	Ile	Ile	Gln	Gln	Gly	Glu	Phe	
				85					90					95		
Val	Cys	Gly	Gly	Pro	Arg	Pro	Thr	Ile	Val	Glu	Gly	Lys	Gly	Lys	Trp	
		100						105					110			
Ala	Glu	Thr	Leu	His	Leu	Val	Glu	Glu	Asn	Met	Phe	Gly	Ser	Ser	Ile	
	115						120					125				
Ala	Asn	Tyr	Arg	Asn	Ser	Ser	Glu	Asp	Arg	Tyr	Val	Ser	Ser	Ile	Phe	
	130					135					140					
His	Gly	Met	Tyr	Lys	Arg	Glu	Val	Phe	Gln	Lys	Val	Gly	Leu	Val	Asn	
145				150					155						160	
Glu	Gln	Leu	Gly	Arg	Thr	Glu	Asp	Asn	Asp	Ile	His	Tyr	Arg	Ile	Arg	
			165					170					175			
Glu	His	Gly	Tyr	Lys	Ile	Arg	Tyr	Ser	Pro	Ser	Ile	Leu	Ser	Tyr	Gln	
	180							185					190			
Tyr	Ile	Arg	Pro	Thr	Phe	Lys	Lys	Met	Leu	His	Gln	Lys	Tyr	Ser	Asn	
	195						200					205				
Gly	Leu	Trp	Ile	Gly	Leu	Thr	Ser	His	Val	Gln	Phe	Lys	Cys	Leu	Ser	
	210				215					220						
Leu	Phe	His	Tyr	Val	Pro	Cys	Leu	Phe	Val	Leu	Ser	Leu	Val	Phe	Ser	
225				230					235						240	
Leu	Ala	Leu	Leu	Pro	Ile	Thr	Phe	Val	Phe	Ile	Thr	Leu	Leu	Leu	Gly	
			245					250						255		
Ala	Tyr	Phe	Leu	Leu	Leu	Ser	Leu	Leu	Thr	Leu	Leu	Thr	Leu	Leu	Lys	
	260						265					270				
His	Lys	Asn	Gly	Phe	Leu	Ile	Val	Met	Pro	Phe	Leu	Leu	Phe	Ser	Ile	
	275						280					285				
His	Phe	Ala	Tyr	Gly	Leu	Gly	Thr	Ile	Val	Gly	Leu	Ile	Arg	Gly	Phe	
	290				295					300						
Lys	Trp	Lys	Lys	Glu	Tyr	Lys	Arg	Thr	Ile	Ile	Tyr	Leu	Asp	Lys	Ile	
305				310					315						320	
Ser	Gln	Ile	Asn	Gln	Asn	Met	Leu	Gln								
				325												

(2) INFORMATION FOR SEQ ID NO:4950:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 225 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...225

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4950:

Glu	Tyr	Tyr	Val	Met	Leu	Ser	Lys	Glu	Asp	Tyr	Thr	Glu	Glu	Ile	Gly
1				5					10					15	
Leu	Ile	Lys	Lys	Gln	Asn	Tyr	Val	Glu	Ala	Glu	Leu	Tyr	Pro	Ile	Val
			20					25					30		
Ala	Asp	Ile	Ile	Lys	Pro	Thr	Leu	Lys	Asp	Ser	Leu	Ser	Lys	Arg	Tyr
		35					40					45			
Val	Phe	Gly	Arg	Gln	Arg	Arg	Gly	Leu	Gly	Gln	Ile	Tyr	Tyr	Gly	Leu
	50					55					60				
Ser	Asn	Phe	Pro	Asp	Ile	Val	Ile	Leu	Asp	Lys	Thr	Tyr	Glu	Asn	Lys
65					70				75					80	
Ser	Arg	Lys	Ser	Ile	Lys	Ile	Glu	Glu	Trp	Lys	Lys	Leu	Arg	Gly	Cys
			85						90					95	
Val	Glu	Val	Lys	Asn	Leu	Asn	Tyr	Ser	Leu	Ile	Thr	Glu	Glu	Lys	Ile
			100					105					110		
Lys	Ser	Thr	Ile	Ser	Asn	Ser	Phe	Glu	His	Ile	Thr	Gly	Glu	Met	Glu
			115				120					125			
Gln	Leu	Thr	Gly	Glu	Met	Gly	Gln	Leu	Ile	Gly	Asp	Leu	Leu	Trp	Tyr
	130					135					140				
Lys	Lys	Val	Ile	Tyr	Thr	Asn	Gly	Ile	Glu	Trp	Arg	Phe	Leu	Ser	Leu
145						150				155				160	
Asp	Asp	Lys	Glu	Glu	Ile	Asp	Asn	Thr	Ile	Val	Glu	Val	Val	Asn	Lys
				165					170					175	
Arg	Ile	Glu	Thr	Glu	Glu	Ala	Gly	Asn	Ser	Phe	Asp	Trp	Trp	Lys	Asn
			180					185					190		
Ile	Lys	Asp	Leu	Ser	Phe	Asn	Tyr	Thr	Asp	Ile	Cys	Leu	Ser	Lys	Asp
		195					200					205			
Cys	Arg	Gln	Glu	Trp	Asn	Glu	Phe	Val	Lys	Arg	Val	Lys	Glu	Ile	Glu
	210					215					220				
Trp															
225															

(2) INFORMATION FOR SEQ ID NO:4951:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 376 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...376

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4951:

Gly	Arg	Asp	Phe	Arg	Ala	Phe	Phe	His	Ser	Arg	Val	Arg	Asn	Asp	Leu
1				5					10					15	
Lys	Tyr	Gly	Ile	Ile	Lys	Gly	Asn	Phe	Tyr	Arg	Lys	Glu	Lys	Ile	Met
			20					25						30	
Ser	Asn	Phe	Ala	Ile	Ile	Leu	Ala	Ala	Gly	Lys	Gly	Thr	Arg	Met	Lys
		35					40						45		
Ser	Asp	Leu	Pro	Lys	Val	Leu	His	Lys	Val	Ala	Gly	Ile	Ser	Met	Leu
	50					55					60				
Glu	His	Val	Phe	Arg	Ser	Val	Gly	Ala	Ile	Gln	Pro	Glu	Lys	Thr	Val
65					70					75					80
Thr	Val	Val	Gly	His	Lys	Ala	Glu	Leu	Val	Glu	Glu	Val	Leu	Ala	Gly
				85					90					95	
Gln	Thr	Glu	Phe	Val	Thr	Gln	Ser	Glu	Gln	Leu	Gly	Thr	Gly	His	Ala
			100					105					110		
Val	Met	Met	Thr	Glu	Pro	Ile	Leu	Glu	Gly	Val	Ser	Gly	His	Thr	Leu
		115					120					125			
Val	Ile	Ala	Gly	Asp	Thr	Pro	Leu	Ile	Thr	Gly	Glu	Ser	Leu	Lys	Asn
	130					135					140				
Leu	Ile	Asp	Phe	His	Ile	Asn	His	Lys	Asn	Val	Ala	Thr	Ile	Leu	Thr
145					150					155					160
Ala	Glu	Thr	Asp	Asn	Pro	Phe	Gly	Tyr	Gly	Arg	Ile	Val	Arg	Asn	Asp
			165						170					175	
Asn	Ala	Glu	Val	Leu	Arg	Ser	Leu	Leu	Ser	Arg	Arg	Met	Leu	Gln	Ile
			180					185					190		
Leu	Lys	Ser	Lys	Ser	Arg	Lys	Ser	Thr	Leu	Val	Thr	Tyr	Val	Phe	Asp
		195				200						205			
Asn	Glu	Arg	Leu	Phe	Glu	Ala	Leu	Lys	Asn	Ile	Asn	Thr	Asn	Asn	Ala
	210					215					220				
Gln	Gly	Glu	Tyr	Tyr	Ile	Thr	Asp	Val	Ile	Gly	Ile	Phe	Arg	Glu	Thr
225					230					235					240
Gly	Glu	Lys	Val	Gly	Ala	Tyr	Thr	Leu	Lys	Asp	Phe	Asp	Glu	Ser	Leu
			245						250					255	
Gly	Val	Asn	Asp	Arg	Val	Ala	Leu	Ala	Thr	Ala	Glu	Ser	Val	Met	Arg
			260					265					270		
Arg	Arg	Ile	Asn	His	Lys	His	Met	Val	Asn	Gly	Val	Ser	Phe	Val	Asn
		275					280					285			
Pro	Glu	Ala	Thr	Tyr	Ile	Asp	Ile	Asp	Val	Glu	Ile	Ala	Pro	Glu	Val
	290					295					300				
Gln	Ile	Glu	Ala	Asn	Val	Ile	Leu	Lys	Gly	Gln	Thr	Lys	Ile	Gly	Ala
305					310					315					320
Glu	Thr	Val	Leu	Thr	Asn	Gly	Thr	Tyr	Val	Val	Asp	Ser	Thr	Ile	Gly
			325						330					335	
Ala	Gly	Ala	Val	Ile	Thr	Asn	Ser	Met	Ile	Glu	Glu	Ser	Ser	Val	Ala
			340					345					350		
Asp	Gly	Val	Thr	Val	Gly	Pro	Tyr	Ala	His	Ile	Arg	Pro	Asn	Ser	Ser
		355					360					365			
Leu	Gly	Ala	Pro	Ser	Ser	Tyr	Trp								
	370					375									

(2) INFORMATION FOR SEQ ID NO:4952:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 78 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...78

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4952:

Tyr	Ser	Tyr	Val	Cys	Val	Val	Leu	Ile	Val	Thr	Ala	Phe	Leu	Met	Ile
1				5					10					15	
Glu	Ser	Ile	Leu	Glu	Ser	Ser	Ser	Gly	Gly	Tyr	Asn	Leu	Phe	Arg	Gly
			20					25					30		
Asn	Ser	Ser	Pro	Ala	Ile	Pro	Cys	Trp	Asn	Asp	Lys	Leu	Leu	Thr	Lys
			35				40					45			
Phe	Pro	Asn	Ser	Val	Glu	Glu	Val	Ile	Leu	Pro	Ser	Glu	Phe	Thr	Val
	50					55				60					
Leu	Ser	Ser	Lys	Asn	Cys	Arg	Thr	Leu	Leu	His	Ser	Val	Leu		
65					70				75						

(2) INFORMATION FOR SEQ ID NO:4953:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 495 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...495

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4953:

Lys	Glu	Tyr	Val	Leu	Lys	Glu	Leu	Asp	Gln	Asn	Gln	Ala	Pro	Ile	Tyr
1				5					10					15	
Glu	Ala	Leu	Val	Lys	Leu	Arg	Lys	Lys	Arg	Ile	Val	Pro	Phe	Asp	Val
			20					25					30		
Pro	Gly	His	Lys	Arg	Gly	Arg	Gly	Asn	Pro	Glu	Leu	Val	Glu	Leu	Leu
			35				40					45			
Gly	Glu	Lys	Cys	Val	Gly	Ile	Asp	Val	Asn	Ser	Met	Lys	Pro	Leu	Asp
	50					55				60					
Asn	Leu	Gly	His	Pro	Ile	Ser	Ile	Ile	Arg	Asp	Ala	Glu	Glu	Leu	Ala
65					70				75					80	
Ala	Asp	Ala	Phe	Gly	Ala	Ser	His	Ala	Phe	Leu	Met	Ile	Gly	Gly	Thr
			85					90					95		
Thr	Ser	Ser	Val	Gln	Thr	Met	Ile	Leu	Ala	Thr	Cys	Lys	Ala	Gly	Asp

				100						105				110		
Lys	Ile	Ile	Leu	Pro	Arg	Asn	Val	His	Lys	Ser	Ala	Ile	Asn	Ala	Leu	
		115					120					125				
Val	Leu	Cys	Gly	Ala	Ile	Pro	Ile	Tyr	Ile	Glu	Met	Ser	Val	Asp	Pro	
	130					135					140					
Lys	Ile	Gly	Ile	Ala	Leu	Gly	Leu	Glu	Asn	Asp	Arg	Val	Ala	Gln	Ala	
145					150					155					160	
Ile	Lys	Asp	His	Pro	Asp	Ala	Lys	Ala	Ile	Leu	Ile	Asn	Asn	Pro	Thr	
				165					170					175		
Tyr	Tyr	Gly	Ile	Cys	Ser	Asp	Leu	Lys	Gly	Leu	Thr	Glu	Met	Ala	His	
			180					185					190			
Glu	Ala	Gly	Met	Met	Val	Leu	Val	Asp	Glu	Ala	His	Gly	Ala	His	Leu	
		195					200					205				
His	Phe	Thr	Gly	Lys	Leu	Pro	Ile	Ser	Ala	Met	Asp	Ala	Gly	Ala	Asp	
	210					215					220					
Met	Ala	Ala	Val	Ser	Met	His	Lys	Ser	Gly	Gly	Ser	Leu	Thr	Gln	Ser	
225					230					235					240	
Ser	Leu	Leu	Leu	Ile	Gly	Glu	Gln	Met	Asn	Pro	Glu	Tyr	Val	Arg	Gln	
				245					250					255		
Ile	Ile	Asn	Leu	Thr	Gln	Ser	Thr	Ser	Ala	Ser	Tyr	Leu	Leu	Met	Ala	
			260					265					270			
Ser	Leu	Asp	Ile	Ser	Arg	Arg	Asn	Leu	Ala	Leu	Arg	Gly	Lys	Glu	Ser	
		275					280					285				
Phe	Glu	Glu	Val	Ile	Glu	Leu	Ser	Glu	Tyr	Ala	Arg	His	Glu	Ile	Asn	
	290					295				300						
Ala	Ile	Gly	Gly	Tyr	Tyr	Ala	Tyr	Ser	Lys	Glu	Leu	Ile	Asp	Gly	Val	
305					310				315						320	
Ser	Val	Cys	Asp	Phe	Asp	Val	Thr	Lys	Leu	Ser	Val	Tyr	Thr	Gln	Gly	
				325					330					335		
Ile	Gly	Leu	Thr	Gly	Ile	Glu	Val	Tyr	Asp	Leu	Leu	Arg	Asp	Glu	Tyr	
			340					345					350			
Asp	Ile	Gln	Ile	Glu	Phe	Gly	Asp	Ile	Gly	Asn	Ile	Leu	Ala	Tyr	Ile	
		355					360					365				
Ser	Ile	Gly	Asp	Arg	Ile	Gln	Asp	Ile	Glu	Arg	Leu	Val	Gly	Ala	Leu	
	370					375					380					
Ala	Asp	Ile	Lys	Arg	Leu	Tyr	Ser	Arg	Asp	Gly	Lys	Asp	Leu	Ile	Ala	
385					390				395						400	
Gly	Glu	Tyr	Ile	Gln	Pro	Glu	Leu	Val	Leu	Ser	Pro	Gln	Glu	Ala	Phe	
				405					410					415		
Tyr	Ser	Glu	Arg	Lys	Ser	Leu	Thr	Leu	Asp	Glu	Ser	Val	Gly	Gln	Val	
			420					425					430			
Cys	Gly	Glu	Phe	Val	Met	Cys	Tyr	Pro	Pro	Gly	Ile	Pro	Ile	Leu	Ala	
		435				</										

(i) SEQUENCE CHARACTERISTICS:

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...102
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4954:

```

Lys Thr Asp Phe Ala Arg Ile Lys Met Thr Leu Ser Asn Tyr Phe Tyr
1      5      10      15
Lys Val Lys Gln Gln Tyr Pro Leu Thr Glu Lys Gln Gln Glu Leu Tyr
20     25     30
Asp Ile Leu Gly Asp Val Asn Pro Glu Tyr Ala Leu Lys Tyr Met Thr
35     40     45
Ala Phe Leu Leu Lys Phe Leu Lys Lys Asp Gln Leu Met Gln Lys Cys
50     55     60
Arg Asp Ile Phe Val Asp Ser Leu Val Val Leu Gly Tyr Ile Val Gln
65     70     75     80
Asn Glu Asp Arg Lys Tyr Glu Leu Ala Ile Asp Phe Asp Lys Glu Arg
85     90     95
Leu Thr Phe Tyr Leu Ala
100

```

(2) INFORMATION FOR SEQ ID NO:4955:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 88 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...88
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4955:

```

Leu Tyr Asn Val Ile Thr Pro Ser Val Ile Val Leu Ala Asp Gln Asn
1      5      10      15
Lys Ala Asp Trp Ser Tyr Asp Glu Asn Thr Val Ile Asn Ile Tyr Asp
20     25     30
Asp Ala Asn Phe Glu Asp Gly Arg Leu His Met Thr Phe Glu Gln Phe
35     40     45
Phe Lys Leu Ala Gln Ile Ala Arg Glu Glu Gly Leu Glu Ile His Ser
50     55     60
Pro Phe Glu Arg Ala Gly Ala Thr Lys Ser Ala Arg Tyr Ile Ala Lys

```

65 Trp Ile Leu Arg Asn Lys Lys His
85

75

80

(2) INFORMATION FOR SEQ ID NO:4956:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 341 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...341

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4956:

Lys	Asn	Asn	Val	Thr	Phe	Ile	Ser	Ala	Asp	Ile	Phe	Arg	Tyr	Gln	Ile
1			5						10					15	
Tyr	Met	Lys	Gly	Arg	Gly	Met	Lys	Leu	Ser	His	Tyr	Leu	Ile	Gly	Leu
			20					25					30		
Leu	Leu	Leu	Leu	Val	Phe	Leu	Ser	Ile	Ser	Ile	Gly	Thr	Ser	Asp	Phe
			35				40					45			
Ser	Trp	Gly	Lys	Leu	Phe	Asp	Phe	Asp	Gln	Gln	Thr	Trp	Leu	Leu	Phe
	50					55					60				
Gln	Glu	Ser	Arg	Leu	Pro	Arg	Thr	Ile	Ser	Ile	Leu	Leu	Thr	Ala	Ser
65					70					75					80
Ser	Met	Ser	Met	Ala	Gly	Leu	Leu	Met	Gln	Thr	Ile	Thr	Gln	Asn	Gln
				85					90					95	
Phe	Ala	Ala	Pro	Ser	Thr	Val	Gly	Thr	Thr	Glu	Ala	Ala	Lys	Leu	Gly
			100					105					110		
Met	Val	Leu	Ser	Leu	Phe	Val	Phe	Pro	Ser	Ala	Ser	Leu	Thr	Gln	Lys
		115					120					125			
Met	Leu	Phe	Ala	Phe	Val	Ser	Ser	Ile	Val	Phe	Thr	Leu	Phe	Phe	Leu
	130					135					140				
Ala	Phe	Met	Thr	Ile	Phe	Thr	Val	Lys	Glu	Arg	Trp	Met	Leu	Pro	Leu
145					150					155					160
Ile	Gly	Ile	Ile	Tyr	Ser	Gly	Ile	Ile	Gly	Ser	Val	Thr	Glu	Val	Ile
			165						170					175	
Ala	Tyr	Arg	Phe	Asn	Leu	Val	Gln	Ser	Met	Thr	Ala	Trp	Thr	Gln	Gly
			180					185					190		
Ser	Phe	Ser	Met	Ile	Gln	Thr	His	Gln	Tyr	Glu	Trp	Leu	Phe	Leu	Gly
		195				200						205			
Leu	Ile	Ile	Leu	Ile	Thr	Val	Trp	Lys	Leu	Ser	Gln	Thr	Phe	Thr	Ile
	210					215					220				
Met	Asn	Leu	Gly	Lys	Glu	Thr	Ser	Glu	Ser	Leu	Gly	Ile	Ser	Tyr	Ser
225					230					235					240
Leu	Leu	Glu	Lys	Leu	Ala	Leu	Phe	Leu	Val	Ala	Leu	Thr	Thr	Ser	Val
			245						250					255	
Thr	Met	Ile	Thr	Val	Gly	Gly	Leu	Pro	Phe	Leu	Gly	Val	Ile	Val	Pro

(2) INFORMATION FOR SEO ID NO:4957:

(A) LENGTH: 279 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Streptococcus pneumoniae*

(A) NAME/KEY: misc_feature
(B) LOCATION 1...279

3837

195					200					205						
Glu	Ile	Ala	Phe	Ser	Ser	Ala	Thr	Asp	Arg	Asp	Ile	Phe	Ile	Thr	Lys	
210					215					220						
Gln	Glu	Phe	Gly	Asp	Ile	Val	Gln	Glu	Glu	Gly	Leu	Arg	Ile	Thr	Met	
225					230					235					240	
Ser	Gly	Asn	Ile	Gln	Ser	Ser	Glu	Leu	Phe	Lys	Phe	Phe	Asn	Glu	Asn	
245					250					255						
Ser	Ile	Lys	Val	Val	Asp	Phe	Glu	Thr	Lys	Lys	Glu	Thr	Leu	Lys	Asp	
260					265					270						
Ile	Tyr	Leu	Asn	Arg	Ser	Lys										
275																

(2) INFORMATION FOR SEQ ID NO:4958:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 141 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4958:

Leu	Thr	Asn	Val	Asp	Phe	Gly	Gly	Met	Val	Met	Gln	Ile	Ser	Asp	Ala
1				5				10					15		
Glu	Trp	Gln	Val	Met	Lys	Ile	Ile	Trp	Met	Gln	Gly	Glu	Gln	Thr	Ser
			20					25					30		
Thr	Asp	Leu	Ile	Arg	Val	Leu	Ala	Glu	Arg	Phe	Asp	Trp	Ser	Lys	Ser
			35				40						45		
Thr	Ile	Gln	Thr	Leu	Leu	Ala	Arg	Leu	Val	Glu	Lys	Glu	Cys	Leu	Thr
	50					55					60				
Arg	Lys	Lys	Glu	Gly	Lys	Phe	Phe	Val	Tyr	Ser	Ala	Leu	Leu	Thr	Leu
65					70						75				80
Asp	Gln	Ser	Arg	Asp	Leu	Leu	Val	Gln	Asp	Ile	Lys	Asp	Lys	Val	Cys
				85					90					95	
Ser	Arg	Arg	Ile	Arg	Asn	Leu	Leu	Ala	Asp	Leu	Ile	Val	Glu	Cys	Glu
			100					105					110		
Phe	Thr	Gln	Thr	Asp	Leu	Glu	Asp	Leu	Glu	Ala	Val	Ile	Ser	Glu	Lys
			115				120						125		
Lys	Ser	Ser	Ala	Val	Thr	Glu	Val	Arg	Cys	Asn	Cys	Met			
			130				135					140			

(2) INFORMATION FOR SEQ ID NO:4959:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 87 amino acids
- (B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...87

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4959:

Lys	Glu	Asn	Val	Met	Ser	Glu	Arg	Arg	Ile	Ser	Glu	Lys	Ser	Leu	Glu
1				5					10					15	
Asn	Leu	Arg	Lys	Ser	Asn	Gln	Glu	Ser	Asn	Leu	Leu	Thr	Arg	Glu	Ala
			20					25					30		
Ile	Glu	Thr	Ala	Leu	Leu	Gln	Leu	Leu	Glu	Lys	Lys	Glu	Leu	Thr	Lys
		35					40					45			
Ile	Ser	Ile	Ser	Glu	Leu	Val	Lys	Arg	Ala	Gly	Val	Ser	Arg	Ala	Ala
	50					55					60				
Phe	Tyr	Arg	Asn	Tyr	Asp	Ser	Lys	Gly	Gly	Ile	Leu	Glu	Arg	Ser	Leu
65				70					75						80
Lys	Glu	Leu	Ser	Thr	Ile	Leu									
				85											

(2) INFORMATION FOR SEQ ID NO:4960:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 88 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...88

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4960:

Met	Lys	Asn	Val	Glu	Leu	Lys	Glu	Lys	Asn	Met	Thr	Phe	Glu	Glu	Ile
1				5					10					15	
Leu	Pro	Gly	Leu	Lys	Ala	Lys	Arg	Lys	Tyr	Val	Arg	Thr	Gly	Trp	Gly
			20					25					30		
Gly	Ala	Glu	Asn	Tyr	Val	Gln	Leu	Phe	Asp	Thr	Ile	Glu	Gln	Asn	Gly
		35					40					45			
Leu	Ala	Leu	Glu	Met	Thr	Pro	Tyr	Phe	Leu	Ile	Asn	Val	Ser	Gly	Glu
	50					55					60				
Gly	Glu	Gly	Phe	Ser	Met	Trp	Ser	Pro	Thr	Val	Cys	Asp	Val	Leu	Ala

65	70	75	80
Thr Asp Trp Val Glu Val His Asp			
85			

(2) INFORMATION FOR SEQ ID NO:4961:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 93 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...93

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4961:

Asn	Arg	Asp	Val	Thr	Ser	Thr	Asp	Ser	His	Ser	Phe	Ile	Ile	Ile	Asp
1			5					10					15		
Ser	Thr	Lys	Glu	Ile	Gln	Asp	Ile	Val	Val	Ile	Ile	Lys	Gly	Leu	Thr
		20					25					30			
Asp	Ser	His	Asp	Asn	Asp	Met	Ala	Asp	Ala	Phe	Ile	Leu	Thr	Thr	Leu
		35				40					45				
Ser	Lys	Val	Phe	Leu	Asn	Gln	His	Asp	Leu	Arg	Tyr	Asp	Phe	Thr	Val
	50				55			60							
Ile	Glu	Val	Thr	Leu	Leu	Leu	Asn	Gln	Thr	Arg	Gly	Thr	Glu	Gly	Thr
65				70				75					80		
Thr	Asp	Ile	Thr	Ala	Asp	Leu	Ser	Gly	His	Thr	Asp	Arg			
			85					90							

(2) INFORMATION FOR SEQ ID NO:4962:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 118 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...118

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4962:

Thr	Arg	Asp	Val	Asp	Leu	Met	Asn	Thr	Ile	Glu	Arg	Thr	Arg	Arg	Leu
1				5					10					15	
Val	Lys	Gly	Cys	Ala	Thr	His	Cys	Phe	Glu	Val	Ala	Asp	Arg	Thr	Asp
			20					25					30		
Glu	Val	Ser	Ser	Lys	His	Cys	Phe	Glu	Val	Val	Asp	Arg	Thr	Asp	Glu
		35					40					45			
Val	Ser	Ser	Lys	His	Cys	Phe	Glu	Val	Ala	Asp	Glu	Thr	Asp	Glu	Val
	50					55					60				
Ser	Ser	Lys	His	Val	Phe	Glu	Val	Val	Asp	Glu	Thr	Asp	Glu	Val	Ser
65					70					75					80
Ser	Lys	His	Val	Phe	Glu	Val	Val	Asp	Glu	Thr	Asp	Glu	Val	Ser	Ser
				85					90					95	
Lys	His	Val	Phe	Glu	Val	Val	Asp	Glu	Thr	Asp	Glu	Val	Ser	Asn	His
			100					105					110		
Thr	Tyr	Gly	Lys	Ala	Thr										
			115												

(2) INFORMATION FOR SEQ ID NO:4963:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 171 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...171

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4963:

Asn	Ser	Cys	Val	Lys	Ser	Leu	Gly	Ile	Asn	Phe	Tyr	Leu	Phe	Leu	Pro
1				5					10					15	
Thr	His	Leu	Ser	Thr	Ile	Leu	Leu	Arg	Lys	His	Gly	Leu	Ile	Ser	Lys
			20					25					30		
Ser	Thr	Ser	Lys	Gly	Tyr	Tyr	Gln	Val	Ala	Ile	Pro	Phe	Met	Arg	Leu
		35					40					45			
Phe	Cys	Leu	Val	Leu	Val	Ser	Ile	Asp	Tyr	Ile	Asn	Cys	Leu	Ser	Glu
	50					55					60				
Thr	Thr	Asp	Lys	Asn	Trp	His	Lys	Ser	Asp	Arg	Val	Phe	Val	Thr	Asn
65					70					75					80
Thr	Gly	Lys	Thr	Val	His	Ser	Ser	Ile	Leu	Ser	Lys	Ser	Leu	Gln	Arg
				85					90					95	
Ala	Asn	Glu	Arg	Leu	Lys	Lys	Pro	Ile	Pro	Lys	His	Leu	Ser	Pro	His
			100					105					110		
Ile	Phe	Arg	His	Thr	Thr	Ile	Ser	Ile	Leu	Ser	Glu	Asn	Lys	Ile	Pro
	115					120						125			
Leu	Lys	Thr	Ile	Thr	Asp	Arg	Val	Gly	His	Ser	Asp	Ser	Glu	Val	Thr
	130					135					140				
Thr	Ser	Ile	Tyr	Thr	His	Val	Thr	Lys	Asn	Met	Lys	Asp	Glu	Ala	Ile
145					150					155					160

Asn Val Leu Asp Lys Val Met Lys Lys Ile Phe
 165 170

(2) INFORMATION FOR SEQ ID NO:4964:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...100
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4964:

Gly	Xaa	Arg	Val	Leu	Phe	Tyr	Asn	Pro	Ala	Lys	Ser	Thr	Val	Asn	Glu
1			5					10					15		
Glu	Asp	Tyr	Leu	Thr	Val	Ile	Pro	His	Leu	Pro	Lys	Lys	Gly	Phe	Ser
		20					25					30			
Arg	Asp	Phe	Leu	Ala	Tyr	Phe	Ala	Leu	Phe	Leu	Lys	Asp	Thr	Ala	Glu
		35				40					45				
Val	Gly	Leu	Asp	Val	Leu	Met	Asp	Phe	Leu	Glu	Asp	Pro	Glu	Ala	Glu
	50				55					60					
Glu	Phe	Val	Met	Glu	Trp	Asn	Gln	Glu	Val	Leu	Glu	Glu	Gly	Lys	Val
65				70				75						80	
Gly	Leu	Glu	Glu	Gly	Glu	Phe	Thr	Leu	Ile	Arg	Asp	Thr	Arg	Ser	Trp
			85					90						95	
Leu	Glu	Val	Leu												
			100												

(2) INFORMATION FOR SEQ ID NO:4965:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 298 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4965:

Met	Glu	Ser	Val	Gly	Asp	Val	Leu	Lys	Arg	Gln	Pro	Ser	Arg	Phe	His
1				5					10					15	
Tyr	Gln	Asp	Leu	Val	Gln	Lys	Ile	Met	Lys	Asp	Pro	Asp	Val	Ala	Ala
			20					25					30		
Phe	Val	Gln	Glu	Ser	Leu	Asn	Gln	Asp	Glu	Leu	Asn	Arg	Ser	Ile	
			35				40					45			
Ser	Lys	Phe	Asn	Gln	Tyr	Ile	Thr	Glu	Arg	Asp	Lys	Phe	Leu	Arg	Gly
	50					55					60				
Asp	Thr	Asp	Tyr	Ile	Ala	Lys	Gly	Tyr	Lys	Pro	Ile	Leu	Val	Met	Asn
65					70					75					80
His	Gly	Tyr	Ala	Asp	Val	Ser	Tyr	Glu	Glu	Thr	Pro	Glu	Leu	Ile	Ala
				85						90				95	
Ala	Glu	Lys	Glu	Ala	Ala	Ile	Lys	Lys	Arg	Leu	Asn	Leu	Ile	Asn	Phe
			100					105					110		
Pro	Ser	Ser	Leu	Lys	Asn	Val	Ser	Phe	Leu	Asp	Val	Tyr	Arg	Asp	Asp
			115				120					125			
Val	Gln	Arg	Leu	Thr	Val	Leu	Lys	Arg	Met	Ile	Glu	Phe	Val	Asn	Asp
	130					135					140				
Tyr	Pro	Asn	Asn	Leu	Lys	Gly	Leu	Tyr	Leu	Tyr	Gly	Asp	Phe	Gly	Val
145					150					155					160
Gly	Lys	Ser	Phe	Met	Val	Ala	Ala	Leu	Ala	His	Asp	Leu	Ser	Glu	Lys
				165						170				175	
Arg	Gly	Val	Ser	Thr	Leu	Leu	His	Tyr	Pro	Ser	Phe	Val	Ile	Asp	
			180				185					190			
Val	Lys	Asn	Ala	Ile	Ser	Asp	Gly	Asn	Val	Lys	Thr	Leu	Val	Asp	Glu
		195					200					205			
Ile	Lys	Leu	Ser	Glu	Val	Leu	Ile	Leu	Asp	Asp	Ile	Gly	Ala	Glu	Gln
	210					215					220				
Ser	Thr	Thr	Trp	Val	Arg	Asp	Glu	Ile	Leu	Gln	Val	Ile	Leu	Gln	Tyr
225					230					235					240
Arg	Met	Gln	Glu	Asn	Leu	Pro	Thr	Phe	Phe	Thr	Ser	Asn	Phe	Asn	Phe
				245						250				255	
Glu	Asp	Leu	Glu	Lys	His	Phe	Ala	Lys	Gly	Lys	Asn	Gly	Asn	Asp	Glu
			260					265					270		
Thr	Trp	Glu	Ala	Arg	Arg	Val	Met	Glu	Arg	Ile	Arg	Tyr	Leu	Ala	Glu
		275				280						285			
Glu	Thr	Arg	Leu	Glu	Gly	Val	Asn	Arg	Arg						
	290					295									

(2) INFORMATION FOR SEQ ID NO:4966:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 202 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...202

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4966:

```
Glu Arg Gly Val Phe Leu Ala Val Asp Asn Glu Ile Lys Gly Leu Leu
1      5      10      15
Ala Leu Gln Asp Ile Pro Lys Glu Asn Ala Lys Leu Ala Ile Ser Gln
20      25      30
Leu Lys Lys Arg Gly Leu Arg Thr Val Met Leu Thr Gly Asp Asn Ala
35      40      45
Gly Val Ala Cys Ala Ile Ala Asp Gln Ile Gly Ile Glu Glu Val Ile
50      55      60
Ala Gly Val Leu Pro Glu Glu Lys Ala His Glu Ile His Lys Leu Gln
65      70      75      80
Gln Ser Gly Lys Val Ala Phe Val Gly Asp Gly Ile Asn Asp Ala Pro
85      90      95
Ala Leu Ser Val Ala Asp Val Gly Ile Ala Met Gly Ala Gly Thr Asp
100     105     110
Ile Ala Ile Glu Ser Ala Asp Leu Val Leu Thr Thr Asn Asn Leu Leu
115     120     125
Gly Val Val Arg Ala Phe Asp Met Ser Lys Lys Thr Phe His Arg Ile
130     135     140
Leu Leu Asn Leu Phe Trp Ala Phe Ile Tyr Asn Val Val Gly Ile Pro
145     150     155     160
Ile Ala Ala Gly Val Phe Ser Gly Val Gly Leu Ala Leu Asn Pro Glu
165     170     175
Leu Ala Gly Leu Ala Met Ala Phe Ser Ser Val Ser Val Leu Thr Ser
180     185     190
Ser Leu Leu Leu Asn Phe Ser Lys Ile Asp
195     200
```

(2) INFORMATION FOR SEQ ID NO:4967:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4967:

```
Ile Gly Gly Val Met Lys Asp Ser His Leu Leu Ala His His Ile Arg
1      5      10      15
Leu Leu Asn Gly Arg Ile Phe Gln Lys Leu Leu Ser Gln Asp Pro Glu
20      25      30
Ala Leu Tyr Arg Gly Glu Gln Gly Lys Ile Leu Ala Val Leu Trp Asn
35      40      45
```

```

Ser Glu Thr Gly Cys Ala Thr Ala Thr Asp Ile Ala Leu Ala Thr Gly
 50          55          60
Leu Ala Asn Asn Thr Leu Thr Thr Met Ile Lys Lys Leu Glu Glu Gln
65          70          75          80
Lys Leu Val Ile Val Ser Pro Cys Gly Lys Asp Lys Arg Lys Lys Tyr
          85          90          95
Leu Val Leu Thr Glu Leu Gly Lys Ser Gln Lys Glu Val Gly His Arg
          100          105          110
Val Ser Gln Lys Leu Asp Thr Ile Phe Tyr Lys Gly Phe Ser Glu Glu
          115          120          125
Glu Ile His Gln Phe Glu Gly Phe Gln Glu Arg Ile Leu Ala Asn Leu
          130          135          140
Lys Glu Lys Gly Asn Glu Val
145          150

```

(2) INFORMATION FOR SEQ ID NO:4968:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...66
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4968:

```

Leu Asp Phe Val Asn Gln Val Leu Cys Leu Phe Pro His Ile Ala Ile
1          5          10          15
Thr Ser Glu Asp Ser Phe Gly Gln Trp Thr Met Leu Gly Asp Leu Val
          20          25          30
Gly Leu Ile Phe Cys Leu Met Leu Val Leu Glu Asn Lys Phe Ser Val
          35          40          45
Ala Ser Lys Ala Thr Leu Phe Ser Lys Ala Gly Gln Ser Ser Leu Arg
          50          55          60
Asn Met
65

```

(2) INFORMATION FOR SEQ ID NO:4969:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4969:

Ala	Asp	Phe	Val	Ser	Phe	Ile	Asp	Asn	Leu	Lys	His	Cys	Phe	Glu	Gln
1				5					10					15	
Pro	Ala	Ala	Asn	Phe	Leu	Val	Cys	Ser	Leu	Ile	Phe	Ile	Glu	Tyr	Asp
			20					25					30		
Phe	Ser	Gly	Cys	Gln	Phe	Ser	Leu	Asp	Lys	Arg	Arg	Val	Gly	Lys	Arg
		35					40					45			
Val	Val	Leu	Pro	Arg	Pro	His	Thr	Tyr	Phe	Leu	Ala	Tyr	Arg	Asn	Cys
	50					55					60				
Asn	Arg	Gly	Arg	Leu	Thr	Cys	His	Arg	Ala	Glu					
65					70					75					

(2) INFORMATION FOR SEQ ID NO:4970:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 261 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...261

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4970:

Arg	Arg	Phe	Val	Met	Lys	Asn	Asn	Arg	Ile	Leu	Ala	Leu	Ser	Gly	Asn
1				5					10					15	
Asp	Ile	Phe	Ser	Gly	Gly	Gly	Leu	Ser	Ala	Asp	Leu	Ala	Thr	Tyr	Thr
			20					25					30		
Leu	Asn	Gly	Leu	His	Gly	Phe	Val	Ala	Val	Thr	Cys	Leu	Thr	Ala	Leu
		35				40					45				
Thr	Glu	Lys	Gly	Phe	Glu	Val	Phe	Pro	Thr	Asp	Asp	Thr	Ile	Phe	Gln
	50				55					60					
His	Glu	Leu	Asp	Ser	Leu	Arg	Asp	Val	Glu	Phe	Gly	Gly	Ile	Lys	Ile
65					70				75					80	
Gly	Leu	Leu	Pro	Thr	Val	Ser	Val	Ala	Glu	Lys	Ala	Leu	Asp	Phe	Ile
			85					90					95		
Lys	Gln	Arg	Pro	Gly	Val	Pro	Val	Val	Leu	Asp	Pro	Val	Leu	Val	Cys
			100					105					110		

Lys Glu Thr His Asp Val Ala Val Ser Glu Leu Cys Gln Glu Leu Ile

130

135

(2) INFORMATION FOR SEQ ID NO:4972:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 184 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...184

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4972:

Ile	Phe	Leu	Val	Arg	Asn	Arg	Cys	Tyr	Gln	Trp	Tyr	Arg	Leu	Val	Arg	1	5	10	15
Val	Ile	Met	Arg	Cys	Trp	Gly	Cys	Ser	Ser	Met	Arg	Arg	Met	Leu	Thr	20	25	30	
Ala	Lys	Leu	Gln	Asn	Arg	Ser	Gly	Val	Leu	Asn	Arg	Phe	Thr	Gly	Val	35	40	45	
Leu	Ser	Arg	Arg	Gln	Val	Asn	Ile	Glu	Ser	Ile	Ser	Val	Gly	Ala	Thr	50	55	60	
Glu	Asp	Pro	Asn	Val	Ser	Arg	Ile	Thr	Ile	Ile	Ile	Asp	Val	Ala	Ser	65	70	75	80
His	Asp	Glu	Val	Glu	Gln	Ile	Ile	Lys	Gln	Leu	Asn	Arg	Gln	Ile	Asp	85	90	95	
Val	Ile	Arg	Ile	Arg	Asp	Ile	Thr	Asp	Lys	Pro	His	Leu	Glu	Arg	Glu	100	105	110	
Val	Ile	Leu	Val	Lys	Met	Ser	Ala	Pro	Ala	Glu	Lys	Arg	Ala	Glu	Ile	115	120	125	
Leu	Ala	Ile	Ile	Gln	Pro	Phe	Arg	Ala	Thr	Val	Val	Asp	Val	Ala	Pro	130	135	140	
Ser	Ser	Ile	Thr	Ile	Gln	Met	Thr	Gly	Asn	Ala	Glu	Lys	Ser	Glu	Ala	145	150	155	160
Leu	Leu	Arg	Val	Ile	Arg	Pro	Tyr	Gly	Ile	Arg	Asn	Ile	Ala	Arg	Thr	165	170	175	
Gly	Ala	Thr	Gly	Phe	Thr	Arg	Asp									180			

(2) INFORMATION FOR SEQ ID NO:4973:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...74

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4973:

```

Asn Pro Leu Val Ala Pro Val Thr Pro Ala Gln Arg Ala Thr Pro Asn
1          5          10          15
Leu Ala Pro Met Tyr Pro His Ala Pro Ile Asn Gly Ala Pro Thr Pro
          20          25          30
Leu Ala Ala Gln Ile Ala Val Pro Asn Pro Gln Pro Pro Lys Ala Ala
          35          40          45
Pro Pro Pro Ser Lys Thr Leu Val Cys Gln Leu Phe Leu Pro Pro Ser
          50          55          60
Ile Leu Asp Asn Ile Val Ile Ser Ile Ser
65          70
  
```

(2) INFORMATION FOR SEQ ID NO:4974:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 232 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...232

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4974:

```

Gln Pro Leu Val Trp Leu Arg Ser Lys Gly Ile Leu Gln Gly Ile Ile
1          5          10          15
Cys Leu Arg Met Glu Pro Leu Pro Ser Lys Thr Ser Pro Val Ser Trp
          20          25          30
Leu Leu Arg Arg Leu Ile Tyr Lys Val Met Ser Glu Cys Leu Ile Leu
          35          40          45
Cys Gly Ser Arg Trp Lys Thr Ala His Ile Ala Ser Tyr Leu Thr Thr
          50          55          60
Gly Gln Val Thr Ala Leu Asp Leu Tyr Asp His Lys Leu Asp Leu Ile
65          70          75          80
Gln Glu Asn Ala Gln Arg Leu Gly Val Ala Asp Arg Val Gln Thr Gln
          85          90          95
Lys Leu Asp Ala Arg Lys Val His Glu Phe Phe Asp Gln Asp Ser Phe
          100          105          110
Asp Lys Ile Leu Val Asp Ala Pro Cys Ser Gly Ile Gly Leu Leu Arg
  
```


- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 670 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...670
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4976:

```

Ala Gln Leu Val Val Lys Thr Arg Trp Leu Lys Arg Ser Ser Asn Ala
1      5      10      15
Ile Thr Asn Asp Leu Asp Asn Ser Pro Thr Val Asn Gln Asn Arg Ser
      20      25      30
Ala Glu Met Ile Ala Ser Asn Ser Thr Thr Asn Gly Leu Asp Asn Ser
      35      40      45
Leu Ser Val Asn Ser Ile Ser Ser Asn Gly Thr Ile Arg Ser Asn Ser
      50      55      60
Gln Leu Asp Asn Arg Thr Val Glu Ser Thr Val Thr Ser Thr Asn Glu
65      70      75      80
Asn Lys Ser Tyr Lys Glu Asp Val Ile Ser Asp Arg Ile Ile Lys Lys
      85      90      95
Glu Phe Glu Asp Thr Ala Leu Ser Val Lys Asp Tyr Gly Ala Val Gly
      100     105     110
Asp Gly Ile His Asp Asp Arg Gln Ala Ile Gln Asp Ala Ile Asp Ala
      115     120     125
Ala Ala Gln Gly Leu Gly Gly Gly Asn Val Tyr Phe Pro Glu Gly Thr
      130     135     140
Tyr Leu Val Lys Glu Ile Val Phe Leu Lys Ser His Thr His Leu Glu
145     150     155     160
Leu Asn Glu Lys Ala Thr Ile Leu Asn Gly Ile Asn Ile Lys Asn His
      165     170     175
Pro Ser Ile Val Phe Met Thr Gly Leu Phe Thr Asp Asp Gly Ala Gln
      180     185     190
Val Glu Trp Gly Pro Thr Glu Asp Ile Ser Tyr Ser Gly Gly Thr Ile
      195     200     205
Asp Met Asn Gly Ala Leu Asn Glu Glu Gly Thr Lys Ala Lys Asn Leu
      210     215     220
Pro Leu Ile Asn Ser Ser Gly Ala Phe Ala Ile Gly Asn Ser Asn Asn
225     230     235     240
Val Thr Ile Lys Asn Val Thr Phe Lys Asp Ser Tyr Gln Gly His Ala
      245     250     255
Ile Gln Ile Ala Gly Ser Lys Asn Val Leu Val Asp Asn Ser Arg Phe
      260     265     270
Leu Gly Gln Ala Leu Pro Lys Thr Met Lys Asp Gly Gln Ile Ile Ser
      275     280     285
Lys Glu Ser Ile Gln Ile Glu Pro Leu Thr Arg Lys Gly Phe Pro Tyr
      290     295     300
Ala Leu Asn Asp Asp Gly Lys Lys Ser Glu Asn Val Thr Ile Gln Asn

```

305					310					315				320
Ser	Tyr	Phe	Gly	Lys	Ser	Asp	Lys	Ser	Gly	Glu	Leu	Val	Thr	Ala
				325					330					335
Gly	Thr	His	Tyr	Gln	Thr	Leu	Ser	Thr	Gln	Asn	Pro	Ser	Asn	Ile
				340				345					350	
Ile	Leu	Asn	Asn	His	Phe	Asp	Asn	Met	Met	Tyr	Ala	Gly	Val	Arg
		355					360					365		
Thr	Gly	Phe	Thr	Asp	Val	Leu	Ile	Lys	Gly	Asn	Arg	Phe	Asp	Lys
	370					375				380				
Val	Lys	Gly	Glu	Ser	Val	His	Tyr	Arg	Glu	Ser	Gly	Ala	Ala	Leu
385					390					395				400
Asn	Ala	Tyr	Ser	Tyr	Lys	Asn	Thr	Lys	Asp	Leu	Leu	Asp	Leu	Asn
				405					410					415
Gln	Val	Val	Ile	Ala	Glu	Asn	Ile	Phe	Asn	Ile	Ala	Asp	Pro	Lys
			420					425					430	
Lys	Ala	Ile	Arg	Val	Ala	Lys	Asp	Ser	Ala	Glu	Tyr	Leu	Gly	Lys
	435						440					445		
Ser	Asp	Ile	Thr	Val	Thr	Lys	Asn	Val	Ile	Asn	Asn	Asn	Ser	Lys
	450					455				460				
Thr	Glu	Gln	Pro	Asn	Ile	Glu	Leu	Leu	Arg	Val	Ser	Asp	Asn	Leu
465				470						475				480
Val	Ser	Glu	Asn	Ser	Ile	Phe	Gly	Gly	Lys	Glu	Gly	Ile	Val	Ile
			485						490					495
Asp	Ser	Lys	Gly	Lys	Ile	Thr	Val	Leu	Asn	Asn	Gln	Phe	Tyr	Asn
			500					505					510	
Ser	Gly	Lys	Tyr	Ile	Ser	Phe	Ile	Lys	Ser	Asn	Ala	Asn	Gly	Lys
	515					520						525		
Pro	Val	Ile	Arg	Asp	Ser	Asp	Gly	Asn	Phe	Asn	Ile	Val	Thr	Glu
	530					535					540			
Gly	Leu	Tyr	Lys	Ile	Val	Thr	Asn	Asn	Leu	Ser	Asp	Lys	Asn	Glu
545				550						555				560
Glu	Lys	Asn	Lys	Glu	Glu	Lys	Gln	Tyr	Asn	Ser	Asn	Asn	Val	Ile
			565						570					575
Ser	Asn	Gln	Lys	Asn	Gly	Glu	Phe	Asn	Ser	Ser	Lys	Asp	Asn	Arg
		580						585					590	
Met	Asn	Asp	Lys	Ile	Asp	Asn	Lys	Gln	Asp	Asn	Lys	Thr	Glu	Glu
	595					600						605		
Asn	Tyr	Lys	Ile	Val	Gly	Asp	Gly	Arg	Glu	Thr	Glu	Asn	His	Ile
	610				615					620				
Lys	Ser	Lys	Glu	Ile	Val	Asp	Val	Lys	Gln	Lys	Leu	Pro	Lys	Arg
625				630						635				640
Ser	Tyr	Lys	Ile	Met	Glu	Leu	Phe	Leu	Thr	Val	Thr	Gly	Ile	Gly
			645						650					655
Leu	Leu	Thr	Leu	Lys	Gly	Leu	Lys	Tyr	Tyr	Gly	Lys	Asp	Lys	
		660					665						670	

(2) INFORMATION FOR SEQ ID NO:4977:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4977:

```

Met Glu Leu Val Leu Pro Asn Asn Tyr Val Val Leu Glu Gln Glu Glu
1          5          10          15
Met Met Tyr Leu Asp Gly Gly Phe Ser Ile Pro Arg Trp Pro Val Ala
          20          25          30
Thr Ala Ile Asn Ile Ala Phe Asn Gly Val Leu Gly Gly Gly Ala Ile
          35          40          45
Ser Leu Val Arg Asn Tyr Ile Arg Asn Tyr Gly Leu Arg Arg Val Thr
          50          55          60
Ser Ala Ile Ala Gly Ala Ala Ala Arg Tyr Val Gly Val Arg Val Ala
65          70          75          80
Asn Arg Val Ala Gly Phe Ala Leu Ser Ala Ile Asn Gly Phe Ala Ala
          85          90          95
Trp Met Ser Ile Gly Asp Ala Ile Thr Thr Ile Trp Ala Asn Asn Asp
          100         105         110
Val Asn Arg Arg Asp Pro Asn Leu Asn Ala Leu Trp
          115         120

```

(2) INFORMATION FOR SEQ ID NO:4978:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 164 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...164

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4978:

```

Arg Glu Leu Val Leu Pro Asn Asn Tyr Val Ala Leu Glu Gln Glu Glu
1          5          10          15
Met Met Tyr Leu Asp Gly Gly Gly Tyr Leu Ser Lys Ser Ala Cys Gln
          20          25          30
Gly Ile Cys Ala Ala Leu Ala Met Ser Pro Gly Thr Phe Ile Ala Leu
          35          40          45
Thr Gly Ala Ala Val Leu Thr Lys Lys Leu Ile Asn Tyr Ile Lys Val
          50          55          60
Gly Gly Leu Gly Gly Trp Leu Ile Gly Ala Ala Ala Gly Val Leu Ala
65          70          75          80
Leu Ile Phe Leu Ile Lys Ile Cys Val Asp Thr Thr Ile Lys Val Leu

```

				85					90					95			
Leu	Asn	Arg	Ile	Phe	Lys	Ala	Ser	Lys	Val	Met	Lys	Arg	Arg	Ile	Phe		
			100					105					110				
Ser	Leu	Phe	Val	Leu	Asp	Leu	Met	Val	Tyr	Ile	Phe	Leu	Gly	Tyr	Val		
		115					120					125					
Leu	Val	Ile	Gln	Lys	Asp	Val	Tyr	Leu	Phe	Ser	Ile	Leu	Ile	Ile	Phe		
	130					135					140						
Ser	Asn	Phe	Ser	Val	Pro	Phe	Ile	Arg	Glu	Lys	Glu	Tyr	Glu	Leu	Phe		
145					150					155					160		
Lys	Asn	Lys	Lys														

(2) INFORMATION FOR SEQ ID NO:4979:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 197 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...197

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4979:

Asn	Ala	Leu	Val	Val	Lys	Leu	Val	Lys	Ala	Ser	Met	Asp	Gly	Gln	Leu		
1				5					10					15			
Glu	Glu	Lys	Gly	Asn	Leu	Thr	Asp	Lys	Ile	Lys	Ser	Leu	Ser	Lys	Gly		
		20						25				30					
Gly	Gln	Gln	Lys	Ile	Gln	Leu	Ile	Ile	Thr	Leu	Ile	His	Glu	Pro	Asp		
	35					40						45					
Leu	Ile	Ile	Leu	Asp	Glu	Pro	Phe	Ser	Gly	Leu	Asp	Pro	Val	Asn	Thr		
	50				55						60						
Glu	Leu	Leu	Lys	Gln	Val	Ile	Phe	Gln	Glu	Lys	Glu	Arg	Gly	Ala	Thr		
65				70					75						80		
Ile	Ile	Phe	Ser	Asp	His	Val	Met	Thr	Asn	Val	Glu	Glu	Leu	Cys	Asp		
			85					90					95				
Asp	Ile	Leu	Met	Ile	Arg	Asp	Gly	Arg	Val	Val	Leu	His	Gly	Pro	Val		
	100						105						110				
Gln	Asp	Val	Arg	Asn	Gln	Tyr	Gly	Lys	Thr	Arg	Leu	Phe	Val	Ser	Ser		
	115						120					125					
Glu	Arg	Ser	Lys	Glu	Glu	Leu	Glu	Asn	Leu	Pro	His	Val	Lys	Gln	Val		
	130					135					140						
Ser	Leu	Thr	Lys	Gln	Gly	Ser	Trp	Lys	Leu	Ile	Leu	Glu	Asp	Glu	Ser		
145				150					155						160		
Ala	Gly	Arg	Glu	Leu	Phe	Pro	Ile	Leu	Thr	Gln	Gly	Gln	Tyr	Ile	Ala		
			165						170					175			
Thr	Phe	Asp	Gln	Gln	Ala	Pro	Thr	Ile	Asp	Glu	Ile	Phe	Lys	Leu	Glu		
		180						185						190			
Ser	Gly	Val	Glu	Val													

(2) INFORMATION FOR SEQ ID NO:4980:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 249 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...249

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4980:

```

Ser Thr Cys Phe Ser Phe Tyr Cys Phe Lys Pro Val Tyr Phe Tyr Lys
1      5      10      15
Gly Val Ile Met Glu Phe Thr Asp Ile Ala Met Glu Leu Ser Lys Lys
      20      25      30
Ala Trp Gln Ala Ser Phe His His Pro Phe Ile Leu Gln Leu Gln Glu
      35      40      45
Gly Asn Leu Glu Pro Ala Ile Phe Arg Tyr Tyr Leu Ile Gln Asp Ala
      50      55      60
Tyr Tyr Leu Lys Ala Phe Ser Glu Ile Tyr His Leu Leu Ala Asp Lys
65      70      75      80
Thr Ser Asn Gln Glu Met Lys Arg Leu Leu Lys Gln Asn Ala Gln Gly
      85      90      95
Leu Val Glu Gly Glu Leu Phe Ile Arg Gln Gln Phe Phe Lys Glu Met
      100     105     110
Glu Ile Ser Asp Gln Glu Met Glu Gln His Pro Ile Ala Pro Thr Cys
      115     120     125
Tyr His Tyr Ile Ser His Ile Tyr Arg Gln Phe Ala Glu Pro Asn Leu
      130     135     140
Ala Ile Ala Phe Ala Ser Leu Leu Pro Cys Pro Trp Leu Tyr His Asp
145     150     155     160
Ile Gly Lys Ser Leu Asn Leu Lys Pro Ser Pro Asn Pro Leu Tyr Gln
      165     170     175
Gln Trp Ile Glu Thr Tyr Ile Thr Asp Glu Leu Glu Gln Gln Ile Arg
      180     185     190
Glu Glu Gly Ala Leu Val Asn Gln Leu Tyr Arg Glu Ser Asp Glu Thr
      195     200     205
Asp Lys Gln Lys Met Leu Asp Ala Phe His Ile Ser Val His Met Glu
      210     215     220
Ala Lys Phe Trp Glu Met Ala Tyr Gln His Gln Thr Trp Lys Ser Asp
225     230     235     240
Leu Gln Ser Leu Glu Lys Gly Glu Glu
      245

```

(2) INFORMATION FOR SEQ ID NO:4981:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 375 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...375
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4981:

```

Ile Leu Cys Phe Tyr Leu Phe Ile Arg Lys Arg Arg Leu Phe Phe Arg
1      5      10      15
Arg Lys Leu Ile Ala Tyr Leu Lys Phe Ser Pro Leu Cys Trp Ile Val
      20      25      30
Pro Ser Ile Tyr Val Ile Met Lys Glu Gly Phe Lys Ile Gly Lys Gly
      35      40      45
Val Phe Met Leu Lys Leu Gly Val Ile Gly Thr Gly Ala Ile Ser His
      50      55      60
His Phe Ile Glu Ala Ala His Thr Ser Gly Glu Tyr Gln Leu Val Ala
65      70      75      80
Ile Tyr Ser Arg Lys Leu Glu Thr Ala Ala Thr Phe Ala Ser Arg Tyr
      85      90      95
Gln Asn Ile Gln Leu Phe Asp Gln Leu Glu Val Phe Phe Lys Ser Ser
      100     105     110
Phe Asp Leu Val Tyr Ile Ala Ser Pro Asn Ser Leu His Phe Ala Gln
      115     120     125
Ala Lys Ala Ala Leu Ser Ala Gly Lys His Val Ile Leu Glu Lys Pro
      130     135     140
Ala Val Thr Gln Pro Gln Glu Trp Phe Asp Leu Ile Gln Thr Ala Glu
145     150     155     160
Lys Asn Asn Cys Phe Ile Phe Glu Ala Ala Arg Asn Tyr His Glu Lys

      165      170      175
Ala Phe Thr Thr Ile Lys Asn Phe Leu Ala Asp Lys Gln Val Leu Gly
      180     185     190
Ala Asp Phe Asn Tyr Ala Lys Tyr Ser Ser Lys Met Pro Asp Leu Leu
      195     200     205
Thr Gly Gln Thr Pro Asn Val Phe Ser Asp Arg Phe Ala Gly Gly Ala
      210     215     220
Leu Met Asp Leu Gly Ile Tyr Pro Leu Tyr Ala Ala Val Arg Leu Phe
225     230     235     240
Gly Lys Ala Asn Asp Ala Thr Tyr His Ala Gln Gln Leu Asp Asn Ser
      245     250     255
Ile Asp Leu Asn Gly Asp Gly Ile Leu Phe Tyr Pro Asp Tyr Gln Val
      260     265     270
His Ile Lys Ala Gly Lys Asn Ile Thr Ser Asn Leu Pro Cys Glu Ile
      275     280     285
Tyr Thr Thr Asp Gly Thr Leu Thr Leu Asn Thr Ile Glu His Ile Arg
290     295     300

```

```

Ser Ala Ile Phe Thr Asp His Gln Gly Asn Gln Val Gln Leu Pro Ile
305                      310                      315                      320
Gln Gln Thr His His Thr Met Thr Glu Glu Val Ala Ala Phe Ala His
                      325                      330                      335
Met Ile Gln Gln Pro Asp Leu Asn Leu Tyr Gln Thr Trp Leu Asp Asp
                      340                      345                      350
Ala Gly Ser Val His Glu Leu Leu Tyr Thr Met Arg Gln Thr Ala Gly
                      355                      360                      365
Ile Arg Phe Glu Ala Glu Lys
                      370                      375

```

(2) INFORMATION FOR SEQ ID NO:4982:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 369 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...369

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4982:

```

Gly Glu Cys Leu Met Leu Glu Arg Leu Lys Ser Ile His Tyr Met Phe
1      5      10      15
Trp Ile Ser Leu Ile Phe Met Val Phe Pro Ile Leu Thr Val Val Thr
      20      25      30
Gly Trp Leu Ser Ala Trp His Leu Leu Ile Asp Ile Leu Phe Val Val
      35      40      45
Ala Tyr Leu Gly Val Leu Thr Thr Lys Ser Gln Arg Leu Ser Trp Leu
      50      55      60
Tyr Trp Gly Ile Leu Leu Thr Tyr Val Val Gly Asn Thr Ala Phe Val
      65      70      75      80
Ala Val Asn Tyr Ile Trp Phe Phe Phe Phe Leu Ser Asn Leu Leu Ser
      85      90      95
Tyr His Phe Ser Val Gly Gly Leu Lys Ser Leu His Val Trp Thr Phe
      100     105     110
Leu Leu Ala Gln Val Leu Val Val Gly Gln Leu Leu Ile Phe Gln Arg
      115     120     125
Ile Glu Val Glu Phe Leu Phe Tyr Leu Leu Val Ile Leu Ala Phe Val
      130     135     140
Asp Leu Met Thr Phe Gly Leu Val Arg Ile Arg Ile Val Glu Asp Leu
      145     150     155     160
Lys Glu Ala Gln Ala Lys Gln Asn Ala Gln Ile Asn Leu Leu Leu Ala
      165     170     175
Glu Asn Glu Arg Asn Arg Ile Gly Gln Asp Leu His Asp Ser Leu Gly
      180     185     190
His Thr Phe Ala Met Leu Ser Val Lys Thr Asp Leu Ala Leu Gln Leu
      195     200     205

```

Phe	Gln	Met	Glu	Ala	Tyr	Pro	Gln	Val	Glu	Lys	Glu	Leu	Lys	Glu	Ile
210						215					220				
His	Gln	Ile	Ser	Lys	Asp	Ser	Met	Asn	Glu	Val	Arg	Thr	Ile	Val	Glu
225					230					235					240
Asn	Leu	Lys	Ser	Arg	Thr	Leu	Thr	Ser	Glu	Leu	Glu	Thr	Val	Lys	Lys
				245					250					255	
Met	Leu	Glu	Ile	Ala	Gly	Ile	Glu	Val	Glu	Thr	Asp	Asn	Gln	Leu	Asp
			260					265					270		
Thr	Ala	Ser	Leu	Thr	Gln	Glu	Leu	Glu	Ser	Met	Ala	Ser	Met	Ile	Leu
	275						280					285			
Leu	Glu	Leu	Val	Thr	Asn	Ile	Ile	Lys	His	Ala	Lys	Ala	Ser	Lys	Ala
	290					295					300				
Tyr	Leu	Lys	Leu	Glu	Arg	Thr	Glu	Lys	Glu	Leu	Ile	Leu	Thr	Val	Ser
305					310					315					320
Asp	Asp	Gly	Cys	Gly	Phe	Ala	Phe	Leu	Lys	Gly	Asp	Glu	Leu	His	Thr
			325						330					335	
Val	Arg	Asp	Arg	Val	Phe	Pro	Phe	Ser	Gly	Glu	Val	Ser	Val	Ile	Ser
		340					345					350			
Gln	Lys	His	Pro	Thr	Glu	Val	Gln	Val	Arg	Leu	Pro	Tyr	Lys	Glu	Arg
		355					360					365			

Asn

(2) INFORMATION FOR SEQ ID NO:4983:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 475 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...475

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4983:

Ala	Arg	Ser	Val	Val	Lys	Thr	Asp	Cys	Leu	Phe	Arg	Glu	Ile	Ile	Asp
1			5					10					15		
Gln	Gly	His	Tyr	His	Tyr	Asn	Tyr	Ser	Lys	Val	Ile	Phe	Asp	Ser	Ile
		20					25				30				
Ser	Tyr	Asp	Ser	Arg	Lys	Val	Thr	Glu	Asp	Thr	Leu	Phe	Phe	Ala	Lys
		35				40					45				
Gly	Ala	Ala	Phe	Lys	Lys	Glu	Tyr	Leu	Leu	Ser	Ala	Ile	Thr	Gln	Gly
	50				55					60					
Leu	Ala	Trp	Tyr	Val	Ala	Glu	Lys	Asp	Tyr	Glu	Val	Asp	Ile	Pro	Val
65				70				75					80		
Ile	Ile	Val	Asn	Asp	Ile	Lys	Lys	Ala	Met	Ser	Leu	Ile	Ala	Met	Glu
			85				90					95			
Phe	Tyr	Gly	Asn	Pro	Gln	Glu	Lys	Leu	Lys	Leu	Leu	Ala	Phe	Thr	Gly

			100					105				110			
Thr	Lys	Gly	Lys	Thr	Thr	Ala	Thr	Tyr	Phe	Ala	Tyr	Asn	Ile	Leu	Ser
		115					120					125			
Gln	Gly	His	Arg	Pro	Ala	Met	Leu	Ser	Thr	Met	Asn	Thr	Thr	Leu	Asp
		130				135					140				
Gly	Glu	Thr	Phe	Phe	Lys	Ser	Ala	Leu	Thr	Thr	Pro	Glu	Ser	Ile	Asp
145					150					155				160	
Leu	Phe	Asp	Met	Met	Asn	Gln	Ala	Val	Leu	Asn	Asp	Arg	Thr	His	Leu
			165					170					175		
Ile	Met	Glu	Val	Ser	Ser	Gln	Ala	Tyr	Leu	Val	His	Arg	Val	Tyr	Gly
		180						185					190		
Leu	Thr	Phe	Asp	Val	Gly	Val	Phe	Leu	Asn	Ile	Thr	Pro	Asp	His	Ile
		195					200					205			
Gly	Pro	Ile	Glu	His	Pro	Ser	Phe	Glu	Asp	Tyr	Phe	Tyr	His	Lys	Arg
		210				215					220				
Leu	Leu	Met	Glu	Asn	Ser	Arg	Ala	Val	Ile	Ile	Asn	Ser	Asp	Met	Asp
225					230					235				240	
His	Phe	Ser	Val	Leu	Lys	Glu	Gln	Val	Glu	Asp	Gln	Asp	His	Asp	Phe
			245						250				255		
Tyr	Gly	Ser	Gln	Phe	Asp	Asn	Gln	Ile	Glu	Asn	Ser	Lys	Ala	Phe	Ser
		260					265						270		
Phe	Ser	Ala	Thr	Gly	Lys	Leu	Ala	Gly	Asp	Tyr	Asp	Ile	Gln	Leu	Ile
		275				280						285			
Gly	Asn	Phe	Asn	Gln	Glu	Asn	Ala	Val	Ala	Ala	Gly	Leu	Ala	Cys	Leu
	290					295					300				
Arg	Leu	Gly	Ala	Ser	Leu	Glu	Asp	Ile	Lys	Lys	Gly	Ile	Ala	Ala	Thr
305					310					315				320	
Arg	Val	Pro	Gly	Arg	Met	Glu	Val	Leu	Thr	Gln	Lys	Asn	Gly	Ala	Lys
			325						330					335	
Val	Phe	Ile	Asp	Tyr	Ala	His	Asn	Gly	Asp	Ser	Leu	Lys	Lys	Leu	Ile
		340						345					350		
Asn	Val	Val	Glu	Thr	His	Gln	Thr	Gly	Lys	Ile	Ala	Leu	Val	Leu	Gly
		355					360					365			
Ser	Thr	Gly	Asn	Lys	Gly	Glu	Ser	Arg	Arg	Lys	Asp	Phe	Gly	Leu	Leu
	370				375						380				
Leu	Asn	Gln	His	Pro	Glu	Ile	Gln	Val	Phe	Leu	Thr	Ala	Asp	Asp	Pro
385					390				395					400	
Asn	Tyr	Glu	Asp	Pro	Met	Ala	Ile	Ala	Asp	Glu	Ile	Ser	Ser	Tyr	Ile
			405						410					415	
Asn	His	Pro	Val	Glu	Lys	Ile	Ala	Asp	Arg	Gln	Glu	Ala	Ile	Lys	Ala
		420						425					430		
Ala	Met	Ala	Ile	Thr	Asn	His	Glu	Leu	Asp	Ala	Val	Ile	Ile	Ala	Gly
		435				440					445				
Lys	Gly	Ala	Asp	Cys	Tyr	Gln	Ile	Ile	Gln	Gly	Lys	Lys	Glu	Ser	Tyr
	450					455					460				
Pro	Gly	Asp	Thr	Ala	Val	Ala	Glu	Asn	Tyr	Leu					
465					470					475					

(2) INFORMATION FOR SEQ ID NO:4984:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 80 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...80

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4984:

Ala	Gln	Pro	Val	Gln	Val	Leu	Val	Val	Ser	Leu	Leu	Lys	Ala	Thr	Ser
1				5					10					15	
Ser	Val	Ser	Met	Ile	Trp	Lys	Lys	Leu	Leu	Thr	Ala	Leu	Lys	Glu	Cys
			20					25					30		
Lys	Leu	Ala	Leu	Pro	Phe	Lys	Gln	Asp	Val	Lys	Phe	Val	Ser	Trp	Ser
		35					40					45			
Ile	Gln	Glu	Lys	Ser	Arg	Thr	Thr	Lys	Ser	Gln	Ser	Trp	Leu	Thr	Lys
	50					55				60					
Phe	Val	Arg	Lys	Leu	Lys	Thr	Ile	Ser	Ile	Ile	Gln	Glu	Ile	Ser	Arg
65					70				75					80	

(2) INFORMATION FOR SEQ ID NO:4985:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 414 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...414

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4985:

Asn	Ser	Thr	Val	Ser	Asn	Asn	Tyr	Ile	His	Asn	Gln	Val	His	Thr	Cys
1				5					10					15	
Glu	Val	Gly	Trp	Asn	Arg	Gly	Pro	Ala	Thr	Pro	Thr	Phe	Cys	Gln	Val
			20					25					30		
Cys	Phe	Phe	His	Lys	Gly	Val	Leu	Met	Leu	Asp	Ile	Lys	Arg	Ile	Arg
		35				40					45				
Thr	Asp	Phe	Glu	Ala	Val	Ala	Glu	Lys	Leu	Ala	Thr	Arg	Gly	Val	Asp
	50					55				60					
Ala	Ala	Val	Leu	Asn	Glu	Met	Lys	Glu	Ile	Asp	Ala	Lys	Arg	Arg	Asn
65					70				75					80	
Ile	Leu	Val	Lys	Val	Glu	Thr	Leu	Lys	Ala	Glu	Arg	Asn	Thr	Val	Ser
			85					90					95		
Ala	Glu	Ile	Ala	Gln	Ala	Lys	Arg	Asn	Lys	Glu	Asn	Thr	Asp	Asp	Lys

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4986:

Ile	Arg	Cys	Phe	Arg	Thr	Trp	Tyr	Gly	Ser	Ile	Lys	Glu	Leu	Ser	Thr
1				5					10					15	
Gly	Glu	His	Glu	Ala	Val	Glu	Leu	Arg	Asp	Gly	Asp	Lys	Ser	Arg	Tyr
			20					25					30		
Gly	Gly	Leu	Gly	Thr	Gln	Lys	Ala	Val	Asp	Asn	Val	Asn	Asn	Ile	Ile
		35					40					45			
Ala	Glu	Ala	Ile	Ile	Gly	Tyr	Asp	Val	Arg	Asp	Gln	Gln	Ala	Ile	Asp
	50					55					60				
Arg	Ala	Met	Ile	Ala	Leu	Asp	Gly	Thr	Pro	Asn	Lys	Gly	Lys	Trp	Gly
65					70					75					80
Ala	Asn	Ala	Ile	Leu	Gly	Val	Ser	Ile	Ala	Val	Ala	Arg	Ala	Ala	Ala
				85					90					95	
Asp	Tyr	Leu	Glu	Ile	Pro	Leu	Tyr	Ser	Tyr	Leu	Gly	Gly	Phe	Asn	Thr
		100						105					110		
Lys	Val	Leu	Pro	Thr	Pro	Met	Met	Asn	Ile	Ile	Asn	Gly	Gly	Ser	His
		115					120					125			
Ser	Asp	Ala	Pro	Ile	Ala	Phe	Gln	Glu	Phe	Met	Ile	Leu	Pro	Val	Gly
	130					135					140				
Ala	Pro	Thr	Phe	Lys	Glu	Ala	Leu	Arg	Tyr	Gly	Ala	Glu	Ile	Phe	His
145					150					155					160
Ala	Leu	Lys	Lys	Ile	Leu	Lys	Ser	Arg	Gly	Leu	Glu	Thr	Ala	Val	Gly
				165					170					175	
Asp	Glu	Gly	Gly	Phe	Ala	Pro	Arg	Phe	Glu	Gly	Thr	Glu	Asp	Gly	Val
		180						185					190		
Glu	Thr	Ile	Leu	Ala	Ala	Ile	Glu	Ala	Ala	Gly	Tyr	Val	Pro	Gly	Lys
		195					200					205			
Asp	Val	Phe	Ile	Gly	Phe	Asp	Cys	Ala	Ser	Ser	Glu	Phe	Tyr	Asp	Lys
	210					215					220				
Glu	Arg	Lys	Val	Tyr	Asp	Tyr	Thr	Lys	Phe	Glu	Gly	Glu	Gly	Ala	Ala
225					230					235					240
Val	Arg	Thr	Ser	Ala	Glu	Gln	Ile	Asp	Tyr	Leu	Glu	Glu	Leu	Val	Asn
				245					250					255	
Lys	Tyr	Pro	Ile	Ile	Thr	Ile	Glu	Asp	Gly	Met	Asp	Glu	Asn	Asp	Trp
			260					265					270		
Asp	Gly	Trp	Lys	Ala	Leu	Thr	Glu	Arg	Leu	Gly	Lys	Lys	Val	Gln	Leu
		275					280					285			
Val	Gly	Asp	Asp	Phe	Phe	Val	Thr	Asn	Thr	Asp	Tyr	Leu	Ala	Arg	Gly
	290					295					300				
Ile	Gln	Glu	Gly	Ala	Ala	Asn	Ser	Ile	Leu	Ile	Lys	Val	Asn	Gln	Ile
305					310					315					320
Gly	Thr	Leu	Thr	Glu	Thr	Phe	Glu	Ala	Ile	Glu	Met	Ala	Lys	Glu	Ala
				325					330				335		
Gly	Tyr	Thr	Ala	Val	Val	Ser	His	Arg	Ser	Gly	Glu	Thr	Glu	Asp	Ser
			340					345					350		
Thr	Ile	Ala	Asp	Ile	Ala	Val	Ala	Thr	Asn	Ala	Gly	Gln	Ile	Lys	Thr
		355					360					365			
Gly	Ser	Leu	Ser	Arg	Thr	Asp	Arg	Ile	Ala	Lys	Tyr	Asn	Gln	Leu	Leu
	370					375					380				
Arg	Ile	Glu	Asp	Gln	Leu	Gly	Glu	Val	Ala	Glu	Tyr	Arg	Gly	Leu	Lys
385					390					395					400
Ser	Phe	Tyr	Asn	Leu	Lys	Lys									
				405											

(2) INFORMATION FOR SEQ ID NO:4987:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 911 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...911
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4987:

Gly	Ala	Arg	Phe	Ser	Ser	Thr	Asp	Ser	Tyr	Gln	Asn	His	Lys	Phe	Thr
1				5					10					15	
Phe	Lys	Thr	Leu	Lys	Phe	Lys	Phe	Arg	Met	Arg	Phe	Tyr	Phe	Met	Glu
			20					25					30		
Asn	Val	Val	Val	His	Ile	Ile	Ser	His	Ser	His	Trp	Asp	Arg	Glu	Trp
			35				40					45			
Tyr	Leu	Pro	Phe	Glu	Ser	His	Arg	Met	Gln	Leu	Val	Glu	Leu	Phe	Asp
	50					55					60				
Asn	Leu	Phe	Asp	Leu	Phe	Glu	Asn	Asp	Pro	Glu	Phe	Lys	Ser	Phe	His
65					70					75					80
Leu	Asp	Gly	Gln	Thr	Ile	Val	Leu	Asp	Asp	Tyr	Leu	Gln	Ile	Arg	Pro
				85					90					95	
Glu	Asn	Arg	Asp	Lys	Val	Gln	Arg	Tyr	Ile	Asp	Glu	Gly	Lys	Leu	Lys
			100					105					110		
Ile	Gly	Pro	Phe	Tyr	Ile	Leu	Gln	Asp	Asp	Tyr	Leu	Ile	Ser	Ser	Glu
		115					120						125		
Ala	Asn	Val	Arg	Asn	Thr	Leu	Ile	Gly	Gln	Gln	Glu	Ala	Ala	Lys	Trp
	130					135					140				
Gly	Lys	Ser	Thr	Gln	Ile	Gly	Tyr	Phe	Pro	Asp	Thr	Phe	Gly	Asn	Met
145					150					155					160
Gly	Gln	Ala	Pro	Gln	Ile	Leu	Gln	Lys	Ser	Gly	Ile	His	Val	Ala	Ala
				165					170					175	
Phe	Gly	Arg	Gly	Val	Lys	Pro	Ile	Gly	Phe	Asp	Asn	Gln	Val	Leu	Glu
		180						185					190		
Asp	Glu	Arg	Phe	Thr	Ser	Gln	Phe	Ser	Glu	Met	Tyr	Trp	Gln	Gly	Val
	195						200					205			
Asp	Gly	Ser	Arg	Val	Leu	Gly	Ile	Leu	Phe	Ala	Asn	Trp	Tyr	Ser	Asn
	210					215					220				
Gly	Asn	Glu	Ile	Pro	Val	Asp	Lys	Asp	Glu	Ala	Leu	Ile	Phe	Trp	Lys
225					230					235					240
Gln	Lys	Leu	Ser	Asp	Val	Arg	Ala	Tyr	Ala	Ser	Thr	Asn	Gln	Trp	Leu
				245					250					255	
Met	Met	Asn	Gly	Cys	Asp	His	Gln	Pro	Val	Gln	Lys	Asn	Leu	Ser	Glu
		260					265						270		
Ala	Ile	Arg	Val	Ala	Asn	Glu	Leu	Phe	Pro	Asp	Val	Ile	Phe	Val	His
		275					280					285			
Ser	Ser	Phe	Asp	Glu	Tyr	Val	Gln	Ala	Val	Glu	Gly	Ala	Leu	Pro	Glu
	290						295				300				

His	Leu	Ser	Thr	Val	Thr	Gly	Glu	Leu	Thr	Ser	Gln	Glu	Thr	Asp	Gly		
305						310				315					320		
Trp	Tyr	Thr	Leu	Ala	Asn	Thr	Ser	Ser	Ser	Arg	Ile	Tyr	Leu	Lys	Gln		
				325					330					335			
Ala	Phe	Gln	Glu	Asn	Ser	Asn	Leu	Leu	Glu	Gln	Val	Val	Glu	Pro	Leu		
			340					345					350				
Thr	Ile	Ile	Thr	Gly	Gly	His	Asn	His	Lys	Asp	Gln	Leu	Thr	Tyr	Ala		
		355				360						365					
Trp	Lys	Thr	Leu	Leu	Gln	Asn	Ala	Pro	His	Asp	Ser	Ile	Cys	Gly	Cys		
	370					375				380							
Ser	Val	Asp	Glu	Val	His	Arg	Glu	Met	Glu	Thr	Arg	Phe	Ala	Lys	Val		
385					390					395					400		
Asn	Gln	Val	Gly	Asn	Phe	Val	Lys	Ser	Asn	Leu	Leu	Asn	Glu	Trp	Lys		
			405					410					415				
Gly	Lys	Ile	Ala	Thr	Asp	Lys	Ala	Gln	Ser	Asp	Tyr	Leu	Phe	Thr	Val		
			420				425					430					
Ile	Asn	Thr	Gly	Leu	His	Asp	Lys	Val	Asp	Thr	Val	Ser	Thr	Val	Ile		
	435					440						445					
Asp	Val	Ala	Thr	Cys	Asp	Phe	Lys	Glu	Leu	His	Pro	Thr	Glu	Gly	Tyr		
	450				455					460							
Lys	Lys	Met	Ala	Ala	Leu	Ile	Leu	Pro	Ser	Tyr	Arg	Val	Glu	Asp	Leu		
465				470					475						480		
Asp	Gly	Arg	Pro	Val	Glu	Ala	Thr	Ile	Glu	Asp	Leu	Gly	Ala	Asn	Phe		
			485					490					495				
Glu	Tyr	Asp	Leu	Pro	Lys	Asp	Lys	Phe	Arg	Gln	Ala	Arg	Ile	Ala	Arg		
		500					505					510					
Gln	Val	Arg	Val	Thr	Ile	Pro	Val	His	Leu	Ala	Pro	Leu	Ser	Trp	Thr		
	515					520						525					
Thr	Phe	Gln	Leu	Leu	Glu	Gly	Lys	Gln	Glu	His	Arg	Glu	Gly	Ile	Tyr		
	530				535				540								
Gln	Asn	Gly	Val	Ile	Asp	Thr	Pro	Phe	Val	Thr	Val	Ser	Val	Asp	Asp		
545				550				555						560			
Asn	Ile	Thr	Val	Tyr	Asp	Lys	Thr	Thr	His	Glu	Ala	Tyr	Glu	Asp	Phe		
			565				570					575					
Ile	Arg	Phe	Glu	Asp	Arg	Gly	Asp	Ile	Gly	Asn	Glu	Tyr	Ile	Tyr	Phe		
		580				585						590					
Gln	Pro	Lys	Gly	Thr	Glu	Pro	Ile	Phe	Ala	Glu	Leu	Lys	Gly	His	Glu		
	595					600						605					
Val	Leu	Glu	Asn	Thr	Ala	Cys	Tyr	Ala	Lys	Ile	Leu	Leu	Lys	His	Glu		
	610				615					620							
Leu	Thr	Val	Pro	Val	Ser	Ala	Asp	Glu	Lys	Leu	Glu	Glu	Glu	Gln	Gln		
625				630				635						640			
Gly	Ile	Ile	Glu	Phe	Met	Lys	Arg	Glu	Ala	Gly	Arg	Ser	Glu	Glu	Leu		
			645					650					655				
Thr	Asn	Ile	Pro	Leu	Glu	Thr	Glu	Leu	Thr	Val	Phe	Val	Asp	Asn	Pro		
		660				665						670					
Gln	Ile	Arg	Phe	Lys	Thr	Arg	Phe	Thr	Asn	Thr	Ala	Lys	Asp	His	Arg		
	675					680					685						
Ile	Arg	Leu	Leu	Val	Lys	Thr	His	Asn	Thr	Arg	Pro	Ser	Asn	Asp	Ser		
	690				695					700							
Glu	Ser	Ile	Tyr	Glu	Val	Val	Thr	Arg	Pro	Asn	Lys	Pro	Ala	Ala	Ser		
705				710				715						720			
Trp	Glu	Asn	Pro	Glu	Asn	Pro	Gln	His	Gln	Gln	Ala	Phe	Val	Ser	Leu		
			725				730					735					
Tyr	Asp	Asp	Glu	Lys	Gly	Val	Thr	Val	Ser	Asn	Lys	Gly	Leu	Asn	Glu		
			740				745					750					

Tyr	Glu	Ile	Leu	Gly	Asp	Asn	Thr	Ile	Ala	Val	Thr	Ile	Leu	Arg	Ala
	755						760					765			
Ser	Gly	Glu	Leu	Gly	Asp	Trp	Gly	Tyr	Phe	Pro	Thr	Pro	Glu	Ala	Gln
	770						775					780			
Cys	Leu	Arg	Glu	Phe	Glu	Val	Glu	Phe	Ala	Leu	Glu	Cys	His	Gln	Ala
	785				790					795					800
Gln	Glu	Arg	Phe	Ser	Ala	Tyr	Arg	Arg	Ala	Lys	Ala	Leu	Gln	Thr	Pro
			805						810					815	
Phe	Thr	Ser	Leu	Gln	Leu	Ala	Arg	Gln	Glu	Gly	Ser	Val	Val	Ala	Thr
			820					825					830		
Gly	Ser	Leu	Leu	Ser	His	Ser	Val	Leu	Ser	Ile	Pro	Gln	Val	Cys	Pro
		835					840					845			
Thr	Ala	Phe	Lys	Val	Ala	Glu	Asn	Glu	Glu	Gly	Tyr	Val	Leu	Arg	Tyr
	850					855					860				
Tyr	Asn	Met	Ser	Gln	Glu	Asn	Val	Arg	Ile	Ser	Glu	His	Gln	Gln	Thr
	865				870					875					880
Ile	Leu	Asp	Leu	Leu	Glu	Arg	Pro	Tyr	Pro	Val	His	Ser	Gly	Leu	Leu
			885						890					895	
Ala	Pro	Gln	Glu	Ile	Arg	Thr	Glu	Phe	Ile	Lys	Lys	Glu	Glu	Ile	
		900					905						910		

(2) INFORMATION FOR SEQ ID NO:4988:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4988:

Phe	Trp	Tyr	Val	Glu	Phe	Trp	Tyr	Leu	Phe	Leu	Ala	Gln	Ile	Leu	Ala
1			5					10					15		
Asn	Met	Ile	Gly	Leu	Thr	Thr	Ile	Tyr	Trp	Leu	Phe	Asn	Gln	Ile	Ile
		20					25					30			
Thr	Tyr	Gly	Val	Ile	Ala	Ala	Val	Val	Ile	Phe	Ser	Pro	Glu	Ile	Arg
		35					40					45			
Thr	Gly	Leu	Glu	Arg	Leu	Gly	Arg	Ala	Thr	Asp	Phe	Phe	Ser	Asn	Ala
	50					55				60					
Pro	Ile	Ser	Ala	Glu	Glu	Gln	Met	Ile	Arg	Ala	Phe	Val	Lys	Ser	Val
	65				70					75					80
Glu	Tyr	Met	Ser	Pro	Arg	Lys	Ile	Gly	Ala	Leu	Val	Ala	Ile	Gln	Arg
			85					90					95		
Val	Arg	Thr	Leu	Gln	Glu	Tyr	Ile	Ser	Thr	Gly	Ile	Pro	Leu	Asp	Ala
		100					105					110			
Lys	Ile	Ser	Ala	Glu	Leu	Leu	Ile	Asn	Ile	Phe	Ile	Pro	Asn	Thr	Pro

(2) INFORMATION FOR SEQ ID NO:4989:

(A) LENGTH: 92 amino acids

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Streptococcus pneumoniae*

(A) NAME/KEY: misc feature

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4989:

(2) INFORMATION FOR SEQ ID NO:4990:

(A) LENGTH: 159 amino acids

(D) TOPOLOGY: linear

3866

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4990:

Ile	Leu	Phe	Leu	Thr	Lys	Lys	Leu	Arg	Asn	Trp	Arg	Thr	Asn	Met	Lys
1				5					10					15	
Leu	Glu	Lys	His	Leu	Ile	Lys	Leu	Asn	Lys	Gln	Phe	Ser	Asn	Lys	Glu
			20					25					30		
Glu	Ala	Ile	Cys	Tyr	Cys	Gly	Gln	Val	Leu	Tyr	Glu	Gly	Gly	Tyr	Val
			35				40						45		
Asn	Glu	Asp	Tyr	Ile	Glu	Ala	Met	Ile	Glu	Arg	Asp	Lys	Glu	Leu	Ser
						55					60				
Val	Tyr	Met	Gly	Asn	Phe	Ile	Ala	Ile	Pro	His	Gly	Thr	Asp	Ala	Ala
65					70					75					80
Lys	Lys	Asp	Val	Leu	Lys	Ser	Gly	Ile	Thr	Val	Val	Gln	Val	Pro	Arg
				85					90					95	
Gly	Val	Asp	Phe	Gly	Asn	Val	Ser	Asn	Pro	Gln	Val	Ala	Thr	Val	Leu
			100					105					110		
Phe	Gly	Ile	Ala	Gly	Ile	Gly	Asn	Glu	His	Leu	Glu	Ile	Ile	Gln	Lys
			115				120						125		
Ile	Ser	Ile	Phe	Cys	Ala	Asp	Val	Asp	Asn	Val	Leu	Lys	Leu	Ala	Asp
	130					135					140				
Ala	Gln	Ser	Lys	Glu	Glu	Val	Leu	Arg	Leu	Phe	Asp	Ala	Val	Glu	
145					150					155					

(2) INFORMATION FOR SEQ ID NO:4991:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 131 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...131

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4991:

Gly	Gly	His	Val	Ile	Asp	Val	Asn	Leu	Ile	Asn	Gly	Ile	Ala	Leu	Ala
1				5					10					15	
Phe	Glu	Gly	Asp	Ala	Val	Tyr	Ser	Met	Tyr	Ile	Arg	Arg	His	Leu	Ile
			20					25					30		

```

Leu Lys Gly Met Thr Lys Pro Asn Lys Leu His Gln Glu Ala Thr Lys
   35              40              45
Tyr Val Ser Ala Lys Ala Gln Ala Arg Leu Ile Ala Leu Met Leu Glu
   50              55              60
Glu Gln Val Leu Thr Glu Lys Glu Glu Glu Ile Tyr Lys Arg Gly Arg
   65              70              75              80
Asn Thr Asn Ser His Thr Lys Ala Lys Asn Ala Asp Val Val Thr Tyr

      85              90              95
Arg Met Ser Thr Gly Phe Glu Ala Val Met Gly Tyr Leu His Met Thr
      100              105              110
Glu Asn Leu Glu Arg Leu Glu Ser Leu Val Ser Trp Cys Ile Gln Lys
      115              120              125
Val Glu Gly
      130

```

(2) INFORMATION FOR SEQ ID NO:4992:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 678 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...678

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4992:

```

Pro Leu His Val His Arg Asp Ala Thr Pro Gln Met Met Val Ile Ser
1              5              10              15
Ser Met His Leu Ile Ser Ser Lys Ile Arg Gly Asp Ala Tyr Ile Val
      20              25              30
Pro His Gly Asp His Tyr His Tyr Ile Pro Lys Asn Glu Leu Ser Ala
      35              40              45
Ser Glu Leu Ala Ala Ala Glu Ala Phe Leu Ser Gly Arg Glu Asn Leu
      50              55              60
Ser Asn Leu Arg Thr Tyr Arg Arg Gln Asn Ser Asp Asn Thr Pro Arg
      65              70              75              80
Thr Asn Trp Val Pro Ser Val Ser Asn Pro Gly Thr Thr Asn Thr Asn
      85              90              95
Thr Ser Asn Asn Ser Asn Thr Asn Ser Gln Ala Ser Gln Ser Asn Asp
      100              105              110
Ile Asp Ser Leu Leu Lys Gln Leu Tyr Lys Leu Pro Leu Ser Gln Arg
      115              120              125
His Val Glu Ser Asp Gly Leu Ile Phe Asp Pro Ala Gln Ile Thr Ser
      130              135              140
Arg Thr Ala Arg Gly Val Ala Val Pro His Gly Asn His Tyr His Phe
      145              150              155              160
Ile Pro Tyr Glu Gln Met Ser Glu Leu Glu Lys Arg Ile Ala Arg Ile

```

				165					170					175			
Ile	Pro	Leu	Arg	Tyr	Arg	Ser	Asn	His	Trp	Val	Pro	Asp	Ser	Arg	Pro		
			180					185						190			
Glu	Glu	Pro	Ser	Pro	Gln	Pro	Thr	Pro	Glu	Pro	Ser	Pro	Ser	Pro	Gln		
		195					200						205				
Pro	Ala	Pro	Asn	Pro	Gln	Pro	Ala	Pro	Ser	Asn	Pro	Ile	Asp	Glu	Lys		
	210					215						220					
Leu	Val	Lys	Glu	Ala	Val	Arg	Lys	Val	Gly	Asp	Gly	Tyr	Val	Phe	Glu		
225					230						235				240		
Glu	Asn	Gly	Val	Ser	Arg	Tyr	Ile	Pro	Ala	Lys	Asn	Leu	Ser	Ala	Glu		
				245					250						255		
Thr	Ala	Ala	Gly	Ile	Asp	Ser	Lys	Leu	Ala	Lys	Gln	Glu	Ser	Leu	Ser		
			260					265						270			
His	Lys	Leu	Gly	Ala	Lys	Lys	Thr	Asp	Leu	Pro	Ser	Ser	Asp	Arg	Glu		
		275					280						285				
Phe	Tyr	Asn	Lys	Ala	Tyr	Asp	Leu	Leu	Ala	Arg	Ile	His	Gln	Asp	Leu		
	290					295					300						
Leu	Asp	Asn	Lys	Gly	Arg	Gln	Val	Asp	Phe	Glu	Ala	Leu	Asp	Asn	Leu		
305					310					315					320		
Leu	Glu	Arg	Leu	Lys	Asp	Val	Ser	Ser	Asp	Lys	Val	Lys	Leu	Val	Asp		
			325						330					335			
Asp	Ile	Leu	Ala	Phe	Leu	Ala	Pro	Ile	Arg	His	Pro	Glu	Arg	Leu	Gly		
		340					345						350				
Lys	Pro	Asn	Ala	Gln	Ile	Thr	Tyr	Thr	Asp	Asp	Glu	Ile	Gln	Val	Ala		
	355					360						365					
Lys	Leu	Ala	Gly	Lys	Tyr	Thr	Glu	Asp	Gly	Tyr	Ile	Phe	Asp	Pro			
	370					375					380						
Arg	Asp	Ile	Thr	Ser	Asp	Glu	Gly	Asp	Ala	Tyr	Val	Thr	Pro	His	Met		
385				390						395					400		
Thr	His	Ser	His	Trp	Ile	Lys	Lys	Asp	Ser	Leu	Ser	Glu	Ala	Glu	Arg		
			405					410						415			
Ala	Ala	Ala	Gln	Ala	Tyr	Ala	Lys	Glu	Lys	Gly	Leu	Thr	Pro	Pro	Ser		
		420					425						430				
Thr	Asp	His	Gln	Asp	Ser	Gly	Asn	Thr	Glu	Ala	Lys	Gly	Ala	Glu	Ala		
	435					440						445					
Ile	Tyr	Asn	Arg	Val	Lys	Ala	Ala	Lys	Lys	Val	Pro	Leu	Asp	Arg	Met		
	450				455						460						
Pro	Tyr	Asn	Leu	Gln	Tyr	Thr	Val	Glu	Val	Lys	Asn	Gly	Ser	Leu	Ile		
465				470					475					480			
Ile	Pro	His	Tyr	Asp	His	Tyr	His	Asn	Ile	Lys	Phe	Glu	Trp	Phe	Asp		
		485						490					495				
Glu	Gly	Leu	Tyr	Glu	Ala	Pro	Lys	Gly	Tyr	Ser	Leu	Glu	Asp	Leu	Leu		
		500					505					510					
Ala	Thr	Val	Lys	Tyr	Tyr	Val	Glu	His	Pro	Asn	Glu	Arg	Pro	His	Ser		
	515					520						525					
Asp	Asn	Gly	Phe	Gly	Asn	Ala	Ser	Asp	His	Val	Arg	Lys	Asn	Lys	Ala		
	530				535						540						
Asp	Gln	Asp	Ser	Lys	Pro	Asp	Glu	Asp	Lys	Glu	His	Asp	Glu	Val	Ser		
545				550					555					560			
Glu	Pro	Thr	His	Pro	Glu	Ser	Asp	Glu	Lys	Glu	Asn	His	Ala	Gly	Leu		
		565					570						575				
Asn	Pro	Ser	Ala	Asp	Asn	Leu	Tyr	Lys	Pro	Ser	Thr	Asp	Thr	Glu	Glu		
	580					585						590					
Thr	Glu	Glu	Glu	Ala	Glu	Asp	Thr	Thr	Asp	Glu	Ala	Glu	Ile	Pro	Gln		
	595					600					605						
Val	Glu	Asn	Ser	Val	Ile	Asn	Ala	Lys	Ile	Ala	Asp	Ala	Glu	Ala	Leu		
	610					615					620						

Leu	Glu	Lys	Val	Thr	Asp	Pro	Ser	Ile	Arg	Gln	Asn	Ala	Met	Glu	Thr
625					630					635					640
Leu	Thr	Gly	Leu	Lys	Ser	Ser	Leu	Leu	Leu	Gly	Thr	Lys	Asp	Asn	Asn
				645					650					655	
Thr	Ile	Ser	Ala	Glu	Val	Asp	Ser	Leu	Leu	Ala	Leu	Leu	Lys	Glu	Ser
			660					665					670		
Gln	Pro	Ala	Pro	Ile	Gln										
			675												

(2) INFORMATION FOR SEQ ID NO:4993:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 504 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...504

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4993:

Glu	Thr	Asn	Val	Lys	Lys	Ile	Ser	Leu	Leu	Leu	Ala	Ser	Leu	Cys	Ala
1				5				10						15	
Leu	Phe	Leu	Val	Ala	Cys	Ser	Asn	Gln	Lys	Gln	Val	Asp	Gly	Lys	Leu
			20					25					30		
Asn	Ile	Val	Thr	Thr	Phe	Tyr	Pro	Val	Tyr	Glu	Phe	Thr	Lys	Gln	Val
			35				40					45			
Ala	Gly	Asp	Thr	Ala	Asn	Val	Glu	Leu	Leu	Ile	Gly	Ala	Gly	Thr	Glu
			50			55				60					
Pro	His	Glu	Tyr	Glu	Pro	Ser	Ala	Lys	Ala	Val	Ala	Lys	Ile	Gln	Asp
65					70				75					80	
Ala	Asp	Thr	Phe	Val	Tyr	Glu	Asn	Glu	Asn	Met	Glu	Thr	Trp	Val	Pro
			85					90					95		
Lys	Leu	Leu	Asp	Thr	Leu	Asp	Lys	Lys	Lys	Val	Lys	Thr	Ile	Lys	Ala
			100					105					110		
Thr	Gly	Asp	Met	Leu	Leu	Leu	Pro	Gly	Gly	Glu	Glu	Glu	Glu	Gly	Asp
			115				120					125			
His	Asp	His	Gly	Glu	Glu	Gly	His	His	His	Glu	Phe	Asp	Pro	His	Val
			130			135					140				
Trp	Leu	Ser	Pro	Val	Arg	Ala	Ile	Lys	Leu	Val	Glu	His	Ile	Arg	Asp
145					150					155				160	
Ser	Leu	Ser	Ala	Asp	Tyr	Pro	Asp	Lys	Lys	Glu	Thr	Phe	Glu	Lys	Asn
			165					170					175		
Ala	Ala	Ala	Tyr	Ile	Glu	Lys	Leu	Gln	Ser	Leu	Asp	Lys	Ala	Tyr	Ala
			180					185					190		
Glu	Gly	Leu	Ser	Gln	Ala	Lys	Gln	Lys	Ser	Phe	Val	Thr	Gln	His	Ala
			195				200					205			
Ala	Phe	Asn	Tyr	Leu	Ala	Leu	Asp	Tyr	Gly	Leu	Lys	Gln	Val	Ala	Ile
			210				215					220			

Ser	Gly	Leu	Ser	Pro	Asp	Ala	Glu	Pro	Ser	Ala	Ala	Arg	Leu	Ala	Glu	225	230	235	240
Leu	Thr	Glu	Tyr	Val	Lys	Lys	Asn	Lys	Ile	Ala	Tyr	Ile	Tyr	Phe	Glu	245	250	255	
Glu	Asn	Ala	Ser	Gln	Ala	Leu	Ala	Asn	Thr	Leu	Ser	Lys	Glu	Ala	Gly	260	265	270	
Val	Lys	Thr	Asp	Val	Leu	Asn	Pro	Leu	Glu	Ser	Leu	Thr	Glu	Glu	Asp	275	280	285	
Thr	Lys	Asp	Gly	Glu	Asn	Tyr	Ile	Ser	Val	Met	Glu	Lys	Asn	Leu	Lys	290	295	300	
Ala	Leu	Lys	Gln	Thr	Thr	Asp	Gln	Glu	Val	Pro	Ala	Ile	Glu	Pro	Glu	305	310	315	320
Lys	Ala	Glu	Asp	Thr	Lys	Thr	Val	Gln	Asn	Gly	Tyr	Phe	Glu	Asp	Ala	325	330	335	
Ala	Val	Lys	Asp	Arg	Thr	Leu	Ser	Asp	Tyr	Ala	Gly	Asn	Trp	Gln	Ser	340	345	350	
Val	Tyr	Pro	Phe	Leu	Glu	Asp	Gly	Thr	Phe	Asp	Gln	Val	Phe	Asp	Tyr	355	360	365	
Lys	Ala	Lys	Leu	Thr	Gly	Lys	Met	Thr	Gln	Ala	Glu	Tyr	Lys	Ala	Tyr	370	375	380	
Tyr	Thr	Lys	Gly	Tyr	Gln	Thr	Asp	Val	Thr	Lys	Ile	Asn	Ile	Thr	Asp	385	390	395	400
Asn	Thr	Met	Glu	Phe	Val	Gln	Gly	Gly	Gln	Ser	Lys	Lys	Tyr	Thr	Tyr	405	410	415	
Lys	Tyr	Val	Gly	Lys	Lys	Ile	Leu	Thr	Tyr	Lys	Lys	Gly	Asn	Arg	Gly	420	425	430	
Val	Arg	Phe	Leu	Phe	Glu	Ala	Thr	Asp	Ala	Asp	Ala	Gly	Gln	Phe	Lys	435	440	445	
Tyr	Val	Gln	Phe	Ser	Asp	His	Asn	Val	Ala	Pro	Val	Lys	Ala	Glu	His	450	455	460	
Phe	His	Ile	Phe	Phe	Gly	Gly	Thr	Ser	Gln	Glu	Ala	Leu	Phe	Glu	Glu	465	470	475	480
Met	Asp	Asn	Trp	Pro	Thr	Tyr	Tyr	Pro	Asp	Asn	Leu	Ser	Gly	Gln	Glu	485	490	495	
Ile	Ala	Gln	Glu	Met	Leu	Ala	His									500			

(2) INFORMATION FOR SEQ ID NO:4994:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 86 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4994:

Gly	Arg	Arg	Leu	Ser	Thr	Glu	Ser	Val	Gly	Trp	Ala	Thr	Thr	Thr	Asp
1				5					10					15	
Cys	Ile	Ala	Arg	Gly	Leu	Ala	Met	Val	Pro	Asp	Val	Leu	Leu	Phe	Asp
			20					25					30		
Glu	Pro	Thr	Ser	Ala	Leu	Asp	Pro	Glu	Met	Val	Gly	Glu	Val	Leu	Ala
		35					40					45			
Val	Met	Gln	Asp	Leu	Ala	Lys	Ser	Gly	Met	Thr	Met	Val	Ile	Val	Thr
	50					55					60				
His	Glu	Met	Gly	Phe	Ala	Arg	Glu	Val	Ala	Asp	Arg	Val	Ile	Phe	Met
65					70					75					80
Ala	Glu	Arg	Cys	Gly	Cys										
					85										

(2) INFORMATION FOR SEQ ID NO:4995:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4995:

Glu	Ala	Ser	Val	Met	Met	Lys	Phe	Ile	Leu	Asp	Ile	Val	Ser	Thr	Pro
1				5					10					15	
Ala	Ile	Leu	Val	Ala	Leu	Ile	Ala	Ile	Leu	Gly	Leu	Val	Leu	Gln	Lys
			20					25					30		
Lys	Lys	Leu	Pro	Asp	Ile	Ile	Lys	Gly	Gly	Ile	Lys	Thr	Phe	Val	Gly
		35				40					45				
Phe	Leu	Val	Val	Ser	Gly	Gly	Ala	Gly	Ile	Val	Gln	Asn	Ser	Leu	Asn
	50				55					60					
Pro	Phe	Gly	Thr	Met	Phe	Glu	His	Ala	Phe	His	Leu	Ser	Gly	Val	Val
65				70						75					80
Pro	Asn	Asn	Glu	Ala	Ile	Val	Ala	Val	Ala	Leu	Thr	Thr	Tyr	Gly	Ser
			85					90					95		
Ala	Thr	Ala	Met	Ile	Met	Phe	Ala	Gly	Met	Val	Phe	Asn	Ile	Leu	Ile
			100					105					110		
Ala	Arg	Phe	Thr	Arg	Phe	Lys	Tyr	Ile	Phe	Leu	Thr	Gly	His	His	Thr
		115				120						125			
Leu	Tyr	Met	Ala	Cys	Met	Ile	Ala	Val	Ile	Leu	Ser	Val	Ala	Gly	Phe
	130				135					140					
Thr	Ser	Leu	Pro	Leu	Ile	Leu	Leu	Gly	Gly	Leu	Ala	Leu	Gly	Ile	Ile
145				150					155						160
Met	Ser	Ile	Ser	Pro	Ala	Phe	Val	Gln	Lys	Tyr	Met	Val	Gln	Leu	Thr
			165					170					175		
Gly	Asn	Asp	Lys	Val	Ala	Leu	Gly	His	Phe	Ser	Ser	Leu	Gly	Tyr	Trp
			180				185						190		

```

Leu Ser Gly Phe Thr Gly Ser Leu Ile Gly Asp Lys Ser Lys Ser Thr
      195                200                205
Glu Asp Ile Lys Phe Pro Lys Ser Leu Ala Phe Leu Arg Asp Ser Thr
      210                215                220
Val Ser Ile Thr Leu Ser Met Ala Val Ile Tyr Ile Ile Val Ala Ile
      225                230                235                240
Phe Ala Gly Ser Glu Tyr Ile Glu Lys Glu Ile Ser Ser Gly Thr Ser
      245                250                255
Gly Leu Val Tyr Ala Leu Gln Leu Ala Gly Gln Phe Ala Ala Gly Val
      260                265                270
Phe Val Ile Leu Ala Gly Val Arg Leu Ile Leu Gly Glu Ile Val Pro
      275                280                285
Ala Phe Lys Gly Ile Ser Glu Arg Leu Val Pro Asn Ser Lys Pro Ala
      290                295                300
Leu Asp Cys Pro Ile Val Tyr Thr Tyr Ala Pro Asn Ala Val Leu Ile
      305                310                315                320
Gly Phe Ile Ser Ser Phe Ile Gly Gly Leu Val Ser Met Ala Ile Met
      325                330                335
Ile Ala Ser Gly Thr Val Val Ile Leu Pro Gly Val Val Pro His Phe
      340                345                350
Phe Cys Gly Ala Thr Ala Gly Val Ile Gly Asn Ala Ser Gly Gly Val
      355                360                365
Arg Gly Ala Thr Ile Gly Ala Phe Leu Gln Gly Ile Leu Ile Ser Phe
      370                375                380
Leu Pro Val Phe Leu Met Pro Val Leu Gly Gly Leu Gly Phe Gln Gly
      385                390                395                400
Ser Thr Phe Ser Asp Ala Asp Phe Gly Leu Ser Gly Ile Ile Leu Gly
      405                410                415
Met Leu Asn Gln Phe Gly Ser Gln Ala Gly Ile Val Ile Gly Leu Val
      420                425                430
Leu Ile Leu Ala Val Met Phe Gly Val Ser Phe Ile Lys Lys Pro Ser
      435                440                445
Ala Lys Glu Glu
      450

```

(2) INFORMATION FOR SEQ ID NO:4996:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...66
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4996:

```

Met Glu Ser Val Leu Glu Ser Leu Lys Gln Glu Lys Asp His Leu Glu
1              5              10              15

```

Lys Ile Ile Lys Val Val Thr Ser Gly Gly Lys Phe Leu Arg Leu Pro
 20 25 30
 Tyr Gln Lys Lys Ser Arg Ser Ile Ser Glu Asn Leu Lys Leu Ile Ser
 35 40 45
 Gln Asn Leu Asp Lys Leu Ser Glu Gln Val Gln Gln Thr Thr Asn Gln
 50 55 60
 His Ser
 65

(2) INFORMATION FOR SEQ ID NO:4997:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 141 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature
 (B) LOCATION 1...141

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4997:

Arg Leu Ser Val Leu Leu Met Leu Ile Leu Arg Ala Arg Arg Tyr His
 1 5 10 15
 Arg Met Cys Leu Ile Cys Gln Arg Ile Glu Leu Ile Lys Ala Gly Gln
 20 25 30
 Asn Pro Tyr Phe Val Lys Glu Leu Glu Thr Gly Tyr Leu Val Ile Gly
 35 40 45
 Asp His Gln Tyr Phe Ala Gly Tyr Ser Leu Phe Leu Ala Lys Glu His
 50 55 60
 Val Thr Glu Leu His His Leu Lys Lys Glu Thr Arg Leu Arg Phe Leu
 65 70 75 80
 Glu Glu Met Ser Leu Val Gln Glu Ala Val Ala Lys Ala Phe Ala Ala
 85 90 95
 Glu Lys Met Asn Ile Glu Leu Leu Glu Asn Gly Asp Ala His Leu His
 100 105 110
 Trp His Leu Phe Pro Arg Arg Arg Gly Asp Met Asn Gly His Gly Leu
 115 120 125
 Lys Gly Arg Gly Pro Val Trp Trp Val Pro Leu Lys Lys
 130 135 140

(2) INFORMATION FOR SEQ ID NO:4998:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 91 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...91

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4998:

Gln	Ala	Gly	Val	Val	Val	Val	Asp	Asn	Thr	Ser	Tyr	Phe	Arg	Gln	Asn	
1				5					10					15		
Pro	Asp	Val	Pro	Leu	Val	Val	Pro	Glu	Val	Asn	Ala	His	Ala	Leu	Asp	
			20					25					30			
Ala	His	Asn	Gly	Ile	Ile	Ala	Cys	Pro	Asn	Cys	Ser	Thr	Ile	Gln	Met	
		35					40					45				
Met	Val	Ala	Leu	Glu	Arg	Phe	Arg	Gln	Lys	Trp	Gly	Leu	Glu	Arg	Ile	
	50					55					60					
Ile	Val	Leu	Thr	Tyr	Gln	Ala	Ser	Ile	Gln	Glu	Leu	Val	Trp	Glu	Gln	
65					70				75						80	
Phe	Leu	Arg	His	Asn	Val	Asn	Phe	Val	Lys	Ser						
				85					90							

(2) INFORMATION FOR SEQ ID NO:4999:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...72

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4999:

Leu	Pro	Ser	Leu	Asp	Gly	Ser	Gln	His	Arg	His	Phe	Ser	Gly	Leu	Arg	
1				5					10					15		
Gln	Val	Lys	Ile	Asn	Ser	Gln	Leu	Ser	Tyr	Tyr	Asn	Val	Phe	Leu	Ser	
			20					25					30			
Leu	Arg	Gln	Leu	Glu	Met	Ile	Ser	Val	Glu	Leu	Asp	Gln	Phe	Pro	Thr	
		35					40					45				
Ser	Leu	Ile	Thr	Phe	Ser	Gly	Tyr	Ile	Phe	Ser	Tyr	Cys	Arg	Phe	Ser	
	50					55					60					
Phe	Tyr	Pro	Lys	Phe	Ser	Tyr	Tyr									
65					70											

(2) INFORMATION FOR SEQ ID NO:5000:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 101 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...101
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5000:

```

Asp Tyr Ser Leu Met Asp Thr Thr Leu Phe Tyr Gly Ile Val Ile Val
1          5          10          15
Leu Ala Val Ser Pro Leu Leu Leu Ser Ser Phe His Ser Ile Arg Gln
          20          25          30
Gln Lys Leu Leu Arg Lys Gln Met Glu Gln Arg Gln Glu Tyr Leu Ala
          35          40          45
Ser Leu Thr Ser Gly Asp Glu Val Leu Leu Leu Ser Gly Ile His Gly
          50          55          60
Lys Ile Ile Ser Ile Gln Asp Asp Leu Val Ser Leu Gln Ile Ala Lys
65          70          75          80
Gly Val Val Ile Tyr Val Glu Lys Glu Ser Val Met Gly Lys Thr Lys
          85          90          95
Glu Leu Leu Phe Lys
          100

```

(2) INFORMATION FOR SEQ ID NO:5001:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 460 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...460
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5001:

```

Tyr Asn Ser Phe Met Asn Lys Lys Arg Thr Val Asp Leu Ile His Gly
1          5          10          15
Pro Ile Leu Pro Ser Leu Leu Ser Phe Thr Phe Pro Ile Leu Leu Ser

```

			20					25				30			
Asn	Ile	Phe	Gln	Gln	Leu	Tyr	Asn	Thr	Ala	Asp	Val	Leu	Ile	Val	Gly
		35					40					45			
Arg	Phe	Leu	Gly	Gln	Glu	Ser	Leu	Ala	Ala	Val	Gly	Ala	Thr	Thr	Ala
	50					55					60				
Ile	Phe	Asp	Leu	Ile	Val	Gly	Phe	Thr	Leu	Gly	Val	Gly	Asn	Gly	Met
65					70					75					80
Gly	Ile	Val	Ile	Ala	Arg	Tyr	Tyr	Gly	Ala	Arg	Asn	Phe	Thr	Lys	Ile
				85					90					95	
Lys	Glu	Ala	Val	Ala	Ala	Thr	Trp	Ile	Leu	Gly	Ala	Leu	Leu	Ser	Ile
			100					105						110	
Leu	Val	Met	Leu	Leu	Gly	Phe	Leu	Gly	Leu	Tyr	Pro	Leu	Leu	Gln	Tyr
		115					120					125			
Leu	Asp	Thr	Pro	Ala	Glu	Ile	Leu	Pro	Gln	Ser	Tyr	Gln	Tyr	Ile	Ser
	130					135					140				
Met	Ile	Val	Thr	Cys	Val	Gly	Val	Ser	Phe	Ala	Tyr	Asn	Leu	Phe	Ala
145					150					155					160
Gly	Leu	Leu	Arg	Ser	Ile	Gly	Asp	Ser	Leu	Ala	Ala	Leu	Gly	Phe	Leu
				165					170					175	
Ile	Phe	Ser	Ala	Leu	Val	Asn	Val	Val	Leu	Asp	Leu	Tyr	Phe	Ile	Thr
			180					185					190		
Gln	Leu	His	Leu	Gly	Val	Gln	Ser	Ala	Gly	Leu	Ala	Thr	Ile	Ile	Ser
		195					200					205			
Gln	Gly	Leu	Ser	Ala	Val	Leu	Cys	Phe	Tyr	Tyr	Ile	Arg	Lys	Ser	Val
	210					215					220				
Pro	Glu	Leu	Leu	Pro	Gln	Phe	Lys	His	Phe	Lys	Trp	Asp	Lys	Ser	Leu
225					230					235					240
Tyr	Ala	Asp	Leu	Leu	Glu	Gln	Gly	Leu	Ala	Met	Gly	Leu	Met	Ser	Ser
				245					250					255	
Ile	Val	Ser	Ile	Gly	Ser	Val	Ile	Leu	Gln	Ser	Ser	Val	Asn	Thr	Phe
			260					265					270		
Gly	Ala	Val	Ile	Ile	Ser	Ala	Gln	Thr	Ala	Ala	Arg	Arg	Ile	Met	Thr
		275					280					285			
Phe	Ala	Leu	Leu	Pro	Met	Thr	Ala	Ile	Ser	Ala	Ser	Met	Thr	Thr	Phe
	290					295					300				
Ala	Ser	Gln	Asn	Leu	Gly	Ala	Lys	Gln	Pro	Asp	Arg	Ile	Val	Gln	Gly
305					310					315					320
Leu	Arg	Ile	Gly	Ser	Arg	Leu	Ser	Ile	Ser	Trp	Ala	Val	Phe	Val	Cys
				325					330					335	
Ile	Phe	Leu	Phe	Phe	Ala	Ser	Pro	Ala	Leu	Val	Ser	Phe	Leu	Ala	Ser
		340						345					350		
Ser	Thr	Asp	Gly	Tyr	Leu	Ile	Glu	Asn	Gly	Ser	Leu	Tyr	Leu	Gln	Ile
		355					360					365			
Ser	Ser	Thr	Phe	Tyr	Pro	Ile	Leu	Ser	Leu	Leu	Leu	Ile	Tyr	Arg	Asn
		370				375					380				
Cys	Leu	Gln	Gly	Leu	Gly	Gln	Lys	Ile	Leu	Pro	Leu	Val	Ser	Ser	Phe
385					390					395					400
Ile	Glu	Leu	Ile	Gly	Lys	Ile	Val	Phe	Val	Val	Leu	Ile	Ile	Pro	Trp
				405				410						415	
Ala	Gly	Tyr	Lys	Gly	Val	Ile	Leu	Cys	Glu	Pro	Leu	Ile	Trp	Val	Ala
			420					425					430		
Met	Thr	Val	Gln	Leu	Tyr	Phe	Ser	Leu	Phe	Arg	His	Pro	Leu	Ile	Lys
		435					440					445			
Glu	Gly	Lys	Ala	Ile	Leu	Ala	Thr	Lys	Val	Gln	Ser				
	450					455					460				

(2) INFORMATION FOR SEQ ID NO:5002:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 295 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...295
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5002:

Ile	Asn	Ser	Phe	Arg	Ala	Thr	Lys	Gly	Lys	Asn	Ser	Met	Ala	Thr	Ile
1				5				10						15	
Gln	Trp	Phe	Pro	Gly	His	Met	Ser	Lys	Ala	Arg	Arg	Gln	Val	Gln	Glu
			20					25					30		
Asn	Leu	Lys	Phe	Val	Asp	Phe	Val	Thr	Ile	Leu	Val	Asp	Ala	Arg	Leu
		35					40					45			
Pro	Leu	Ser	Ser	Gln	Asn	Pro	Met	Leu	Thr	Lys	Ile	Val	Gly	Asp	Lys
	50					55					60				
Pro	Lys	Leu	Leu	Ile	Leu	Asn	Lys	Ala	Asp	Leu	Ala	Asp	Pro	Ala	Met
65				70					75						80
Thr	Lys	Glu	Trp	Arg	Gln	Tyr	Phe	Glu	Ser	Gln	Gly	Ile	Gln	Thr	Leu
				85				90						95	
Ala	Ile	Asn	Ser	Lys	Glu	Gln	Val	Thr	Val	Lys	Val	Val	Thr	Asp	Ala
			100					105					110		
Ala	Lys	Lys	Leu	Met	Ala	Asp	Lys	Ile	Ala	Arg	Gln	Lys	Glu	Arg	Gly
		115					120					125			
Ile	Gln	Ile	Glu	Thr	Leu	Arg	Thr	Met	Ile	Ile	Gly	Ile	Pro	Asn	Ala
130						135					140				
Gly	Lys	Ser	Thr	Leu	Met	Asn	Arg	Leu	Ala	Gly	Lys	Lys	Ile	Ala	Val
145				150						155					160
Val	Gly	Asn	Lys	Pro	Gly	Val	Thr	Lys	Gly	Gln	Gln	Trp	Leu	Lys	Thr
			165						170					175	
Asn	Lys	Asp	Leu	Glu	Ile	Leu	Asp	Thr	Pro	Gly	Ile	Leu	Trp	Pro	Lys
			180					185					190		
Phe	Glu	Asp	Glu	Thr	Val	Ala	Leu	Lys	Leu	Ala	Leu	Thr	Gly	Ala	Ile
		195					200						205		
Lys	Asp	Gln	Leu	Leu	Pro	Met	Asp	Glu	Val	Thr	Ile	Phe	Gly	Ile	Asn
	210					215					220				
Tyr	Phe	Lys	Glu	His	Tyr	Pro	Glu	Lys	Leu	Ala	Glu	Arg	Phe	Lys	Gln
225				230						235					240
Met	Lys	Ile	Glu	Glu	Glu	Pro	Ser	Val	Ile	Ile	Met	Asp	Met	Thr	Arg
			245						250					255	
Ala	Leu	Gly	Phe	Arg	Asp	Asp	Tyr	Asp	Arg	Phe	Tyr	Ser	Leu	Phe	Val
			260					265					270		
Lys	Glu	Val	Arg	Asp	Gly	Lys	Leu	Gly	Asn	Tyr	Thr	Leu	Asp	Thr	Leu
		275					280						285		
Glu	Asp	Leu	Asp	Gly	Asn	Asp									
	290					295									

(2) INFORMATION FOR SEQ ID NO:5003:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 652 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...652

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5003:

Thr	Ser	Leu	Val	Lys	Gly	Val	Arg	Leu	Met	Asn	Lys	Arg	Lys	Val	Ser
1				5					10					15	
Leu	Glu	Asp	Phe	Tyr	Lys	Trp	Tyr	Ser	Leu	Asn	Lys	Glu	Glu	Leu	Leu
			20					25					30		
Asn	Lys	Ala	Thr	Val	Gly	Glu	Lys	Phe	Asn	Asp	Lys	Leu	Lys	Glu	Glu
		35					40					45			
Phe	Leu	Gln	Glu	Trp	Pro	Leu	Asp	Arg	Ile	Leu	Thr	Met	Ser	Ile	Asp
	50					55					60				
Glu	Tyr	Val	Ile	Gly	Lys	Gly	Gln	Gln	Asn	Lys	Ser	Leu	Cys	Tyr	Ala
65					70				75						80
Leu	Glu	Lys	Gly	Lys	Tyr	Lys	Asn	Leu	Phe	Leu	Gly	Ile	Ser	Gly	Gly
			85					90					95		
Ser	Ala	Ser	Lys	Phe	Gly	Ile	Tyr	Trp	Asn	Lys	Lys	Thr	Asn	Lys	Tyr
		100						105					110		
Lys	Asp	Gln	Ala	Asn	Asn	Glu	Ile	Ser	Glu	Leu	Asp	Gln	Arg	Phe	Ser
	115					120						125			
Lys	Leu	Lys	Ser	Asp	Leu	Tyr	Glu	Ile	Ile	Lys	Glu	Gly	Ile	Arg	Phe
	130					135					140				
Asn	Phe	Glu	Asn	Pro	Ile	Phe	Asp	Met	Lys	Arg	Ser	Thr	Asn	Glu	Phe
145				150					155						160
Ile	Gly	Arg	Ser	Ala	Met	Val	Thr	Lys	Leu	Leu	Cys	Ile	Tyr	Thr	Glu
			165					170					175		
Gly	Asp	Pro	Phe	Gly	Val	Asn	Ile	Asn	Ser	Gln	Lys	Glu	Phe	Trp	
		180					185					190			
Asn	His	Phe	Val	Ser	Gln	Thr	Asn	Gln	Gly	Gly	Pro	Tyr	Leu	Gln	Asn
	195						200					205			
His	Lys	Ile	Ile	Glu	Leu	Val	Ser	Lys	Thr	Tyr	Pro	Glu	Leu	Glu	Pro
	210					215					220				
Ser	Lys	Leu	Gly	Thr	Met	Leu	Phe	Glu	Tyr	Ser	Lys	Leu	Phe	Met	Glu
225				230					235						240
Asn	Lys	Glu	Asp	Asn	Ser	Thr	Met	Asp	Ser	Ser	Asn	Asn	Phe	Ser	His
			245					250					255		
Gln	Leu	Thr	Gln	Ser	Leu	Leu	Lys	Ser	Pro	Asn	Leu	Ile	Leu	Arg	Gly
		260					265					270			
Ala	Pro	Gly	Thr	Gly	Lys	Thr	Tyr	Leu	Ala	Lys	Glu	Ile	Ala	Lys	Glu
		275					280					285			

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION: 1...296

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5004:

Asn	Gln	Leu	Val	Ser	Ser	Phe	Leu	Ser	Ile	Ser	Ser	Pro	Lys	Tyr	Ala	
1				5					10					15		
Ile	Ile	Ile	Ala	Lys	Asp	Lys	Glu	Gly	Arg	Pro	Met	Ile	Lys	Leu	Leu	
			20					25					30			
Ala	Leu	Asp	Met	Asp	Gly	Thr	Leu	Leu	Asn	Glu	Ala	Lys	Glu	Ile	Pro	
			35				40					45				
Gln	Ala	His	Ile	Ala	Ala	Ile	His	Gln	Ala	Ile	Glu	Lys	Gly	Val	Lys	
			50				55				60					
Leu	Val	Leu	Cys	Thr	Gly	Arg	Pro	Leu	Phe	Gly	Val	Leu	Pro	Tyr	Tyr	
65					70				75					80		
Lys	Lys	Leu	Gly	Leu	Asp	Leu	Gln	Asn	Glu	Tyr	Val	Ile	Val	Asn	Asn	
				85					90					95		
Gly	Cys	Ser	Thr	His	Gln	Thr	Ser	Asp	Trp	Gly	Leu	Val	Asp	Trp	Gln	
			100					105					110			
Glu	Leu	Ser	Pro	Ala	Asp	Ile	Glu	Tyr	Leu	Tyr	Asp	Leu	Ala	Glu	Lys	
			115				120					125				
Ser	Asp	Val	Gln	Leu	Thr	Leu	Phe	Asp	Glu	Ser	His	Tyr	Phe	Val	Leu	
			130				135					140				
Gly	Gly	Lys	Pro	Asn	Gln	Val	Ile	Glu	Asn	Asp	Ala	Lys	Leu	Val	Phe	
145					150				155						160	
Ser	Asp	Leu	Thr	Glu	Ile	Ser	Leu	Glu	Glu	Ala	Thr	Ser	Gly	Lys	Leu	
				165				170						175		
Arg	Met	Phe	Gln	Gly	Met	Phe	Leu	Gly	Thr	Lys	Glu	Gln	Thr	Asp	Asp	
			180					185					190			
Phe	Glu	Gln	Arg	Phe	Ala	Glu	Glu	Leu	Cys	Gln	Arg	Phe	Ser	Gly	Val	
			195				200					205				
Arg	Ser	Gln	Pro	Val	Ile	Tyr	Glu	Ala	Met	Pro	Leu	Gly	Thr	Thr	Lys	
			210			215					220					
Ala	Thr	Ala	Leu	Ser	Arg	Leu	Ala	Glu	Ile	Leu	Lys	Ile	Asp	Ser	Ser	
225					230					235					240	
Glu	Ile	Met	Ala	Met	Gly	Asp	Ala	Asn	Asn	Asp	Ile	Glu	Met	Leu	Gln	
				245					250					255		
Phe	Ala	Gly	Leu	Gly	Ile	Ala	Met	Gly	Asn	Ala	Ser	Asp	Tyr	Val	Lys	
			260					265					270			
Ser	Leu	Ala	Asp	Ala	Val	Thr	Ser	Ser	Asn	Glu	Glu	Asp	Gly	Val	Ala	
			275				280					285				
Arg	Ala	Ile	Glu	Lys	Tyr	Ile	Leu									
			290				295									

(2) INFORMATION FOR SEQ ID NO:5005:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 287 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...287
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5005:

```

His Met Leu Val Phe Ser Glu Tyr Gln Thr Gly Thr Ile Asp Leu Ala
1      5      10      15
Leu Ser Phe Tyr Gly Tyr Glu Glu Cys Thr Pro Asn Tyr Ser Phe Gly
      20      25      30
Pro Ala Ile Arg Asp Thr Tyr Val Leu His Tyr Ile Thr Lys Gly Gln
      35      40      45
Gly Lys Phe Tyr Tyr Lys Gly Lys Ile Val Asp Leu Lys Glu Gly Asp
      50      55      60
Phe Phe Leu Leu Lys Pro Glu Glu Leu Thr Phe Tyr Gln Ala Asp Ser
      65      70      75      80
Lys Glu Pro Trp Ala Tyr Tyr Trp Leu Gly Ile Thr Gly Gly Lys Ser
      85      90      95
Pro Asp Tyr Phe Ala Leu Ser Gln Ile Ser Asp Gln Ser Tyr Leu Ile
      100     105     110
Gln Ser Glu Thr Cys His Thr Gln Thr Thr Ala Lys Leu Ile Ser Asp
      115     120     125
Ile Val Arg Phe Ala Gln Ile Thr Lys Ser Ser Glu Leu Ala Gln Leu
      130     135     140
His Ile Met Gly Gln Leu His Glu Leu Met Phe His Leu Gly Thr Ile
      145     150     155     160
Ala Pro Asn Gln Lys Lys Lys Asn Ile Ser Ser Thr His Gln Leu Tyr
      165     170     175

Leu Glu Cys Lys Arg Leu Ile Asp Ser His Tyr Pro Gln Ser Leu Thr
      180     185     190
Ile Gln Asp Leu Ala Lys Glu Leu Ser Val His Arg Ser Tyr Leu Ser
      195     200     205
Ser Val Phe Lys Glu Phe Asn Thr Leu Ser Pro Lys Glu Tyr Leu Leu
      210     215     220
Tyr Val Arg Met His Arg Ala Arg Gln Leu Leu Glu Asn Thr Gln Glu
      225     230     235     240
Ser Ile Lys Val Ile Ala Tyr Ser Val Gly Phe Ser Asp Pro Leu His
      245     250     255
Phe Ser Lys Ala Tyr Lys Gln Tyr Phe Asn Gln Thr Pro Ser His Thr
      260     265     270
Arg Lys Glu Tyr Ser Gln Tyr Gln Leu Val Arg Lys Ala Thr Leu
      275     280     285

```

- (2) INFORMATION FOR SEQ ID NO:5006:
 - (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 138 amino acids
 - (B) TYPE: amino acid

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...138
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5006:

```

Pro Met Leu Val Pro Lys Arg Val Lys His Arg Arg Glu Phe Arg Gly
1          5          10          15
Lys Met Arg Gly Glu Ala Lys Gly Gly Lys Glu Val Ala Phe Gly Glu
20          25          30
Tyr Gly Leu Gln Ala Thr Thr Ser His Trp Ile Thr Asn Arg Gln Ile
35          40          45
Glu Ala Ala Arg Ile Ala Met Thr Arg Tyr Met Lys Arg Gly Gly Lys
50          55          60
Val Trp Ile Lys Ile Phe Pro His Lys Ser Tyr Thr Ala Lys Ala Ile
65          70          75          80
Gly Val Arg Met Gly Ser Gly Lys Gly Ala Pro Glu Gly Trp Val Xaa
85          90          95
Pro Val Lys Arg Gly Lys Met Met Phe Glu Ile Ala Gly Val Ser Glu
100         105         110
Glu Ile Ala Arg Glu Ala Leu Arg Leu Ala Ser His Lys Leu Pro Val
115         120         125
Lys Cys Lys Phe Val Lys Arg Glu Ala Lys
130         135

```

(2) INFORMATION FOR SEQ ID NO:5007:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 86 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...86
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5007:

```

Ser Thr Ile Val Lys Phe Asn Ile Lys Lys Met Leu Lys Gln Ser Glu
1          5          10          15
Lys Arg Leu Lys Ser Ser Lys Glu Ser Asn Met Gly Leu Ile Lys Thr

```

		20					25				30				
Leu	Ala	Lys	Ile	Tyr	Gly	Asn	Tyr	Phe	Leu	Thr	Val	Gln	Gly	Val	Lys
		35					40					45			
Val	Met	Lys	Thr	Ile	Lys	Lys	Ala	Asp	His	Val	Val	Val	Gly	Leu	Gly
		50				55					60				
Lys	Leu	Phe	Ile	Ala	Asp	Lys	Leu	Met	Asp	Thr	Ala	Arg	Trp	Leu	Ile
65					70					75					80
Lys	Pro	Glu	Glu	Arg	Glu										
					85										

(2) INFORMATION FOR SEQ ID NO:5008:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 91 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...91
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5008:

His	Ile	Ile	Val	Ser	Lys	Ala	Leu	Leu	Glu	Ile	Thr	Leu	Lys	Ser	Ser
1				5					10					15	
Tyr	Gln	Phe	Val	His	Ile	Leu	Phe	Gln	Ser	Thr	Ile	Tyr	Ile	Pro	Ser
			20					25					30		
Thr	Met	His	His	Asn	Leu	Gly	Asn	Ser	Tyr	Ser	Ile	Lys	Ile	Lys	Lys
			35				40					45			
Gln	Thr	Arg	Lys	Leu	Gly	Thr	Asp	Cys	Ser	Lys	His	Arg	Phe	Lys	Val
			50			55					60				
Val	Asp	Arg	Thr	Asp	Glu	Val	Ser	Ser	Lys	His	Cys	Phe	Glu	Val	Val
65					70					75					80
Asp	Thr	Thr	His	Ile	Tyr	Thr	Thr	Arg	Gln	Arg					
			85						90						

(2) INFORMATION FOR SEQ ID NO:5009:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 68 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...68

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5009:

```
Ser Thr Ile Val Gln Val Leu Ser Glu Val Asp Asn Leu Asn Leu Val
1           5           10           15
Trp Tyr Thr Ile Phe Val Ile Gly Tyr Arg Leu Arg Ser Tyr Gly Phe
          20           25           30
Val Arg Gly Gly Glu Thr Asn Glu Pro Tyr Thr Arg Ala Arg Ser Tyr
          35           40           45
Tyr Tyr Ser Arg Cys Tyr Ser Trp Asn Tyr Leu Val Phe Arg Leu Gln
          50           55           60
Met Ala Arg Trp
65
```

(2) INFORMATION FOR SEQ ID NO:5010:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5010:

```
Gln Trp Ile Val Gly Cys Thr Thr Ile Thr Ser Val Val Pro Asn Pro
1           5           10           15
Ser Ile Phe Leu Val Val Thr Asp Lys Ala Gly Asp Gly Thr Val Asp
          20           25           30
Thr Phe Ile Gly Val Ala Thr Val Gly Gln Val Ser Cys Pro Val Met
          35           40           45
Glu Gly Arg Val Val Leu Thr Thr Met Ala Pro Leu Asp Arg Lys Ala
          50           55           60
Pro Ala Leu Phe Val Asn Phe Phe Ser Lys Asn Val Gly Ser Pro Gly
          65           70           75           80
Thr Val Ile Thr
```

(2) INFORMATION FOR SEQ ID NO:5011:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 131 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...131
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5011:

```

Arg Arg Val Val Met Asp Arg Asn Ile Asp Gln Glu Leu Val Ser Ile
1      5      10      15
Ile Ile Pro Thr His Asn Arg Tyr Glu Ser Leu Ile Arg Ala Val Lys
20      25      30
Ser Cys Leu His Gln Ser Tyr Lys Asn Ile Glu Val Ile Ile Ile Asp
35      40      45
Asp Asn Tyr Ser Asn Val Asn Leu Arg Asn Lys Ile Ile His Gln Phe
50      55      60
Gly Tyr Thr Asn His Arg Ile Lys Leu Ile Leu Ser Asn Glu Asp Leu
65      70      75      80
Gly Ala Thr Asn Ala Arg Asn Ile Gly Ile Lys Asn Ser Arg Gly Lys
85      90      95
Tyr Ile Ser Phe Leu Asp Asp Asp Asp Glu Tyr Met Pro Asp Arg Ile
100      105      110
Leu Lys Leu Met Ala Cys Leu Lys Lys Pro Trp Asn Glu Glu Cys Ser
115      120      125
Ser Ser Leu
130

```

(2) INFORMATION FOR SEQ ID NO:5012:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 152 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...152
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5012:

```

Ala Glu Xaa Val Gly Val Gly Val Gly Arg Ala Leu Pro Thr Leu Xaa
1      5      10      15
Gly Met Asn Gln Val Leu Lys Val Leu Ser Glu Val Gly Ile Gln Lys
20      25      30
Ile Met Phe Phe Leu Xaa Val Leu Phe Tyr Gly Asn Asn Cys Ile Asp

```


Tyr	Lys	Ile	Gln	Glu	Asp	Leu	Asp	Leu	His	Asp	Ser	Glu	Ile	Leu	Arg
				165					170					175	
Ala	Ile	Glu	Val	His	Thr	Val	Gly	Ala	Gly	Gln	Met	Thr	Asp	Leu	Asp
			180					185					190		
Lys	Val	Ile	Tyr	Val	Ala	Asp	Tyr	Ile	Glu	His	Asn	Arg	Ala	Phe	Pro
		195					200					205			
Gly	Val	Asp	Val	Ala	Arg	Glu	Ile	Ala	Ser	Leu	Ser	Leu	Asn	Lys	Ala
	210					215					220				
Val	Ala	Tyr	Glu	Thr	Ala	Arg	Thr	Val	Glu	Tyr	Leu	Ala	His	Gln	Gly
225					230					235					240
Phe	Pro	Ile	Tyr	Pro	Gln	Thr	Leu	Glu	Thr	Tyr	Asn	Ala	Phe	Val	His
				245					250					255	
Tyr	Leu	Lys	Glu	Asp											
			260												

(2) INFORMATION FOR SEQ ID NO:5014:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 357 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...357
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5014:

Ile	Leu	Pro	Val	Arg	Leu	Pro	Arg	Cys	Val	Arg	Ala	Ala	Pro	Gly	Ala
1				5				10						15	
Arg	Arg	Arg	Arg	Gly	Ala	Pro	Val	Arg	Arg	Thr	Ser	Pro	Val	Ala	Ala
			20					25					30		
Gly	Val	Pro	Ala	Val	Leu	Ala	Gly	Thr	Ala	Ala	Gly	Ala	Arg	Ala	Pro
	35					40						45			
Leu	Arg	Gly	Ala	Ala	Arg	Ser	Arg	Arg	Ser	Pro	Val	Pro	Gly	Arg	Leu
	50					55					60				
Pro	Phe	Pro	Ala	Ala	Val	Leu	Pro	Ala	Ala	Ala	Arg	Leu	Pro	Gly	Ala
65					70					75					80
Gly	Gly	Arg	Ala	Trp	Pro	Pro	Gly	Arg	Arg	Glu	Thr	Ala	Val	Ala	Leu
				85					90					95	
Arg	Pro	Val	Ala	Ser	Arg	Gly	Ser	Pro	Val	Ala	Pro	Pro	Gly	Ala	Arg
			100					105					110		
Cys	Val	Pro	Ala	Pro	Arg	Arg	Glu	Pro	Val	Ala	Ile	Gly	Gly	Pro	Gly
	115						120					125			
Arg	Ala	Arg	Pro	Gly	Pro	Gly	Ala	Gly	Val	Gly	Arg	Ala	Thr	Ala	Ala
	130					135					140				
Pro	Gly	Ser	Cys	Ala	Glu	Ala	Pro	Gln	Leu	Arg	Ala	Gly	Leu	Cys	Val
145					150					155					160
Ile	Ala	Gly	Phe	Val	Gly	Thr	Leu	Ala	Gln	Pro	Leu	Ala	Asp	Arg	Arg
				165					170					175	

```

Asp Leu Leu Asp Gly Leu Val Gly Phe Ala Val Leu Ala Phe Leu Val
180 185 190
Phe Ala Asp Leu Gln Gln Gln Leu Asp Phe Leu Val Leu Arg Gln Pro
195 200 205
Phe Ala Gln Ala Ser Gly Arg Met Ala Leu Ile Val Val Asp Asp Leu
210 215 220
Val His Asp Pro Ala His Arg Val Gln His Val Asp Gly Arg Ile Val
225 230 235 240
Val Gly Gly Gly Gln Leu Ala Arg Gln His Asp Val Pro Val Glu Asn
245 250 255
Arg Ala Gly Leu Val Gly His Arg Leu Ala His Val Val Ala Phe His
260 265 270
Gln His Gly Val Glu Arg Gly Asp Arg Ala Pro Leu Gly Leu Pro Gly
275 280 285
Thr Leu His Gln Ala Trp Gln Arg Gly Glu His Arg Trp Arg Ile Ala
290 295 300
Ala Ala Gly Gly Arg Phe Thr Gly Arg Gln Ala Asp Phe Ala Leu Gly
305 310 315 320
Pro Gly Glu Ala Gly Gln Arg Val His Gln Gln Gln Asp Ala Ala Ser
325 330 335
Leu Val Ala Asp Ile Leu Gly Asp Ala Gly Gly Asp Glu Ile Gly Ile
340 345 350
Glu Leu Tyr Thr Thr
355

```

(2) INFORMATION FOR SEQ ID NO:5015:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 525 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...525

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5015:

```

Tyr Phe Ala Val Val Gly Gly Gln Ile Met Thr Pro Glu Gln Leu Lys
1 5 10 15
Ala Ser Ile Leu Gln Arg Ala Met Glu Gly Lys Leu Val Pro Gln Asn
20 25 30
Pro Asn Asp Glu Pro Ala Ser Glu Leu Leu Lys Arg Ile Lys Ala Glu
35 40 45
Lys Glu Lys Leu Ile Ser Glu Gly Lys Ile Lys Arg Asp Lys Lys Glu
50 55 60
Thr Glu Ile Phe Arg Gly Asp Asp Gly Lys His Tyr Gly Lys Phe Ala
65 70 75 80
Asp Gly Ser Thr Gln Glu Ile Asp Val Pro Tyr Asp Ile Pro Asp Thr
85 90 95

```

Trp	Glu	Trp	Val	Arg	Ile	Lys	Ser	Ile	Tyr	Trp	Asn	Phe	Gly	Gln	Asn		
			100					105					110				
Lys	Pro	Glu	Lys	Ser	Phe	Arg	Tyr	Ile	Asp	Thr	Ser	Ser	Ile	Asp	Arg		
		115					120					125					
Lys	Lys	Asn	Ile	Ile	Asn	Tyr	Lys	Asn	Leu	Gln	Tyr	Leu	Ser	Pro	Glu		
		130				135					140						
Gln	Ala	Pro	Ser	Arg	Ala	Arg	Lys	Leu	Val	Ser	Gln	Asn	Ser	Val	Leu		
145					150					155					160		
Phe	Ser	Thr	Val	Arg	Pro	Tyr	Leu	Lys	Asn	Ile	Ala	Val	Val	Arg	Glu		
			165						170					175			
Leu	Lys	Glu	Tyr	Leu	Ile	Ala	Ser	Thr	Ala	Phe	Ile	Val	Leu	Asp	Thr		
		180						185					190				
Leu	Leu	Asn	Glu	Thr	Tyr	Leu	Lys	Tyr	Tyr	Leu	Leu	Ser	Asp	Asn	Phe		
		195					200					205					
Ile	Asn	Arg	Val	Asn	Asn	Lys	Ser	Thr	Gly	Thr	Ser	Tyr	Pro	Ala	Ile		
	210					215					220						
Asn	Asp	Tyr	Asn	Phe	Asn	Leu	Leu	Leu	Ile	Ala	Leu	Pro	Pro	Leu	Ser		
225				230						235					240		
Glu	Gln	Gln	Arg	Ile	Val	Glu	Ala	Ile	Glu	Ser	Ala	Leu	Glu	Lys	Val		
			245						250					255			
Asp	Glu	Tyr	Ala	Glu	Ser	Tyr	Asn	Arg	Leu	Glu	Gln	Leu	Asp	Lys	Glu		
		260						265					270				
Phe	Pro	Asp	Lys	Leu	Lys	Lys	Ser	Ile	Leu	Gln	Tyr	Ala	Met	Gln	Gly		
		275					280					285					
Lys	Leu	Val	Glu	Gln	Asp	Pro	Asn	Asp	Glu	Ser	Val	Glu	Val	Leu	Leu		
	290					295					300						
Glu	Lys	Ile	Arg	Ala	Glu	Lys	Gln	Lys	Leu	Phe	Glu	Glu	Gly	Lys	Ile		
305					310					315					320		
Lys	Lys	Lys	Asp	Leu	Asp	Ile	Ser	Ile	Val	Ser	Gln	Gly	Asp	Asp	Asn		
			325						330				335				
Ser	Tyr	Tyr	Glu	Glu	Val	Pro	Cys	Glu	Ile	Pro	Glu	Ser	Trp	Glu	Trp		
		340						345					350				
Val	Arg	Leu	Asn	Asp	Ile	Thr	Ser	Tyr	Ile	Gln	Arg	Gly	Lys	Ser	Pro		
	355						360					365					
Lys	Tyr	Ser	Asn	Ile	Pro	Ile	Tyr	Pro	Val	Ile	Ala	Gln	Lys	Cys	Asn		
	370					375					380						
Gln	Trp	Ser	Gly	Phe	Ser	Ile	Asp	Leu	Ala	Arg	Phe	Ile	Asp	Pro	Glu		
385					390					395					400		
Thr	Val	His	Ser	Tyr	Gln	Lys	Glu	Arg	Leu	Leu	Arg	Asp	Gly	Asp	Leu		
			405					410					415				
Met	Trp	Asn	Ser	Thr	Gly	Leu	Gly	Thr	Leu	Gly	Arg	Leu	Ala	Ile	Tyr		
		420						425					430				
His	Glu	Asn	Lys	Asn	Pro	Tyr	Gly	Trp	Ala	Val	Ala	Asp	Ser	His	Val		
	435						440					445					
Thr	Val	Ile	Arg	Val	Leu	Ser	Gly	Val	Ile	Asn	Cys	His	Phe	Ile	Tyr		
	450					455					460						
Asn	Phe	Leu	Ser	Ser	Pro	Ile	Val	Gln	Ser	Val	Ile	Glu	Glu	Lys	Ala		
465					470					475					480		
Ser	Gly	Ser	Thr	Lys	Gln	Lys	Glu	Leu	Leu	Thr	Lys	Thr	Ile	Lys	Glu		
			485					490					495				
Tyr	Leu	Ile	Pro	Leu	Pro	Pro	Leu	Pro	Glu	Gln	Ser	Arg	Ile	Val	Asp		
		500					505						510				
Lys	Ile	Glu	Gln	Phe	Phe	Ala	His	Ile	Asp	Ala	Leu	Ile					
	515						520					525					

(2) INFORMATION FOR SEQ ID NO:5016:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 531 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...531
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5016:

```

Tyr Phe Ala Val Val Gly Gly Gln Ile Met Thr Pro Glu Gln Leu Lys
1      5      10      15
Ala Ser Ile Leu Gln Arg Ala Met Glu Gly Lys Leu Val Pro Gln Asn
20      25      30
Pro Asn Asp Glu Pro Ala Ser Glu Leu Leu Lys Arg Ile Lys Ala Glu
35      40      45
Lys Glu Lys Leu Ile Ser Glu Gly Lys Ile Lys Arg Asp Lys Lys Glu
50      55      60
Thr Glu Ile Phe Arg Gly Asp Asp Gly Lys His Tyr Gly Lys Phe Ala
65      70      75      80
Asp Gly Ser Thr Gln Glu Ile Asp Val Pro Tyr Asp Ile Pro Asp Thr
85      90      95
Trp Glu Trp Val Arg Phe Ser Thr Leu Val Glu Ile Val Arg Gly Gly
100     105     110
Ser Pro Arg Pro Ile Lys Asp Tyr Leu Thr Ser Glu Val Asp Gly Ile
115     120     125
Asn Trp Ile Lys Ile Gly Asp Thr Glu Lys Gly Glu Lys Tyr Ile Asn
130     135     140
Asn Val Lys Glu Lys Ile Lys Lys Ser Gly Leu Asn Lys Thr Arg Phe
145     150     155     160
Val Lys Lys Gly Thr Phe Leu Leu Thr Asn Ser Met Ser Phe Gly Arg
165     170     175
Pro Tyr Ile Leu Asn Val Asp Gly Ala Ile His Asp Gly Trp Leu Ala
180     185     190
Ile Ser Asn Tyr Glu Asn Ser Leu Asn Lys Asp Tyr Leu Phe Tyr Ile
195     200     205
Leu Ser Ser Asn Val Val Tyr Ser Gln Phe Leu Ser Leu Ile Ser Gly
210     215     220
Ala Val Val Lys Asn Leu Asn Ser Asp Lys Val Ala Ser Ile Leu Ile
225     230     235     240
Pro Leu Pro Pro Leu Ser Glu Gln Gln Arg Ile Ile Glu Ala Ile Glu
245     250     255
Ser Ala Leu Glu Lys Val Asp Glu Tyr Ala Glu Ser Tyr Asn Arg Leu
260     265     270
Glu Gln Leu Asp Lys Glu Phe Pro Asp Lys Leu Lys Lys Ser Ile Leu
275     280     285
Gln Tyr Ala Met Arg Gly Lys Leu Val Glu Gln Asp Pro Asn Asp Glu
290     295     300
Ser Val Glu Val Leu Leu Glu Lys Ile Arg Ala Glu Lys Gln Lys Leu

```

```

305          310          315          320
Phe Glu Glu Gly Lys Ile Lys Lys Lys Asp Leu Asp Ile Ser Ile Val
          325          330          335
Ser Gln Gly Asp Asp Asn Ser Tyr Tyr Gly Asn Lys Asp Glu Thr Thr
          340          345          350
Ser Tyr Pro Ile Tyr Lys Ile Pro Glu Ala Trp Arg Tyr Ile Lys Phe
          355          360          365
Ala Ser Leu Val Asn Phe Arg Ile Gly Lys Thr Pro Pro Arg Ser Glu
          370          375          380
Ala Thr Phe Trp Gly Thr Glu Ile Pro Trp Val Ser Ile Ser Asp Met
385          390          395          400
Pro Ile Ser Gly Tyr Val Thr Asn Thr Arg Glu Ser Ile Ser Lys Leu
          405          410          415
Ala Leu Lys Ser Lys Lys Ile Asp Ile Ser Pro Lys Gly Thr Leu Leu
          420          425          430
Met Ser Phe Lys Leu Ser Ile Gly Lys Val Ala Ile Leu Asp Ile Pro
          435          440          445
Ala Thr His Asn Glu Ala Ile Ile Ser Ile Phe Pro Tyr Ala Asn Lys
          450          455          460
Glu Asn Ile Ile Arg Asp Tyr Leu Met Ile Phe Leu Pro Leu Ile Ser
465          470          475          480
Thr Leu Gly Asp Ser Lys Asp Ala Ile Lys Gly Lys Thr Leu Asn Ser
          485          490          495
Thr Ser Ile Ser Glu Leu Leu Ile Pro Ile Ser Asn His Glu Glu Met
          500          505          510
Lys Arg Ile Phe Lys Val Asp Leu Leu Phe Gln Lys Val Ser Gln
          515          520          525
Leu Phe Glu
          530

```

(2) INFORMATION FOR SEQ ID NO:5017:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 74 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...74

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5017:

```

Asn Met Ala Val Lys Ile Ser Gly Val Leu Lys Asp Gly Thr Gly Lys
1          5          10          15
Pro Val Gln Asn Cys Thr Ile Gln Leu Lys Ala Arg Arg Asn Ser Thr
          20          25          30
Thr Val Val Val Asn Thr Val Gly Ser Glu Asn Pro Asp Glu Ala Cys
          35          40          45
Phe Phe Ile Leu Ser Trp His Tyr Lys Lys Ala Leu Leu Ile Asn Leu

```

50 55 60
Leu Gln Arg Thr Gly His Tyr Gln Ser Lys
65 70

(2) INFORMATION FOR SEQ ID NO:5018:

- ```
(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 62 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...62

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5018:
```

|     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |     |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Phe | Leu | Gly | Leu | Cys | Ile | Ala | Cys | Met | Gly | Val | Ser | Val | Gly | Glu | Gly |
| 1   |     |     |     | 5   |     |     |     |     | 10  |     |     |     |     | 15  |     |
| Leu | Leu | Met | Thr | Gly | Leu | Phe | Lys | Ser | Val | Ala | Arg | Gln | Pro | Asp | Asn |
|     |     |     | 20  |     |     |     |     | 25  |     |     |     |     | 30  |     |     |
| Ala | Ser | Glu | Phe | Arg | Ser | Leu | Met | Phe | Leu | Gly | Val | Ala | Phe | Ile | Glu |
|     |     | 35  |     |     |     |     | 40  |     |     |     |     | 45  |     |     |     |
| Gly | Thr | Phe | Phe | Val | Thr | Leu | Val | Phe | Ser | Phe | Ile | Ile | Lys |     |     |
|     | 50  |     |     |     |     | 55  |     |     |     |     | 60  |     |     |     |     |

(2) INFORMATION FOR SEQ ID NO:5019:

- ```
(i) SEQUENCE CHARACTERISTICS:
      (A) LENGTH: 344 amino acids
      (B) TYPE: amino acid
      (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
      (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
      (A) NAME/KEY: misc_feature
      (B) LOCATION 1...344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5019:
```

Arg	Gln	Gly	Phe	Gly	Ala	Asp	Ile	Asp	Val	Thr	Gly	Glu	Ile	Val	Phe
1				5					10					15	
Asn	Thr	Gly	Met	Thr	Gly	Tyr	Gln	Glu	Ser	Ile	Thr	Asp	Gln	Ser	Tyr
			20					25					30		

Asn	Gly	Gln	Ile	Leu	Thr	Phe	Thr	Tyr	Pro	Leu	Val	Gly	Asn	Tyr	Gly
	35						40					45			
Ile	Asn	Arg	Asp	Asp	Tyr	Glu	Ser	Ile	Ile	Pro	Thr	Cys	Lys	Gly	Val
	50					55					60				
Val	Val	Phe	Glu	Glu	Ala	Arg	Arg	Ala	Ser	Asn	Trp	Arg	Asn	Gln	Met
65					70					75					80
Thr	Leu	Asp	Glu	Phe	Leu	Lys	Ala	Lys	Lys	Ile	Pro	Gly	Ile	Ser	Gly
			85						90					95	
Ile	Asp	Thr	Arg	Ala	Leu	Thr	Lys	Ile	Ile	Arg	Lys	His	Gly	Thr	Met
			100					105					110		
Arg	Ala	Thr	Leu	Thr	His	Val	Gly	Asp	Ser	Met	Asp	His	Val	Thr	Asp
			115				120					125			
Gln	Leu	Gln	Ala	Thr	Val	Leu	Pro	Thr	Asp	Asn	Ile	Lys	Gln	Val	Ser
	130					135					140				
Thr	Lys	Thr	Ser	Tyr	Pro	Ala	Pro	Gly	Val	Gly	Leu	Ser	Val	Val	Leu
145					150					155					160
Val	Asp	Phe	Gly	Leu	Lys	His	Ser	Ile	Leu	Arg	Glu	Leu	Ser	Lys	Arg
				165					170					175	
Asn	Cys	Asn	Val	Thr	Val	Val	Pro	Tyr	Ser	Thr	Thr	Ala	Glu	Glu	Ile
			180					185					190		
Leu	His	Leu	Asn	Pro	Asp	Gly	Val	Met	Leu	Ser	Asn	Gly	Pro	Gly	Asn
		195				200						205			
Pro	Glu	Asp	Val	Pro	Gln	Ala	Leu	Asp	Met	Ile	Arg	Gly	Val	Gln	Gly
	210					215					220				
Lys	Ile	Pro	Ile	Phe	Gly	Ile	Cys	Met	Gly	His	Gln	Leu	Phe	Ala	Met
225					230					235					240
Ala	Asn	Gly	Ala	Lys	Thr	Tyr	Lys	Met	Lys	Phe	Gly	His	Arg	Gly	Phe
				245					250					255	
Asn	His	Ala	Val	Arg	Glu	Ile	Ala	Thr	Gly	Arg	Val	Asp	Phe	Thr	Ser
			260					265					270		
Gln	Asn	His	Gly	Tyr	Ala	Val	Ser	Arg	Glu	Asp	Leu	Pro	Glu	His	Leu
		275					280					285			
Ile	Ile	Thr	His	Glu	Glu	Ile	Asn	Asp	Lys	Ser	Val	Glu	Gly	Val	Arg
	290					295					300				
His	Arg	Tyr	Gln	Pro	Ala	Phe	Ser	Val	Gln	Tyr	His	Pro	Asp	Ala	Ala
305					310					315					320
Pro	Gly	Pro	His	Asp	Ala	Ser	Tyr	Leu	Phe	Asp	Glu	Phe	Ile	Glu	Met
				325					330					335	
Met	Glu	Ile	Phe	Lys	Gln	Ser	Asn								
					340										

(2) INFORMATION FOR SEQ ID NO:5020:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 94 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...94

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5020:

Thr	Cys	Gln	Val	Cys	Asn	Lys	Thr	Asn	Ile	Lys	Asn	Lys	Lys	Glu	Val
1				5					10					15	
Phe	Val	Met	Asn	Thr	Lys	Lys	Met	Ser	Gln	Phe	Glu	Ile	Met	Asp	Thr
			20					25					30		
Glu	Met	Leu	Ala	Cys	Val	Glu	Gly	Gly	Gly	Cys	Asn	Trp	Gly	Asp	Phe
		35					40					45			
Ala	Lys	Ala	Gly	Val	Gly	Gly	Gly	Val	Ala	Arg	Gly	Leu	Gln	Leu	Gly
	50					55					60				
Ile	Lys	Thr	Arg	Thr	Trp	Gln	Gly	Ala	Ala	Thr	Gly	Ala	Ala	Gly	Gly
65					70					75					80
Ala	Ile	Leu	Gly	Gly	Val	Ala	Tyr	Ala	Ala	Thr	Cys	Trp	Trp		
				85						90					

(2) INFORMATION FOR SEQ ID NO:5021:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 104 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...104

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5021:

Ser	Phe	Gln	Val	Leu	Met	Lys	Val	Lys	Ile	Ala	Arg	Ala	Ala	Asn	Pro
1				5					10					15	
Gly	Phe	Thr	Ile	Gly	Lys	Ala	Thr	Leu	Gln	Lys	Val	Arg	Ile	Ser	Pro
			20					25					30		
Gln	Pro	Ser	Ile	Leu	Ala	Asp	Ser	Ser	Asn	Ser	Val	Gly	Ile	Phe	Ser
		35					40					45			
Leu	Asn	Cys	Phe	Met	Arg	Lys	Thr	Pro	Asn	Gly	His	Pro	Ile	Lys	Gly
	50					55					60				
Lys	Ile	Thr	Ala	Gln	Arg	Val	Ser	Trp	Ile	Pro	Met	Lys	Leu	Thr	Ile
65					70					75					80
Arg	Thr	Asn	Gly	Thr	Arg	Thr	Thr	Cys	Phe	Gly	Ser	Ala	Ile	Ala	Ala
				85					90					95	
Ile	Lys	Ile	Ala	Asn	Arg	Met	Arg								
						100									

(2) INFORMATION FOR SEQ ID NO:5022:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 635 amino acids

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...635

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5022:

```

Lys Lys Gln Val Tyr Thr Val Phe Ala Asp Ser Ile Lys Asp Glu Leu
1      5      10      15
Asp Tyr Thr Asn Phe Lys Glu Lys Ala Gln Leu Ala Cys Val Val Tyr
      20      25      30
Thr Met Cys Gly Ile Val Gly Val Val Gly Asn Thr Asn Ala Thr Asp
      35      40      45
Ile Leu Ile Gln Gly Leu Glu Lys Leu Glu Tyr Arg Gly Tyr Asp Ser
      50      55      60
Ala Gly Ile Phe Val Leu Asp Gly Ala Asp Asn His Leu Val Lys Ala
65      70      75      80
Val Gly Arg Ile Ala Glu Leu Ser Ala Lys Thr Ala Gly Val Glu Gly
      85      90      95
Thr Thr Gly Ile Gly His Thr Arg Trp Ala Thr His Gly Lys Pro Thr
      100      105      110
Glu Asp Asn Ala His Pro His Arg Ser Glu Thr Glu Arg Phe Val Leu
      115      120      125
Val His Asn Gly Val Ile Glu Asn Tyr Leu Glu Ile Lys Glu Glu Tyr
      130      135      140
Leu Ala Gly His His Phe Lys Gly Gln Thr Asp Thr Glu Ile Ala Val
145      150      155      160
His Leu Ile Gly Lys Phe Ala Glu Glu Glu Gly Leu Ser Val Leu Glu
      165      170      175
Ala Phe Lys Lys Ala Leu His Ile Ile Arg Gly Ser Tyr Ala Phe Ala
      180      185      190

Leu Ile Asp Ser Glu Asn Pro Asp Val Ile Tyr Val Ala Lys Asn Lys
      195      200      205
Ser Pro Leu Leu Ile Gly Leu Gly Glu Gly Tyr Asn Met Val Cys Ser
      210      215      220
Asp Ala Met Ala Met Ile Arg Glu Thr Asn Gln Tyr Met Glu Ile His
225      230      235      240
Asp Gln Glu Leu Val Ile Val Lys Ala Asp Ser Val Glu Val Gln Asp
      245      250      255
Tyr Asp Gly Asn Ser Arg Glu Arg Ala Ser Tyr Thr Ala Glu Leu Asp
      260      265      270
Leu Ser Asp Ile Gly Lys Gly Thr Tyr Pro Tyr Tyr Met Leu Lys Glu
      275      280      285
Ile Asp Glu Gln Pro Thr Val Met Arg Lys Leu Ile Gln Ala Tyr Thr
      290      295      300
Asp Asp Ala Gly Gln Val Val Val Ala Pro Ala Ile Ile Lys Ala Val

```

305					310					315				320
Gln	Asp	Ala	Asp	Arg	Ile	Tyr	Ile	Leu	Ala	Ala	Gly	Thr	Ser	Tyr
				325					330					335
Ala	Gly	Phe	Ala	Ser	Lys	Lys	Met	Leu	Glu	Glu	Leu	Thr	Asp	Thr
			340					345					350	
Val	Glu	Leu	Gly	Ile	Ser	Ser	Glu	Trp	Gly	Tyr	Gly	Met	Pro	Leu
		355					360					365		
Ser	Lys	Lys	Pro	Leu	Phe	Ile	Phe	Ile	Ser	Gln	Ser	Gly	Glu	Thr
	370					375					380			
Asp	Ser	Arg	Gln	Val	Leu	Val	Lys	Ala	Asn	Glu	Met	Gly	Ile	Pro
385				390					395					400
Leu	Thr	Val	Thr	Asn	Val	Pro	Gly	Ser	Thr	Leu	Ser	Arg	Glu	Ala
			405					410					415	
Tyr	Thr	Met	Leu	Leu	His	Ala	Gly	Pro	Glu	Ile	Ala	Val	Ala	Ser
		420					425					430		
Lys	Ala	Tyr	Thr	Ala	Gln	Ile	Ala	Ala	Leu	Ala	Phe	Leu	Ala	Lys
	435					440					445			
Val	Gly	Glu	Ala	Asn	Gly	Asn	Ala	Lys	Ala	Gln	Ala	Phe	Asp	Leu
450					455				460					
His	Glu	Leu	Ser	Ile	Val	Ala	Gln	Ser	Ile	Glu	Ser	Thr	Leu	Ser
465				470				475					480	
Lys	Glu	Thr	Ile	Glu	Ala	Lys	Val	Arg	Glu	Leu	Leu	Glu	Thr	Thr
			485				490						495	
Asn	Ala	Phe	Tyr	Ile	Gly	Arg	Gly	Gln	Asp	Tyr	Tyr	Val	Ala	Met
		500					505					510		
Ala	Ser	Leu	Lys	Leu	Lys	Glu	Ile	Ser	Tyr	Ile	Gln	Cys	Glu	Gly
		515				520					525			
Ala	Ala	Gly	Glu	Leu	Lys	His	Gly	Thr	Ile	Ala	Leu	Ile	Glu	Glu
	530				535				540					
Thr	Pro	Val	Leu	Ala	Leu	Leu	Ser	Asp	Pro	Val	Leu	Ala	Asn	His
545					550				555					560
Arg	Gly	Asn	Ile	Gln	Glu	Val	Ala	Ala	Arg	Gly	Ala	Lys	Val	Leu
			565					570					575	
Ile	Ala	Glu	Glu	Asn	Val	Ala	Lys	Asp	Thr	Asp	Asp	Ile	Val	Leu
			580					585				590		
Thr	Val	His	Pro	Tyr	Leu	Ser	Pro	Ile	Ser	Met	Val	Val	Pro	Thr
		595				600					605			
Leu	Val	Ala	Tyr	Phe	Ala	Thr	Leu	His	Arg	Gly	Leu	Asp	Val	Asp
610					615				620					
Pro	Arg	Asn	Leu	Ala	Lys	Ser	Val	Thr	Val	Glu				
625					630				635					

(2) INFORMATION FOR SEQ ID NO:5023:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 167 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...167

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5023:

```

Lys Thr Gly Phe Thr Arg Glu Ile Ser Asn Tyr Leu Val Lys Thr Leu
1      5      10      15
Glu Gly Phe Gly Tyr Gln Pro Val Arg Thr Ala Lys Gly Gly Val Asn
      20      25      30
Val Thr Ile Lys Gly Gln Asn Asp Glu Gln His Arg Tyr Val Thr Ala
      35      40      45
His Val Asp Thr Leu Gly Ala Ile Val Arg Ala Val Lys Pro Asp Gly
      50      55      60
Arg Leu Lys Leu Asp Arg Ile Gly Gly Phe Pro Trp Asn Met Ile Glu
65      70      75      80
Gly Glu Asn Cys Thr Val His Val Ala Ser Thr Gly Gln Lys Val Ser
      85      90      95
Gly Thr Ile Leu Ile His Gln Thr Ser Cys His Val Tyr Lys Asp Ala
      100     105     110
Gly Thr Ala Glu Arg Thr Gln Asp Asn Met Glu Val Arg Leu Asp Val
      115     120     125
Lys Val Ser Asn Glu Lys Glu Thr Arg Ala Leu Gly Ile Glu Val Gly
130     135     140
Asp Phe Ile Ser Phe Asp Pro Arg Thr Val Val Thr Asp Thr Gly Phe
145     150     155     160
Tyr Gln Val Ser Ser Phe Gly
      165

```

(2) INFORMATION FOR SEQ ID NO:5024:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 144 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...144

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5024:

```

Glu Val Lys Val Leu Ala Lys Pro Thr Arg Lys Arg Arg Val Lys Lys
1      5      10      15
Asn Ile Glu Ser Gly Ile Ala His Ile His Ala Thr Phe Asn Asn Thr
      20      25      30
Ile Val Met Ile Thr Asp Val His Gly Asn Ala Ile Ala Trp Ser Ser
      35      40      45
Ala Gly Ala Leu Gly Phe Lys Gly Ser Arg Lys Ser Thr Pro Phe Ala
50      55      60

```


Ala	Gln	Met	Ala	Ser	Glu	Ala	Ala	Ala	Lys	Ser	Ala	Gln	Glu	His	Gly
65					70				75					80	
Leu	Lys	Ser	Val	Glu	Val	Thr	Val	Lys	Gly	Pro	Gly	Ser	Gly	Arg	Glu
			85						90					95	
Ser	Ala	Ile	Arg	Ala	Leu	Ala	Ala	Ala	Gly	Leu	Glu	Val	Thr	Ala	Ile
			100					105					110		
Arg	Asp	Val	Thr	Pro	Val	Pro	Thr	Gln	Trp	Cys	Ser	Ser	Ser	Lys	Thr
		115					120					125			
Ser	Pro	Cys	Ile	Ile	Ile	Ala	Leu	His	Cys	Phe	Ser	Phe	Lys	Arg	Glu
		130				135					140				

(2) INFORMATION FOR SEQ ID NO:5025:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 193 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...193

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5025:

Arg	Leu	Lys	Val	Phe	Ser	Ile	Thr	Ser	Val	Lys	Pro	Gly	Glu	Gly	Lys
1				5				10					15		
Thr	Thr	Thr	Ser	Thr	Asn	Ile	Ala	Arg	Ala	Phe	Ala	Arg	Ala	Gly	Tyr
			20					25					30		
Lys	Thr	Leu	Leu	Ile	Asp	Ala	Asp	Met	Arg	Asn	Ser	Val	Met	Ser	Gly
		35				40						45			
Val	Phe	Lys	Ser	Arg	Glu	Arg	Ile	Thr	Gly	Leu	Thr	Glu	Phe	Leu	Ser
	50					55					60				
Gly	Thr	Thr	Asp	Leu	Ser	Gln	Gly	Leu	Cys	Asp	Thr	Asn	Ile	Glu	Asn
65				70					75					80	
Leu	Phe	Val	Ile	Gln	Ala	Gly	Ser	Val	Ser	Pro	Asn	Pro	Thr	Ala	Leu
			85					90						95	
Leu	Gln	Ser	Arg	Asn	Phe	Ser	Thr	Met	Leu	Glu	Thr	Val	Arg	Lys	Tyr
			100					105					110		
Phe	Asp	Tyr	Ile	Val	Val	Asp	Thr	Ala	Pro	Val	Gly	Val	Val	Ile	Asp
		115					120					125			
Ala	Ala	Ile	Ile	Thr	Gln	Lys	Cys	Asp	Ala	Ser	Ile	Leu	Val	Thr	Lys
		130				135					140				
Ala	Gly	Glu	Thr	Lys	Arg	Arg	Asp	Ile	Gln	Lys	Ala	Lys	Glu	Gln	Ile
145					150					155					160
Glu	Gln	Thr	Gly	Lys	Pro	Cys	Leu	Gly	Val	Val	Leu	Asn	Lys	Phe	Asp
			165						170					175	
Thr	Ser	Val	Asp	Glu	Tyr	Gly	Ser	Tyr	Gly	Ser	Tyr	Gly	Lys	Lys	Lys
			180					185					190		

Lys

(2) INFORMATION FOR SEQ ID NO:5026:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 157 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...157
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5026:

Lys	Lys	Lys	Val	Lys	Asn	Tyr	Lys	Gly	Val	Pro	Met	Ile	Pro	Gln	Glu
1				5					10					15	
Met	Trp	Asn	Lys	Tyr	Lys	Gln	Ile	Asn	Pro	Leu	Ile	Gly	Asp	Glu	Ile
		20						25					30		
Asp	Ala	Trp	Ala	Phe	Gly	Val	Glu	Pro	Asp	Leu	Leu	Ala	Asp	Leu	Val
		35					40					45			
Phe	Lys	Gly	Glu	Lys	Thr	Ala	Thr	Ala	Ser	Ala	Tyr	Asp	Leu	Tyr	Val
	50					55				60					
Leu	Glu	Asp	Glu	Pro	Leu	Pro	Gln	Val	Gly	Thr	Phe	Asp	Ile	Ile	Leu
65					70				75					80	
Asp	Ser	Gln	Asn	Gln	Ser	Val	Cys	Ile	Val	Glu	Ile	Thr	Lys	Val	Ser
			85						90					95	
Val	Glu	Leu	Phe	Asn	Gln	Val	Ser	Ala	Gln	His	Ala	Phe	Lys	Glu	Gly
			100					105					110		
Glu	Gly	Asp	Lys	Ser	Leu	Ala	Tyr	Trp	Arg	Gln	Val	His	Glu	Asp	Phe
		115				120						125			
Phe	Thr	Asp	Cys	Leu	Gly	Glu	Val	Gly	Leu	Thr	Phe	Thr	Ser	Glu	Ser
	130					135					140				
Lys	Val	Val	Leu	Glu	Glu	Phe	Arg	Lys	Val	Tyr	Pro	Leu			
145					150					155					

(2) INFORMATION FOR SEQ ID NO:5027:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 255 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...255

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5027:

Lys	Glu	Lys	Val	Ser	Met	Ser	Lys	Glu	Ile	Lys	Phe	Ser	Ser	Asp	Ala
1				5					10					15	
Arg	Ser	Ala	Met	Val	Arg	Gly	Val	Asp	Ile	Leu	Ala	Asp	Thr	Val	Lys
			20					25					30		
Val	Thr	Leu	Gly	Pro	Lys	Gly	Arg	Asn	Val	Val	Leu	Glu	Lys	Ser	Phe
		35				40					45				
Gly	Ser	Pro	Leu	Ile	Thr	Asn	Asp	Gly	Val	Thr	Ile	Ala	Lys	Glu	Ile
	50					55					60				
Glu	Leu	Glu	Asp	His	Phe	Glu	Asn	Met	Gly	Ala	Lys	Leu	Val	Ser	Glu
65					70					75					80
Val	Ala	Ser	Lys	Thr	Asn	Asp	Ile	Ala	Gly	Asp	Gly	Thr	Thr	Thr	Ala
				85					90					95	
Thr	Val	Leu	Thr	Gln	Ala	Ile	Val	Arg	Glu	Gly	Ile	Lys	Asn	Val	Thr
		100					105						110		
Ala	Gly	Ala	Asn	Pro	Ile	Gly	Ile	Arg	Arg	Gly	Ile	Glu	Thr	Ala	Val
	115					120						125			
Ala	Ala	Ala	Val	Glu	Ala	Leu	Lys	Asn	Asn	Ala	Ile	Pro	Val	Ala	Asn
	130					135					140				
Lys	Glu	Ala	Ile	Ala	Gln	Val	Ala	Ala	Val	Ser	Ser	Arg	Ser	Glu	Lys
145					150					155					160
Val	Gly	Glu	Tyr	Ile	Ser	Glu	Ala	Met	Glu	Lys	Val	Gly	Lys	Glu	Gly
			165						170					175	
Val	Ile	Thr	Ile	Glu	Glu	Ser	Arg	Gly	Met	Glu	Thr	Glu	Leu	Glu	Val
		180						185					190		
Val	Glu	Gly	Met	Gln	Phe	Asp	Arg	Gly	Tyr	Leu	Ser	Gln	Tyr	Met	Val
	195						200					205			
Thr	Asp	Ser	Glu	Lys	Met	Val	Ala	Asp	Leu	Glu	Asn	Pro	Tyr	Ile	Leu
	210					215					220				
Ile	Thr	Asp	Lys	Lys	Ile	Ser	Asn	Ile	Gln	Glu	Ile	Leu	Pro	Leu	Leu
225					230					235					240
Glu	Ser	Ile	Leu	Gln	Glu	His	Cys	Ser	Ile	Trp	Asp	Tyr	Ala	Gly	
				245					250					255	

(2) INFORMATION FOR SEQ ID NO:5028:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 475 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...475

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5028:

Trp 1	Arg	Lys	Val	Met 5	Thr	Ile	Phe	Pro	Asp 10	Asp	Phe	Leu	Trp	Gly 15	Gly
Ala	Val	Ala	Ala	Asn	Gln	Val	Glu	Gly	Ala	Tyr	Asn	Glu	Asp	Gly	Lys
			20					25					30		
Gly	Leu	Ser	Val	Gln	Asp	Val	Leu	Pro	Lys	Gly	Gly	Leu	Gly	Glu	Ala
		35					40					45			
Thr	Glu	Asn	Pro	Thr	Glu	Asp	Asn	Leu	Lys	Leu	Ile	Gly	Ile	Asp	Phe
	50					55					60				
Tyr	His	Lys	Tyr	Lys	Glu	Asp	Ile	Ser	Leu	Phe	Ser	Glu	Met	Gly	Phe
65				70						75				80	
Asn	Val	Phe	Arg	Thr	Ser	Ile	Ala	Trp	Ser	Arg	Ile	Phe	Pro	Lys	Gly
			85						90					95	
Asp	Glu	Glu	Glu	Pro	Asn	Glu	Ala	Gly	Leu	Lys	Tyr	Tyr	Asp	Glu	Leu
			100					105					110		
Phe	Asp	Glu	Leu	His	Ala	His	Gly	Ile	Glu	Pro	Leu	Val	Thr	Leu	Ser
		115					120					125			
His	Tyr	Glu	Thr	Pro	Leu	Tyr	Leu	Ala	Arg	Lys	Tyr	His	Gly	Trp	Val
		130				135					140				
Asp	Arg	Arg	Met	Ile	His	Phe	Tyr	Glu	Lys	Phe	Ala	Arg	Thr	Val	Leu
145				150						155				160	
Glu	Arg	Tyr	Lys	Asp	Lys	Val	Lys	Tyr	Trp	Leu	Thr	Phe	Asn	Glu	Val
			165						170					175	
Asn	Ser	Val	Leu	Glu	Leu	Pro	Phe	Thr	Ser	Gly	Gly	Ile	Asp	Ile	Pro
		180						185					190		
Lys	Glu	Asn	Leu	Ser	Lys	Gln	Glu	Leu	Tyr	Gln	Ala	Ile	His	His	Glu
		195					200					205			
Leu	Val	Ala	Ser	Ser	Leu	Val	Thr	Lys	Ile	Ala	Arg	Glu	Ile	Asn	Ser
	210					215					220				
Glu	Phe	Lys	Val	Gly	Cys	Met	Val	Leu	Ala	Met	Pro	Ala	Tyr	Pro	Met
225				230						235				240	
Thr	Pro	Asn	Pro	Lys	Asp	Val	Trp	Ala	Thr	His	Glu	Tyr	Glu	Asn	Leu
			245						250					255	
Asn	Tyr	Leu	Phe	Ser	Asp	Val	His	Val	Arg	Gly	Tyr	Tyr	Pro	Asn	Tyr
		260						265					270		
Ala	Lys	Arg	Tyr	Phe	Lys	Glu	Asn	Asp	Ile	Asn	Ile	Glu	Phe	Ala	Ala
		275					280					285			
Glu	Asp	Ala	Glu	Leu	Leu	Lys	Asn	Tyr	Thr	Val	Asp	Phe	Leu	Ser	Phe
	290					295					300				
Ser	Tyr	Tyr	Met	Ser	Val	Thr	Gln	Ser	Ala	Ile	Pro	Thr	Gln	Tyr	Asn
305				310						315				320	
Ser	Gly	Glu	Gly	Asn	Ile	Ile	Gly	Gly	Leu	Val	Asn	Pro	Tyr	Leu	Glu
			325						330					335	
Ser	Ser	Glu	Trp	Gly	Trp	Gln	Ile	Asp	Pro	Ile	Gly	Leu	Arg	Ile	Ile
		340						345					350		
Leu	Asn	Arg	Tyr	Tyr	Asp	Arg	Tyr	Gln	Ile	Pro	Leu	Phe	Ile	Val	Glu

Ser	Lys	Arg	Tyr	Gly	Leu	Ile	Tyr	Val	Asp	Arg	Asn	Asp	Asp	Gly	Asn
		435					440					445			
Gly	Thr	Phe	Asn	Arg	Tyr	Lys	Lys	Met	Ser	Phe	Thr	Trp	Tyr	Lys	Gly
	450					455					460				
Val	Ile	Glu	Ser	Asn	Gly	Asp	Ser	Leu	Phe	Lys					
465					470					475					

(2) INFORMATION FOR SEQ ID NO:5029:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 236 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...236

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5029:

Lys	Val	Glu	Val	Ala	Gly	Asp	Gly	Thr	Ala	Thr	Ile	Thr	Phe	Pro	Asp
1				5				10						15	
Gly	Ser	Val	Val	Thr	Ile	Leu	Gly	Lys	Asp	Thr	Val	Gln	Gln	Ser	Ala
			20				25					30			
Lys	Gly	Glu	Ser	Val	Thr	Gln	Glu	Ala	Thr	Pro	Glu	Tyr	Lys	Pro	Glu
	35					40					45				
Thr	Thr	Pro	Gly	Gly	Asp	Lys	Gly	Gly	Asn	Thr	Gly	Asn	Ser	Asp	Ala
	50				55					60					
Asn	Ala	Asn	Ala	Gly	Gly	Gly	Ser	Gln	Ala	Gly	Gly	Ser	Ala	His	Thr
65				70				75						80	
Gly	Ser	Gln	Asn	Ser	Ala	Gln	Ser	Gln	Ala	Ser	Lys	Gln	Leu	Ala	Thr
			85					90						95	
Glu	Lys	Glu	Ser	Ala	Lys	Asn	Ala	Ile	Glu	Lys	Ala	Ala	Lys	Asp	Lys
			100					105					110		
Gln	Asp	Glu	Ile	Lys	Gly	Ala	Pro	Leu	Ser	Asp	Lys	Glu	Lys	Ala	Glu
	115					120						125			
Leu	Leu	Ala	Arg	Val	Glu	Ala	Glu	Lys	Gln	Ala	Ala	Leu	Lys	Glu	Ile
	130				135						140				
Glu	Asn	Ala	Lys	Thr	Met	Glu	Asp	Val	Lys	Glu	Ala	Glu	Thr	Ile	Gly
145				150				155						160	
Val	Gln	Ala	Ile	Ala	Met	Val	Thr	Val	Pro	Lys	Arg	Pro	Val	Ala	Pro
			165					170						175	
Lys	Thr	Thr	Ser	Ala	Pro	Gln	Ala	Thr	Ala	Gly	Thr	Met	Gln	Asp	Val
			180					185					190		
Thr	Tyr	Gln	Ser	Pro	Ala	Gly	Lys	Gln	Leu	Pro	Asn	Thr	Gly	Ser	Ala
	195					200						205			
Ser	Ser	Ala	Ala	Leu	Ala	Ser	Leu	Gly	Leu	Val	Val	Ala	Thr	Ser	Gly
	210					215					220				
Phe	Ala	Leu	Leu	Gly	Arg	Lys	Thr	Arg	Arg	Arg	Lys				
225					230						235				

(2) INFORMATION FOR SEQ ID NO:5030:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 74 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...74
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5030:

Trp	Val	Glu	Val	Thr	Leu	Val	Gln	Ser	Gly	Val	Thr	Ile	Ser	Arg	Thr
1				5					10					15	
Pro	Leu	Ser	Ser	Glu	Ala	Thr	Val	Met	Ile	Asp	Ala	Thr	Glu	Val	Lys
			20					25					30		
Ile	Asn	Arg	Pro	Lys	Lys	Glu	Leu	Ala	Asn	Tyr	Ser	Cys	Lys	Lys	Met
		35					40					45			
Pro	Arg	Tyr	Glu	Gly	Ser	Ser	Asp	Cys	His	Lys	Ser	Arg	Glu	Asn	Cys
	50					55					60				
Phe	Phe	Gly	Tyr	His	Cys	Glu	Leu	Leu	Ser						
65					70										

(2) INFORMATION FOR SEQ ID NO:5031:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 328 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...328
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5031:

Tyr	Asn	Glu	Val	Leu	Glu	Lys	Gln	Val	Ser	Phe	Ala	Trp	Lys	Gly	Lys
1				5					10					15	
Ile	Met	Ser	Glu	Lys	Asn	Phe	Tyr	Ile	Thr	Thr	Pro	Ile	Tyr	Tyr	Pro
			20					25					30		
Ser	Gly	Lys	Leu	His	Ile	Gly	Ser	Ala	Tyr	Thr	Thr	Ile	Ala	Cys	Asp

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5032:

```
Thr Phe Glu Val Cys Tyr Asn Lys Glu Asn Lys Asn Lys Arg Phe Ile
1      5      10      15
Met Thr Lys Leu Tyr Gly Ser Leu Glu Ala Gly Gly Thr Lys Phe Val
      20      25      30
Cys Ala Val Gly Asp Glu Asn Phe Asn Val Val Glu Lys Thr Gln Phe
      35      40      45
Pro Thr Thr Thr Pro Ile Glu Thr Ile Asp Lys Thr Ile Glu Ser Ser
      50      55      60
Gln Asn Ser Ile Thr Phe Leu Val Leu Gln Leu Val His Leu Gly Arg
65      70      75      80
Leu Ile Leu Thr Lys Thr Gln Lys Leu Met Ala Leu Ser Arg Arg Leu
      85      90      95
Gln Asn Gln Thr Gly Gln Met Trp Thr Cys Leu Val Pro Phe Val Ala
      100      105      110
Pro
```

(2) INFORMATION FOR SEQ ID NO:5033:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 142 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5033:

```
Trp Thr Glu Val Ile Glu Phe Asn Ala Arg Phe Gly Asp Pro Glu Thr
1      5      10      15
Gln Leu Ile Leu Pro Arg Leu Thr Ser Asp Phe Ala Gln Asn Ile Thr
      20      25      30
Asp Ile Leu Asp Ser Lys Glu Pro Asn Ile Thr Trp Thr Asp Lys Gly
      35      40      45
Val Thr Leu Gly Val Val Val Ala Ser Lys Gly Tyr Pro Leu Asp Tyr
      50      55      60
Ser Lys Gly Val Glu Leu Pro Val Lys Thr Asp Gly Asp Ile Ile Thr
65      70      75      80
Tyr Tyr Ala Gly Ala Lys Phe Ala Glu Asn Ser Arg Ala Leu Leu Ser
      85      90      95
Asn Gly Gly Arg Val Tyr Met Leu Val Thr Thr Ala Asp Thr Val Lys
      100      105      110
Glu Ala Gln Ala Ser Ile Tyr Gln Glu Leu Ser Gln Gln Lys Ile Glu
      115      120      125
Gly Leu Phe Tyr Arg Thr Asp Ile Gly Ser Lys Ala Ile Lys
```


140

(i) SEQUENCE CHARACTERISTICS:

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Streptococcus pneumoniae*

(A) NAME/KEY: misc feature

(B) LOCATION 1...604

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5034:

3907

	275		280		285												
Asp	Gly	Tyr	Tyr	Phe	His	Val	Thr	Asn	Ser	Gln	Leu	Gly	Asn	Val	Pro		
	290					295					300						
Ala	His	Phe	Phe	Arg	Lys	Ala	Thr	Leu	Lys	Asn	Ser	Glu	Arg	Phe	Gly		
305					310					315					320		
Thr	Glu	Glu	Leu	Ala	Arg	Ile	Glu	Gly	Asp	Met	Leu	Glu	Ala	Arg	Glu		
				325					330					335			
Lys	Ser	Ala	Asn	Leu	Glu	Tyr	Glu	Ile	Phe	Met	Arg	Ile	Arg	Glu	Glu		
			340					345				350					
Val	Gly	Lys	Tyr	Ile	Gln	Arg	Leu	Gln	Ala	Leu	Ala	Gln	Gly	Ile	Ala		
	355						360					365					
Thr	Val	Asp	Val	Leu	Gln	Ser	Leu	Ala	Val	Val	Ala	Glu	Thr	Gln	His		
	370					375					380						
Leu	Ile	Arg	Pro	Glu	Phe	Gly	Asp	Asp	Ser	Gln	Ile	Asp	Ile	Arg	Lys		
385					390					395					400		
Gly	Arg	His	Ala	Val	Val	Glu	Lys	Val	Met	Gly	Ala	Gln	Thr	Tyr	Ile		
				405					410					415			
Pro	Asn	Thr	Ile	Gln	Met	Ala	Glu	Asp	Thr	Ser	Ile	Gln	Leu	Val	Thr		
			420					425				430					
Gly	Pro	Asn	Met	Ser	Gly	Lys	Ser	Thr	Tyr	Met	Arg	Gln	Leu	Ala	Met		
	435						440					445					
Thr	Ala	Val	Met	Ala	Gln	Leu	Gly	Ser	Tyr	Val	Pro	Ala	Glu	Ser	Ala		
	450					455					460						
His	Leu	Pro	Ile	Phe	Asp	Ala	Ile	Phe	Thr	Arg	Ile	Gly	Ala	Ala	Asp		
465					470					475					480		
Asp	Leu	Val	Ser	Gly	Gln	Ser	Thr	Phe	Met	Val	Glu	Met	Met	Glu	Ala		
				485					490					495			
Asn	Asn	Ala	Ile	Ser	His	Ala	Thr	Lys	Asn	Ser	Leu	Ile	Leu	Phe	Asp		
			500					505					510				
Glu	Leu	Gly	Arg	Gly	Thr	Ala	Thr	Tyr	Asp	Gly	Met	Ala	Leu	Ala	Gln		
	515						520					525					
Ser	Ile	Ile	Glu	Tyr	Ile	His	Glu	His	Ile	Gly	Ala	Lys	Thr	Leu	Phe		
	530					535					540						
Ala	Thr	His	Tyr	His	Glu	Leu	Thr	Ser	Leu	Glu	Ser	Ser	Leu	Gln	His		
545					550					555					560		
Leu	Val	Asn	Val	His	Val	Ala	Thr	Leu	Glu	Gln	Asp	Gly	Gln	Val	Thr		
				565					570					575			
Phe	Leu	His	Lys	Ile	Glu	Pro	Gly	Pro	Ala	Asp	Lys	Ser	Thr	Val	Ser		
			580					585					590				
Met	Leu	Pro	Arg	Leu	Leu	Ala	Cys	Gln	Gln	Thr	Phe						
	595					600											

(2) INFORMATION FOR SEQ ID NO:5035:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 123 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...123

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5035:

Leu	Gly	Glu	Val	Met	Arg	Leu	Ile	Tyr	Leu	Ile	Ile	Gly	Phe	Leu	Ser
1				5					10					15	
Leu	Ala	Leu	Ala	Ile	Val	Gly	Val	Val	Leu	Pro	Leu	Leu	Pro	Thr	Thr
			20				25						30		
Pro	Phe	Leu	Leu	Leu	Ser	Ile	Ala	Cys	Phe	Ser	Arg	Ser	Ser	Lys	Arg
		35				40						45			
Phe	Glu	Asp	Trp	Leu	Tyr	His	Thr	Lys	Leu	Tyr	Gln	Thr	Tyr	Val	Ala
	50					55					60				
Asp	Phe	Arg	Glu	Thr	Lys	Ser	Ile	Thr	Arg	Glu	Arg	Lys	Lys	Lys	Ile
65					70					75					80
Ile	Val	Ser	Ile	Tyr	Val	Leu	Met	Gly	Ile	Ser	Ile	Tyr	Phe	Ala	Pro
			85					90						95	
Leu	Leu	Pro	Val	Lys	Ile	Gly	Leu	Gly	Ala	Leu	Thr	Ile	Phe	Ile	Thr
		100					105							110	
Tyr	Tyr	Leu	Phe	Lys	Val	Ile	Pro	Asp	Lys	Glu					
		115					120								

(2) INFORMATION FOR SEQ ID NO:5036:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5036:

Lys	Leu	Arg	Val	Val	Arg	Leu	Ala	Ile	Met	Leu	Arg	Asp	Leu	Asp	Leu
1				5					10					15	
Tyr	Lys	Val	Ile	Phe	Glu	Gly	Asn	Tyr	Arg	Ala	Thr	Ala	Gly	Arg	Glu
			20				25						30		
Glu	Met	Lys	Glu	Ala	Ile	Leu	Glu	Tyr	Gln	Ala	Asn	Pro	Ala	Ala	Leu
		35				40						45			
Lys	Asp	Leu	Lys	Glu	Lys	Ala	Lys	Asn	Ile	Ser	Arg	Glu	Tyr	Ser	Glu
	50					55					60				
Glu	His	Leu	Leu	Gln	Ile	Trp	Leu	Asp	Phe	Tyr	Glu	Lys	Gln	Ala	Ala
65				70					75						80
Leu	Gly	Arg	Lys												

(2) INFORMATION FOR SEQ ID NO:5037:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 85 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...85
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5037:

```

Asn Arg Arg Val Met Gly Ile Glu Pro Thr His Ala Arg Ala Thr Ile
1          5          10          15
Trp Cys Val Asn His Phe Thr Thr Pro Ala Ile Ile Leu Leu Thr Arg
          20          25          30
Ala Val Gly Ile Glu Pro Thr Leu Lys Val Leu Glu Thr Leu Val Leu
          35          40          45
Pro Leu Asn Tyr Ala Arg Lys Met Glu Gly Glu Gly Phe Glu Pro Pro
          50          55          60
Asn Pro Lys Glu Arg Ile Tyr Ser Pro Pro Arg Leu Ala Ser Ser Leu
65          70          75          80
Pro Phe Gln Asn Ile
          85

```

(2) INFORMATION FOR SEQ ID NO:5038:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 121 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...121
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5038:

```

Ile Phe Arg Val His Tyr Arg Phe Trp Trp Glu Leu Arg Pro Arg Ile
1          5          10          15
Trp Cys Asp Asn Ser Met Met Arg Asn Glu Phe Arg Glu Arg Val Glu
          20          25          30
Gln Leu Leu Gln Gln Lys Glu Ile Asn Glu Asn Ser Glu Leu Ser His

```

		35					40				45						
Leu	Phe	Arg	Leu	Ala	Ile	Gln	Asn	Leu	Asp	Arg	Asn	Glu	Lys	Tyr	Gln		
	50					55					60						
Ser	Val	Met	Ala	Asn	Leu	Ser	Gln	Gly	Leu	Ser	Leu	Tyr	Leu	Met	Thr		
65					70					75					80		
His	His	Tyr	Gln	Ala	Pro	Lys	Ser	Val	Ile	Asp	Phe	Gly	Leu	Trp	Ile		
			85						90					95			
Ala	Lys	Ala	Pro	Ser	Gln	Glu	Arg	Gly	Arg	Leu	Ala	Phe	Leu	Gln	Met		
			100					105					110				
Leu	Ala	Gln	Thr	Leu	Gln	Gly	Phe	Arg									
			115					120									

(2) INFORMATION FOR SEQ ID NO:5039:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 445 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...445

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5039:

Gly	Glu	Arg	Val	Met	Asp	Leu	Phe	Gly	Phe	Gly	Thr	Val	Ile	Val	His		
1				5				10					15				
Phe	Leu	Ile	Ile	Ser	His	Ser	Tyr	His	Phe	Ile	Cys	Lys	Gly	Gln	Ile		
		20					25					30					
Asn	Arg	Lys	Glu	Leu	Phe	Val	Phe	Gly	Ala	Tyr	Thr	Leu	Leu	Thr	Glu		
		35				40					45						
Ile	Val	Phe	Asp	Phe	Pro	Leu	Tyr	Ile	Leu	Tyr	Leu	Asp	Gly	Leu	Gly		
	50			55				60									
Ile	Glu	Arg	Phe	Leu	Phe	Pro	Leu	Gly	Leu	Tyr	Ser	Tyr	Phe	Arg	Trp		
65				70				75						80			
Met	Lys	Gln	Tyr	Glu	Arg	Asp	Arg	Gly	Leu	Phe	Leu	Ser	Leu	Leu	Leu		
		85					90					95					
Ser	Leu	Leu	Tyr	Glu	Ser	Thr	His	Asn	Phe	Leu	Ser	Val	Thr	Phe	Ser		
		100					105					110					
Ser	Ile	Thr	Gly	Asp	Asn	Phe	Val	Leu	Gln	Tyr	His	Phe	Pro	Phe	Phe		
	115					120					125						
Phe	Val	Val	Thr	Val	Leu	Thr	Tyr	Phe	Val	Thr	Leu	Lys	Ile	Ile	Tyr		
	130				135					140							
Tyr	Phe	His	Leu	Glu	Leu	Ala	Tyr	Phe	Asp	Glu	Asp	Tyr	Leu	Tyr	Pro		
145				150				155						160			
Phe	Leu	Lys	Lys	Val	Phe	Phe	Ala	Leu	Leu	Leu	Leu	His	Ile	Val	Ser		
		165					170					175					
Phe	Val	Ser	Asp	Met	Val	Ser	Thr	Ile	Lys	His	Leu	Asn	Ser	Phe	Gly		
		180					185				190						
Ser	Ile	Leu	Ser	Ser	Ile	Val	Phe	Ile	Ser	Leu	Leu	Leu	Thr	Phe	Phe		

		35				40					45				
Gly	Phe	Phe	Gly	Asp	Lys	Thr	Asp	Ser	Ser	Thr	Met	Ile	Lys	Asn	Glu
	50					55					60				
Val	Arg	Met	Met	Met	Gly	Cys	Leu	Ala	Tyr	Asn	Leu	Tyr	Leu	Phe	Leu
65					70					75					80
Lys	Gln	Leu	Ala	Gly	Asp	Glu	Val	Lys	Ala	Leu	Thr	Ile	Lys	Arg	Phe
				85					90					95	
Arg	Arg	Leu	Phe	Leu	His	Ile	Ala	Gly	Lys	Tyr	Val	Ser	Thr	Ala	Arg
		100						105					110		
Arg	His	Ile	Leu	Lys	Phe	Ser	Ser	Leu	Tyr	Ala	Tyr	Ser	Lys	Gln	Phe
	115					120						125			
Gln	Ala	Leu	Phe	Asp	Thr	Ile	Cys	Gln	Ile	Asn	Leu	Ile	Leu	Pro	Val
	130					135					140				
Pro	Tyr	Arg	Ala	Arg	Gly	Gln	Gly	Lys	Thr	Cys	Leu	Thr	Glu		
145					150					155					

(2) INFORMATION FOR SEQ ID NO:5041:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 87 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...87

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5041:

Met	Gly	Arg	Val	Asp	Arg	Ala	Ser	Val	Glu	Arg	Val	Asp	Arg	Pro	Asp
1				5				10				15			
Leu	Val	Leu	Ser	Ile	Asp	Phe	Arg	Phe	Phe	Val	Asn	Tyr	Ser	Trp	Phe
		20				25					30				
Val	Lys	Lys	Leu	Ile	Phe	Gly	Glu	Glu	Asp	Cys	Tyr	Leu	Leu	His	Phe
	35					40					45				
Tyr	Val	Gln	Ser	Tyr	Ser	Gly	Leu	Met	Leu	Gly	Lys	Tyr	Thr	Val	Thr
	50					55					60				
Ala	Lys	Thr	Phe	Leu	Glu	Val	Ala	Leu	Ile	Tyr	Leu	Ile	Tyr	Leu	Cys
65				70					75						80
Lys	Phe	Tyr	Val	Ile	Leu	Leu									
				85											

(2) INFORMATION FOR SEQ ID NO:5042:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 629 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...629

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5042:

Val	Glu	Arg	Val	Val	Tyr	Met	Lys	Ile	Glu	Asn	Lys	Asn	Val	Arg	Arg
1				5					10					15	
Asn	Phe	Phe	Trp	Gly	Asp	Gly	Arg	Phe	Tyr	Thr	Thr	Asp	Ile	Val	Asn
			20					25					30		
Lys	Arg	Ala	Gly	Val	Met	Ile	Glu	Asn	Val	Ser	Lys	Glu	Glu	Phe	Thr
			35					40					45		
Ile	Thr	Leu	Glu	Asn	Gly	Ile	Arg	Leu	Ser	Ser	Asn	His	Phe	Ser	Ala
			50					55				60			
Ile	Val	Arg	Glu	Glu	Gly	Asp	Thr	Arg	Ile	Gln	Val	Ser	Phe	Val	Cys
65					70					75					80
Pro	Ser	Ile	Arg	Leu	Arg	Leu	Ile	Phe	Glu	Ser	Arg	Asp	Asp	Val	Leu
				85					90					95	
Ser	Lys	Gln	Leu	Val	Leu	Glu	Ser	Ser	Thr	Glu	Val	Ile	Lys	Ser	Val
			100						105				110		
Glu	Val	Glu	Ser	Phe	Glu	Phe	Glu	Thr	Glu	Asp	Asn	Ile	Phe	Tyr	Pro
			115					120				125			
Lys	Arg	Gln	Asp	Cys	Ile	Lys	Glu	Met	Ala	Asn	Phe	Ser	Gly	His	Tyr
			130					135				140			
Val	Glu	Leu	Gly	Gln	Pro	Val	Tyr	Ala	Asn	Ser	Leu	Phe	Leu	Gly	Met
145					150					155					160
Glu	Phe	Pro	Met	Ser	Glu	Asn	Lys	Val	Asp	Gly	Arg	His	Tyr	Val	Ser
				165					170					175	
Arg	Tyr	Tyr	Leu	Gly	Thr	Val	Val	Asn	Gln	Glu	Lys	Ser	Leu	Trp	Ser
			180					185					190		
Cys	Ile	Ile	Gly	Gly	Ala	Cys	Ser	Tyr	Lys	Lys	Glu	Glu	Ile	Gln	Glu
			195					200				205			
Ala	Phe	Phe	Glu	Tyr	Val	Glu	Gly	Ile	Ala	Gln	Pro	Ser	Tyr	Phe	Arg
	210					215					220				
Lys	Gln	Tyr	Asn	Ser	Trp	Tyr	Asp	His	Met	Thr	Asp	Ile	Thr	Glu	Glu
225					230					235					240
Gly	Ile	Leu	Lys	Ser	Phe	Ser	Glu	Ile	Arg	Asp	Gly	Phe	Glu	Asn	His
				245					250					255	
Gly	Val	His	Leu	Asp	Ala	Tyr	Val	Val	Asp	Asp	Gly	Trp	Thr	Asn	Tyr
			260						265				270		
Gln	Ser	Val	Trp	Glu	Phe	Asn	His	Lys	Phe	Pro	Asn	Gly	Leu	Arg	Asn
			275					280				285			
Ile	Lys	His	Leu	Val	Asn	Gly	Phe	Gly	Ser	Ser	Leu	Gly	Leu	Trp	Ile
			290					295				300			
Gly	Pro	Arg	Gly	Gly	Tyr	Asn	Gly	Thr	Glu	Ile	Ile	Met	Ser	Asp	Trp
305					310					315					320
Leu	Glu	Ala	His	Pro	Glu	Leu	Asn	Ile	Gly	Ser	Lys	Asn	Leu	Ile	Ser
				325					330				335		
Asn	Asp	Val	Asn	Val	Ala	Asp	Phe	Asn	Tyr	Leu	Asn	Gln	Met	Lys	Lys
			340					345					350		


```

Lys Met Leu Glu Tyr Gln Lys Glu Phe Asp Ile Ser Tyr Trp Lys Ile
    355                                360                                365
Asp Gly Trp Leu Leu Gln Pro Asp Lys Pro Asp Lys Ser Gly Pro His
    370                                375                                380
Gly Met Tyr Thr Met Thr Ala Val Tyr Glu Phe Leu Ile Gln Leu Leu
    385                                390                                395                                400
Ile Asp Leu Arg Lys Glu Arg Gly Gly Lys Asp Cys Trp Leu Asn Leu
    405                                410                                415
Thr Ser Tyr Val Asn Pro Ser Pro Trp Phe Leu Gln Trp Val Asn Ser
    420                                425                                430
Leu Trp Ile Gln Ile Ser Gln Asp Val Gly Phe Thr Glu Asn Ala Gly
    435                                440                                445
Asn Asp Ile Asn Arg Met Ile Thr Tyr Arg Asp Ser Gln Tyr Gln Glu
    450                                455                                460
Phe Leu Glu Lys Arg Glu Ile Gln Leu Pro Met Trp Ser Leu Tyr Asn
    465                                470                                475                                480
His Glu Pro Ile Tyr Ala Val Ser Ala Asn Thr Trp Tyr Met Asp His
    485                                490                                495
Gln Met Phe Ala Ser Ile Pro Asp Phe Glu Ala Tyr Leu Leu Phe Ile
    500                                505                                510
Ser Thr Arg Gly Asn Ala Phe Trp Glu Phe His Tyr Ser Phe Asp Met
    515                                520                                525
Phe Asp Glu Glu Arg Trp Lys Ala Asn Ala Arg Ala Val Lys Trp Ile
    530                                535                                540
Glu Glu Asn Tyr Gln Thr Leu Lys Tyr Ser Lys Lys Ile Gly Gly Ser
    545                                550                                555                                560
Pro Glu Lys Phe Glu Ile Tyr Gly Tyr Lys Cys His Asn Gln Lys Thr
    565                                570                                575
Ser Thr Glu Ile Leu Ser Leu Arg Asn Pro Ala Gln Ile Lys Gln Lys

    580                                585                                590
Ile Lys Ile Glu Asn Leu Ser Ile Glu Asn Phe Thr Arg Val Ile Gly
    595                                600                                605
Asp Phe Thr Ile Gln Glu Asp Glu Ile Glu Leu Ala Pro Tyr Ser Ile
    610                                615                                620
Val Ile Leu Lys Lys
    625

```

(2) INFORMATION FOR SEQ ID NO:5043:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 295 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5043:

Ile	Glu	Arg	Val	Asn	Leu	Met	Leu	Gln	Gln	Leu	Val	Asn	Gly	Leu	Ile
1				5					10					15	
Leu	Gly	Ser	Val	Tyr	Ala	Leu	Leu	Ala	Leu	Gly	Tyr	Thr	Met	Val	Tyr
			20					25					30		
Gly	Ile	Ile	Lys	Leu	Ile	Asn	Phe	Ala	His	Gly	Asp	Ile	Tyr	Met	Met
		35					40					45			
Gly	Ala	Phe	Ile	Gly	Tyr	Phe	Leu	Ile	Asn	Ser	Phe	Gln	Met	Asn	Phe
	50					55					60				
Phe	Val	Ala	Leu	Ile	Val	Ala	Met	Leu	Val	Thr	Ala	Ile	Leu	Gly	Val
65					70					75					80
Val	Ile	Glu	Phe	Leu	Ala	Tyr	Arg	Pro	Leu	Arg	His	Ser	Thr	Arg	Ile
				85					90					95	
Ala	Val	Leu	Ile	Thr	Ala	Ile	Gly	Val	Ser	Phe	Leu	Leu	Glu	Asn	Gly
			100					105					110		
Met	Val	Tyr	Leu	Val	Gly	Ala	Asn	Thr	Arg	Ala	Phe	Pro	Gln	Ala	Ile
		115					120					125			
Gln	Thr	Val	Arg	Tyr	Asp	Leu	Gly	Pro	Ile	Ser	Leu	Thr	Asn	Val	Gln
	130					135					140				
Leu	Met	Ile	Leu	Ala	Ile	Ser	Leu	Ile	Leu	Met	Ile	Leu	Leu	Gln	Val
145					150					155					160
Ile	Val	Gln	Lys	Thr	Lys	Met	Gly	Lys	Ala	Met	Arg	Ala	Val	Ser	Val
			165					170					175		
Asp	Ser	Asp	Ala	Ala	Gln	Leu	Met	Gly	Ile	Asn	Val	Asn	Arg	Thr	Ile
			180					185				190			
Ser	Phe	Thr	Phe	Ala	Leu	Gly	Ser	Ala	Leu	Ala	Gly	Ala	Ala	Gly	Val
		195					200					205			
Leu	Ile	Ala	Leu	Tyr	Tyr	Asn	Ser	Leu	Glu	Pro	Leu	Met	Gly	Val	Thr
	210					215					220				
Pro	Gly	Leu	Lys	Ser	Phe	Val	Ala	Ala	Val	Leu	Gly	Gly	Ile	Gly	Ile
225					230					235					240
Ile	Pro	Gly	Ala	Ala	Leu	Gly	Gly	Phe	Val	Ile	Gly	Leu	Leu	Glu	Thr
			245					250						255	
Phe	Ala	Thr	Ala	Phe	Gly	Met	Ser	Asp	Phe	Arg	Asp	Ala	Ile	Val	Tyr
		260						265				270			
Gly	Ile	Leu	Leu	Leu	Ile	Leu	Ile	Val	Arg	Pro	Ala	Gly	Ile	Leu	Gly
		275					280					285			
Lys	Asn	Val	Lys	Glu	Lys	Val									
	290					295									

(2) INFORMATION FOR SEQ ID NO:5044:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5044:

```
Ser Gly Gly Val Val Asn Val Lys Glu Tyr Pro Leu Tyr Phe Phe Ser
1      5      10
Tyr Ser Met Glu Ile Lys Glu Gln Thr Arg Lys Leu Ala Ala Gly Cys
20    25    30
Ser Lys His Cys Phe Glu Val Val Asp Arg Thr Asp Glu Val Ser Asn
35    40    45
His Ile Tyr Gly Asn Val Thr Leu Thr Trp Phe Glu Glu Ile Phe Glu
50    55    60
Glu Tyr Tyr Ile Ser Lys Gly Arg Ser Lys Phe Thr Pro Thr Cys
65    70    75
```

(2) INFORMATION FOR SEQ ID NO:5045:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 313 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...313

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5045:

```
Glu Lys Gly Val Gly Ser Leu Thr Leu Arg Ser His Ser Glu Arg Leu
1      5      10      15
Met Gly Thr Thr Ile Thr Ile Ser Leu Val Asp Glu Gln Ala Asp Ile
20    25    30
Phe Leu Gln Lys Ser Phe Asp Leu Leu Lys Glu Leu Glu Tyr Arg Phe
35    40    45
Asn Ala Asn Ser Gln Glu Ser Glu Leu Met Glu Ile Asn Tyr Gln Ala
50    55    60
Gly Val Ser Pro Val Thr Val His Pro Asp Leu Phe Glu Leu Ile Ser
65    70    75    80
Leu Gly Leu Glu His Ser Leu Ala Leu Ser Ser His Leu Asn Ile Ser
85    90    95
Ile Gly Pro Leu Ile Gln Thr Trp Arg Ile Gly Phe Ser Asp Ala Lys
100   105   110
Val Ala Gln Pro Gln Glu Ile Glu Ser Val Leu Pro Leu Ile Asn Pro
115   120   125
His Gly Ile Glu Leu Asp Ser Ser Thr Ser Thr Val Phe Leu Lys Gln
130   135   140
Lys Gly Met Lys Ile Asp Leu Gly Cys Leu Ala Lys Gly Tyr Ser Ala
145   150   155   160
Asp Lys Val Ala Gln Phe Leu Arg Lys Glu Gly Val Thr Ser Ala Leu
165   170   175
```

```

Ile Asn Leu Gly Gly Asn Ile Leu Thr Ile Gly Lys Asn Gln Ala Arg
      180                      185                      190
Gly Asp Asn Pro Trp Gln Ile Gly Ile Gln Asp Pro Ala Asn Pro Arg
      195                      200                      205
Gly Asn His Leu Met Thr Ile Pro Val Val Asn Lys Ser Val Val Thr
      210                      215                      220
Ser Gly Ile Tyr Glu Arg His Leu Thr Val Asp Gly Gln Asp Tyr His
      225                      230                      235                      240
His Ile Phe Asp Ser Gln Thr Gly Tyr Pro Val Glu Thr Glu Leu Ala
      245                      250                      255
Ser Leu Thr Ile Ile Ser Asp Lys Ser Val Asp Gly Glu Ile Trp Thr
      260                      265                      270
Thr Arg Leu Phe Gly Glu Arg Pro Ala Ser Ile Leu Trp Gln Val Glu
      275                      280                      285
Ser Leu Glu Gly Ile Glu Val Ile Leu Ile Asp Lys Glu Gly His Leu
      290                      295                      300
Ser Cys Ser Ser Gly Ile Pro Thr Leu
      305                      310

```

(2) INFORMATION FOR SEQ ID NO:5046:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 68 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...68

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5046:

```

Lys Gly Gly Val Phe Met Lys Ser Phe Lys Asp Phe Arg Glu Ser Leu
1      5      10      15
Thr Ala Glu Asp Met Gln Ala Ile Ser Ala Lys Ala Asn Glu Ala Thr
      20      25      30
Lys Gln Ile Asp His Thr Asp Gly Leu Gln Leu Gly Lys Val Ser Gly
      35      40      45
Leu Thr Ser Val Ile Thr Thr Ile Glu Leu Leu Glu Lys Tyr His Glu
      50      55      60
Trp Leu His Ser
65

```

(2) INFORMATION FOR SEQ ID NO:5047:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 124 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...124

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5047:

His	Ser	Gly	Val	Lys	Gln	Ser	Gly	Arg	Leu	Phe	Gln	Pro	Glu	Pro	Arg
1				5					10					15	
Asn	Leu	Lys	Ala	Lys	Leu	Phe	Ser	Gln	Val	Ile	Val	Arg	Ala	Lys	His
			20					25					30		
Ile	His	Ser	Asn	Asp	Phe	Asp	Ala	Thr	Ser	Asp	Gly	Ser	Ile	Ile	Phe
			35				40					45			
Lys	Lys	Val	Ile	Ser	Asp	Asp	Ser	Leu	Cys	Ser	Thr	Phe	Lys	Asn	Ser
			50			55					60				
Asp	Asp	Ile	Glu	Leu	Phe	Lys	Ile	Leu	Arg	Asn	Lys	Ala	His	Leu	His
65					70				75					80	
Leu	Pro	Ile	Glu	Thr	Val	Thr	Pro	Arg	Thr	Val	Ser	Thr	Ser	Gln	Asp
				85					90					95	
Ile	Ile	Leu	Gly	Arg	Phe	Leu	Lys	Leu	His	Ser	Lys	Trp	Lys	Ser	Leu
			100					105					110		
Ser	Phe	Arg	Met	Thr	Val	Glu	Val	Glu	Met	Glu	Ser				
			115					120							

(2) INFORMATION FOR SEQ ID NO:5048:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 108 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5048:

His	Ser	Gly	Val	Lys	Gln	Ser	Gly	Arg	Leu	Phe	Gln	Pro	Glu	Pro	Arg
1				5					10					15	
Asn	Leu	Lys	Ala	Lys	Leu	Phe	Ser	Gln	Ala	Ile	Val	Arg	Ala	Lys	His
			20					25					30		
Ile	His	Ser	Asn	Asp	Phe	Asp	Ala	Thr	Ser	Asp	Gly	Ser	Ile	Val	Ala
			35				40					45			

Lys	Lys	Val	Ile	Ser	Asn	Asp	Ser	Leu	Cys	Ser	Ser	Leu	Lys	Asn	Ser
50						55					60				
Asp	Asp	Ile	Glu	Leu	Val	Lys	Ile	Leu	Arg	Asn	Lys	Ala	His	Leu	His
65					70				75					80	
Leu	Pro	Ile	Glu	Thr	Val	Thr	Thr	Arg	Thr	Val	Ser	Thr	Ser	Gln	Asp
				85					90					95	
Ile	Ile	Ser	Gly	Arg	Gln	Glu	Lys	Ser	Cys	Leu	Lys				
			100					105							

(2) INFORMATION FOR SEQ ID NO:5049:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5049:

His	Ser	Gly	Val	Lys	Gln	Ser	Gly	Arg	Leu	Phe	Gln	Pro	Glu	Pro	Arg
1				5					10					15	
Asn	Leu	Lys	Ala	Lys	Leu	Phe	Ser	Gln	Val	Ile	Val	Arg	Ala	Lys	His
			20					25					30		
Ile	His	Ser	Asn	Asn	Phe	Asp	Ala	Thr	Ser	Asp	Ser	Ser	Ile	Val	Ala
			35				40					45			
Lys	Lys	Val	Ile	Ser	Asn	Asp	Ser	Leu	Cys	Ser	Ser	Leu	Lys	Asn	Ser
			50			55					60				
Asp	Asp	Ile	Glu	Ile	Val	Lys	Ile	Leu	Arg	Asn	Glu	Ala	His	Leu	His
65					70				75					80	
Leu	Pro	Ile	Glu	Thr	Val	Thr	Pro	Arg	Thr	Val	Ser	Thr	Ser	Gln	Asp
				85					90					95	
Ile	Ile	Ser	Gly	Arg	Arg	Glu	Lys	Ser	Cys	Ser	Lys				
			100					105							

(2) INFORMATION FOR SEQ ID NO:5050:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5050:

```
His Ser Gly Val Lys Gln Ser Gly Arg Leu Phe Gln Pro Glu Pro Arg
1          5          10          15
Asn Leu Lys Ala Lys Leu Phe Ser Gln Ala Ile Val Arg Ala Lys His
          20          25          30
Ile His Ser Asn Asp Phe Asp Ala Thr Ser Asp Gly Ser Ile Val Ala
          35          40          45
Lys Lys Val Ile Ser Asn Asp Ser Leu Cys Ser Ser Leu Lys Asn Ser
          50          55          60
Asp Asp Ile Glu Ile Val Lys Ile Leu Arg Asn Glu Ala His Leu His
65          70          75          80
Leu Pro Ile Glu Thr Val Thr Pro Arg Thr Val Ser Thr Ser Gln Asp
          85          90          95
Ile Ile Ser Gly Arg Gln Glu Lys Ser Cys Leu Lys
          100          105
```

(2) INFORMATION FOR SEQ ID NO:5051:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 108 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...108

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5051:

```
His Ser Gly Val Lys Gln Ser Arg Arg Leu Phe Gln Pro Glu Pro Arg
1          5          10          15
Asn Leu Lys Ala Lys Leu Phe Ser Gln Val Ile Val Arg Ala Lys His
          20          25          30
Ile His Ser Asn Asp Phe Asp Ala Thr Ser Asp Gly Ser Ile Ile Phe
          35          40          45
Lys Lys Val Ile Ser Asp Asp Ser Leu Cys Ser Thr Phe Lys Asn Ser
          50          55          60
Asp Asp Ile Glu Leu Phe Lys Ile Leu Arg Asn Lys Ala His Leu His
65          70          75          80
Leu Pro Ile Glu Thr Val Thr Pro Arg Thr Val Ser Thr Ser Gln Asp
          85          90          95
Ile Ile Leu Gly Arg Phe Leu Lys Leu His Ser Lys
          100          105
```

(2) INFORMATION FOR SEQ ID NO:5052:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 111 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5052:

His	Ser	Gly	Val	Lys	Gln	Ser	Gly	Arg	Leu	Phe	Gln	Pro	Glu	Pro	Arg
1				5					10					15	
Asn	Leu	Lys	Ala	Lys	Leu	Phe	Ser	Gln	Val	Ile	Val	Arg	Thr	Lys	His
			20					25					30		
Ile	His	Ser	Asn	Asn	Phe	Asp	Ala	Thr	Ser	Asp	Asn	Ser	Ile	Val	Ala
			35				40					45			
Lys	Lys	Val	Ile	Ser	Asn	Asp	Ser	Leu	Cys	Ser	Thr	Leu	Lys	Asn	Ser
			50			55					60				
Asp	Asp	Ile	Glu	Leu	Val	Lys	Ile	Leu	Arg	Asn	Glu	Ala	His	Leu	Ser
65					70				75					80	
Leu	Cys	Lys	Ser	Ile	Leu	Ile	Pro	Arg	His	Asn	Leu	Arg	Lys	Thr	Arg
				85				90						95	
Lys	Ile	Met	Phe	Lys	Val	Lys	Ile	Ile	Glu	Leu	Thr	Asn	Asp	Ser	
				100				105					110		

(2) INFORMATION FOR SEQ ID NO:5053:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 321 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...321

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5053:

Asn Gly Gly Val Phe Leu Lys Pro Phe Lys Thr Ile Glu Glu Gln Ile

1				5				10					15			
Ala	Thr	Leu	Lys	Ile	Arg	Gly	Leu	Ser	Ile	Thr	Asp	Glu	Ser	Lys	Ala	
			20					25					30			
Ala	Lys	Tyr	Leu	Leu	Ser	Asn	Asn	Tyr	Tyr	Asn	Ile	Ile	Asn	Gly	Tyr	
		35					40					45				
Ser	Lys	Phe	Phe	Gln	His	Pro	Gly	Thr	Asp	Thr	Tyr	Ile	Asp	Gly	Val	
	50					55					60					
Thr	Phe	Asp	Glu	Val	Ser	Ser	Leu	Tyr	Thr	Phe	Asp	Lys	Asp	Val	Lys	
65					70					75					80	
Arg	Ala	Ile	Leu	Gln	Ala	Ile	Leu	Glu	Ala	Glu	His	His	Ile	Lys	Ser	
				85					90					95		
Ile	Thr	Ala	His	Arg	Phe	Ala	Glu	Ala	Tyr	Pro	Ser	Gln	Lys	Tyr	Ala	
			100					105					110			
Tyr	Leu	Asn	Thr	Asn	Ser	Tyr	Ala	Asp	Asn	Lys	Ile	Leu	Asp	Val	Gly	
		115					120					125				
Phe	Ile	Val	Ser	Lys	Leu	Ser	Lys	Ile	Ile	Asn	Thr	Asn	Lys	Arg	Tyr	
	130					135					140					
Arg	Gly	Asn	Ser	Ile	His	His	Tyr	Ala	His	Thr	His	Ser	Asp	Val	Pro	
145					150					155					160	
Ile	Trp	Val	Leu	Thr	Asp	Tyr	Leu	Glu	Phe	Gly	Asp	Leu	Arg	Thr	Ile	
				165					170					175		
Ile	Glu	Asn	Leu	Pro	Asn	Ser	Leu	Gln	Asn	Glu	Ile	Ala	Arg	Asp	Leu	
		180						185					190			
Val	Ser	Phe	Ile	Ser	Thr	Asn	Ile	Pro	Asp	Phe	Asn	Asp	Val	Phe	Pro	
		195					200					205				
Pro	Glu	Thr	Leu	Ile	Ser	Phe	Leu	Lys	Asn	Ile	Asn	Glu	Val	Arg	Asn	
	210					215					220					
Lys	Cys	Ala	His	Asn	Asn	Arg	Leu	Leu	Asn	Phe	Arg	Cys	Arg	Ser	Asn	
225					230					235					240	
Ser	Thr	Phe	Trp	Glu	Thr	Ile	His	Asn	Lys	Glu	Ile	Leu	Met	Gly	Asp	
			245						250					255		
Asp	Ser	Arg	Lys	Thr	Val	Tyr	Ser	Thr	Ile	Ile	Ser	Leu	Gln	Cys	Phe	
			260					265					270			
Ile	Ser	Lys	Ala	Ala	Phe	Asn	Ile	Leu	Trp	Asn	Thr	Leu	Arg	Lys	Lys	
		275					280						285			
Val	Ile	Lys	Leu	Glu	Lys	Lys	Leu	Pro	Ser	Ile	Asp	Ile	Asn	Val	Ile	
	290					295					300					
Asn	Gln	Ser	Leu	Gly	Phe	Pro	Asn	Asp	Trp	His	Arg	Asn	Glu	Pro	Lys	
305					310					315					320	
Val																

(2) INFORMATION FOR SEQ ID NO:5054:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 113 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...113

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5054:

```
Val Phe Leu Val Tyr Leu Ile Ile Thr Val His Lys Leu Gly Arg Val
1      5      10      15
Ile Asp Glu Thr Glu Lys Thr Ile Lys Thr Leu Thr Ser Asp Val Asp
      20      25      30
Val Thr Leu His His Thr Asn Glu Leu Leu Ala Lys Val Asn Val Leu
      35      40      45
Ala Asp Asp Ile Asn Val Lys Val Ala Thr Ile Asp Pro Leu Phe Ser
      50      55      60
Ala Val Ala Asp Leu Ser Leu Ser Val Ser Asp Leu Asn Asp His Ala
65      70      75      80
Arg Val Leu Ser Lys Lys Ala Ser Ser Ala Gly Ser Lys Thr Leu Lys
      85      90      95
Thr Gly Ala Ser Leu Ser Ala Leu Arg Leu Ala Ser Lys Phe Phe Lys
      100      105      110
Lys
```

(2) INFORMATION FOR SEQ ID NO:5055:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 92 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...92

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5055:

```
Leu Phe Leu Val Arg Lys Tyr Leu Tyr His Gln Pro Ser Leu Leu Gln
1      5      10      15
Asp Ile Cys Trp Gly Leu Arg Arg Ala Val Glu Ala Ile Val Thr Ile
      20      25      30
Glu Ala Met Arg His Asn Phe Val Pro Met Thr Ala Gly Thr Ser Glu
      35      40      45
Val Ser Asp Tyr Ile Glu Ala Asn Val Val Tyr Gly Gln Gly Leu Glu
      50      55      60
Lys Glu Ile Pro Tyr Ala Ile Ser Asn Thr Phe Gly Phe Gly Gly His
65      70      75      80
Asn Ala Val Leu Ala Phe Lys Arg Trp Glu Asn Arg
      85      90
```

(2) INFORMATION FOR SEQ ID NO:5056:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...64
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5056:

```

Leu Ser Leu Val Glu Tyr Leu Val Trp Asp Gln Gly Val Ala Gly Ser
1          5          10          15
Asn Pro Val Phe Pro Ile His Gly Gly Val Ala Gln Leu Ala Arg Ala
20          25          30
Ser Gly Ser Tyr Pro Gly Gly Arg Gly Phe Asp Pro Leu Arg Arg Tyr
35          40          45
Asn Asp Leu Val Gly Pro Leu Ala Gln Leu Val Arg Ala Leu Gly Ser
50          55          60

```

(2) INFORMATION FOR SEQ ID NO:5057:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 84 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...84
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5057:

```

Leu Arg Leu Val Ile Lys Asn Ile Gly Arg Asn Val Leu Asn Lys Lys
1          5          10          15
Tyr Asn Ile Val Leu Phe Leu Leu Phe Ile Val Tyr Leu Phe Gly Tyr
20          25          30
Phe Ser Ile Ser Lys Thr Leu Ile Pro Ile Met Cys Val Phe Gln Val
35          40          45
Phe Leu Ile Glu His Ile Phe Arg Ile Arg Asn Arg Met Met Gln Ile
50          55          60
Gly Glu Ile Ile Ile Ile Val Ala Ser Ile Ile Leu Phe Ile Asp Ser

```

65
Ile Leu Ser Leu

(2) INFORMATION FOR SEQ ID NO:5058:

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 82 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Streptococcus pneumoniae

```
(ix) FEATURE:
      (A) NAME/KEY: misc_feature
      (B) LOCATION 1...82
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5058:

[illegible]

(2) INFORMATION FOR SEQ ID NO:5059:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 815 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Streptococcus pneumoniae

```
(ix) FEATURE:
      (A) NAME/KEY: misc_feature
      (B) LOCATION 1...815
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5059:

Pro	Ser	Leu	Val	Lys	His	Lys	Ser	Asp	Arg	Ile	Ser	Leu	His	Gln	Lys
1				5					10					15	
Asp	Leu	Glu	Ile	Thr	Ser	Val	Glu	Val	Ala	Gly	Gln	Ala	Arg	Pro	Phe
			20					25					30		
Thr	Val	Asp	His	Asp	Asn	Glu	Ala	Leu	His	Ile	Glu	Leu	Ala	Glu	Ala
		35					40					45			
Gly	Gln	Val	Glu	Leu	Val	Leu	Ala	Phe	Ser	Gly	Lys	Ile	Thr	Asp	Asn
	50					55					60				
Met	Thr	Gly	Ile	Tyr	Pro	Ser	Tyr	Tyr	Thr	Val	Asp	Gly	Val	Lys	Lys
65					70					75					80
Glu	Val	Leu	Ser	Thr	Gln	Phe	Glu	Ser	His	Phe	Ala	Arg	Glu	Ala	Phe
				85					90					95	
Pro	Cys	Val	Asp	Glu	Pro	Glu	Ala	Lys	Ala	Thr	Phe	Asp	Leu	Ser	Leu
			100					105					110		
Arg	Phe	Asp	Gln	Ala	Glu	Gly	Glu	Leu	Ala	Leu	Ser	Asn	Met	Pro	Glu
		115					120					125			
Ile	Asp	Val	Glu	Asn	Arg	Lys	Glu	Thr	Gly	Ile	Trp	Lys	Phe	Glu	Thr
	130					135					140				
Thr	Pro	Arg	Met	Ser	Ser	Tyr	Leu	Leu	Ala	Phe	Val	Ala	Gly	Asp	Leu
145				150						155					160
Gln	Gly	Val	Thr	Ala	Lys	Thr	Lys	Asn	Gly	Thr	Leu	Val	Gly	Val	Tyr
				165					170					175	
Ser	Thr	Lys	Ala	His	Pro	Leu	Ser	Asn	Leu	Asp	Phe	Ser	Leu	Asp	Ile
			180					185					190		
Ala	Val	Arg	Ser	Ile	Glu	Phe	Tyr	Glu	Asp	Tyr	Tyr	Gly	Val	Lys	Tyr
		195					200					205			
Pro	Ile	Pro	Gln	Ser	Leu	His	Ile	Ala	Leu	Pro	Asp	Phe	Ser	Ala	Gly
	210					215					220				
Ala	Met	Glu	Asn	Trp	Gly	Leu	Val	Thr	Tyr	Arg	Glu	Val	Tyr	Leu	Val
225				230						235					240
Val	Asp	Glu	Asn	Ser	Thr	Phe	Ala	Ser	Arg	Gln	Gln	Val	Ala	Leu	Val
			245						250					255	
Val	Ala	His	Glu	Leu	Ala	His	Gln	Trp	Phe	Gly	Asn	Leu	Val	Thr	Met
			260					265				270			
Lys	Trp	Trp	Asp	Asp	Leu	Trp	Leu	Asn	Glu	Ser	Phe	Ala	Asn	Met	Met
	275						280					285			
Glu	Tyr	Val	Cys	Val	Asp	Thr	Ile	Glu	Pro	Ser	Trp	Asn	Ile	Phe	Glu
	290					295					300				
Asp	Phe	Gln	Thr	Gly	Gly	Val	Pro	Leu	Ala	Leu	Glu	Arg	Asp	Ala	Thr
305				310						315					320
Asp	Gly	Val	Gln	Ser	Val	His	Val	Glu	Val	Lys	His	Pro	Asp	Glu	Ile
			325						330					335	
Asn	Thr	Leu	Phe	Asp	Gly	Ala	Ile	Val	Tyr	Ala	Lys	Gly	Ser	Arg	Leu
		340						345					350		
Met	His	Met	Leu	Arg	Arg	Trp	Leu	Gly	Asp	Ala	Asp	Phe	Ala	Lys	Gly
		355					360					365			
Leu	His	Ala	Tyr	Phe	Glu	Lys	His	Gln	Tyr	Ser	Asn	Thr	Ile	Gly	Ser
	370					375					380				
Asp	Leu	Trp	Asp	Ala	Leu	Gly	Gln	Ala	Ser	Gly	Arg	Asp	Val	Ala	Ala
385				390						395					400
Phe	Met	Asp	Ser	Trp	Leu	Glu	Gln	Pro	Gly	Tyr	Pro	Val	Leu	Thr	Val
			405						410					415	
Lys	Val	Glu	Asn	Asp	Val	Leu	Lys	Ile	Ser	Gln	Lys	Gln	Phe	Phe	Ile
			420					425					430		
Gly	Glu	Asn	Glu	Asp	Lys	Asn	Arg	Leu	Trp	Val	Val	Pro	Leu	Asn	Ser
		435					440					445			

Asn	Trp	Lys	Gly	Leu	Pro	Asp	Thr	Leu	Glu	Thr	Glu	Ser	Ile	Glu	Ile
450						455					460				
Pro	Gly	Tyr	Ala	Ala	Leu	Leu	Ala	Glu	Asn	Glu	Gly	Ala	Leu	Arg	Leu
465					470					475					480
Asn	Thr	Glu	Asn	Thr	Ala	His	Tyr	Ile	Thr	Asp	Tyr	Gln	Gly	Asp	Leu
				485					490					495	
Leu	Glu	Ala	Val	Leu	Ala	Glu	Leu	Glu	Thr	Leu	Asp	Asn	Thr	Ser	Lys
			500					505					510		
Leu	Gln	Ile	Val	Gln	Glu	Arg	Arg	Leu	Leu	Ala	Glu	Ala	Gly	His	Ile
	515						520					525			
Ser	Tyr	Ala	Asp	Leu	Leu	Pro	Val	Leu	Asp	Lys	Leu	Ala	Lys	Glu	Glu
	530					535					540				
Ser	Tyr	Leu	Val	Val	Ser	Ala	Val	Ser	Gln	Val	Ile	Ser	Ala	Leu	Glu
545					550				555						560
Arg	Phe	Ile	Asp	Glu	Gly	Thr	Asp	Ala	Glu	Thr	Ala	Phe	Lys	Gly	Leu
			565						570					575	
Val	Ala	Lys	Leu	Ala	Arg	His	Asn	Tyr	Asp	Arg	Leu	Gly	Phe	Glu	Ala
			580				585					590			
Lys	Asp	Gly	Glu	Ser	Asp	Glu	Asp	Glu	Leu	Val	Arg	Gln	Leu	Ala	Val
	595					600					605				
Ser	Met	Met	Ile	Arg	Ser	Asn	Asp	Ala	Glu	Ala	Arg	Gln	Val	Ala	Ser
610						615					620				
Gln	Ile	Phe	Ala	Thr	His	Lys	Glu	Asn	Leu	Ala	Glu	Leu	Pro	Ala	Ala
625					630					635					640
Ile	Arg	Ser	Gln	Val	Leu	Ile	Asn	Glu	Met	Lys	His	His	Glu	Thr	Lys
			645						650					655	
Asp	Leu	Leu	Ala	Leu	Tyr	Leu	Asp	Thr	Tyr	Thr	His	Ala	Thr	Asp	Ala
			660					665					670		
Val	Phe	Lys	Arg	Gln	Leu	Thr	Ala	Ala	Leu	Ala	Tyr	Ser	Thr	Asp	Ala
	675						680				685				
Asp	Asn	Ile	Gln	Asn	Leu	Ile	Thr	Ser	Trp	Lys	Asp	Lys	Phe	Val	Val
690					695					700					
Lys	Pro	Gln	Asp	Leu	Ser	Ala	Trp	Tyr	Tyr	Gln	Phe	Leu	Ala	His	Gln
705					710					715					720
Ala	Thr	Gln	Lys	Thr	Ala	Trp	Ser	Trp	Ala	Arg	Glu	Asn	Trp	Ala	Trp
			725						730					735	
Ile	Lys	Ala	Ala	Leu	Gly	Gly	Asp	Met	Ser	Phe	Asp	Ser	Phe	Val	Ile
		740					745					750			
Leu	Pro	Ala	His	Val	Phe	Lys	Thr	Gln	Gln	Arg	Leu	Ala	Glu	Tyr	Lys
	755						760					765			
Glu	Phe	Phe	Glu	Pro	Gln	Leu	Ser	Asp	Leu	Ala	Leu	Ser	Arg	Asn	Ile
770						775					780				
Gly	Met	Gly	Ile	Lys	Glu	Ile	Ala	Ala	Arg	Val	Asp	Leu	Ile	Ser	Arg
785					790					795					800
Glu	Lys	Ala	Ala	Val	Glu	Ala	Val	Val	Leu	Gln	Tyr	Gly	Asn	Ala	
			805						810					815	

(2) INFORMATION FOR SEQ ID NO:5060:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 314 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...314

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5060:

```
Pro Gly Leu Val Cys Trp Val Leu Ile Val Phe Leu Val Ala Val Asn
1          5          10          15
Ser Leu Ser Asp Tyr Lys Thr Asp Phe Arg Leu Phe Glu Phe Ser Lys
          20          25          30
Ile Phe Gly Asp Glu Glu Tyr Gly Phe Gln Leu Ser Val Thr Val Leu
          35          40          45
Arg Tyr Gly Tyr Thr Tyr Arg Leu Phe Ser Phe Val Val Asp Met Leu
          50          55          60
Asn Gln Asp Met Gly Arg Asn Leu Glu Val Ile Gln Arg His Gly Ala
65          70          75          80
Leu Leu Leu Val Glu Asn Gly Gln Leu Leu Tyr Val Glu Leu Pro Lys
          85          90          95
Glu Gly Val Asn Val His Asp Phe Phe Glu Thr Ser Lys Val Arg Glu
          100          105          110
Thr Leu Leu Ile Ala Thr Arg Asn Glu Gly Lys Thr Lys Glu Phe Arg
          115          120          125
Ala Ile Phe Asp Lys Leu Gly Tyr Asp Val Glu Asn Leu Asn Asp Tyr
          130          135          140
Pro Asp Leu Pro Glu Val Ala Glu Thr Gly Met Thr Phe Glu Glu Asn
145          150          155          160
Ala Arg Leu Lys Ala Glu Thr Ile Ser Gln Leu Thr Gly Lys Met Val
          165          170          175
Leu Ala Asp Asp Ser Gly Leu Lys Val Asp Val Leu Gly Gly Leu Pro
          180          185          190
Gly Val Trp Ser Ala Arg Phe Ala Gly Val Gly Ala Thr Asp Arg Glu
          195          200          205
Asn Asn Ala Lys Leu Leu His Glu Leu Ala Met Val Phe Glu Leu Lys
          210          215          220
Asp Arg Ser Ala Gln Phe His Thr Thr Leu Val Val Ala Ser Pro Asn
225          230          235          240
Lys Glu Ser Leu Val Leu Asn Thr Arg Pro Gly Gln Val Ile Leu Thr
          245          250          255
Leu Lys Pro Lys Gly Glu Asn Gly Phe Gly Tyr Asp Pro Leu Phe Leu
          260          265          270
Val Gly Glu Thr Gly Glu Ser Ser Ala Glu Leu Thr Leu Glu Glu Lys
          275          280          285
Asn Ser Gln Ser His Arg Ala Leu Ala Val Lys Lys Leu Leu Glu Val
          290          295          300
Phe Pro Ser Trp Gln Ser Lys Pro Ser Leu
305          310
```

(2) INFORMATION FOR SEQ ID NO:5061:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 68 amino acids

(B) TYPE: amino acid

- (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...68
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5061:

```

Phe Leu Leu Val Gly Lys Glu Leu Val Ser Val Asn Ser Leu Lys Ala
1          5          10          15
Ser Gln Asn Gln Leu Cys Asn Leu Gly Gly Ala Thr Val Ser Leu Thr
          20          25          30
Leu Pro Tyr Gln Thr Val Pro Thr Gln Gly Phe Ile Met Leu Gly Ser
          35          40          45
Leu His Ser Ile Asn His Leu Leu Ser Thr Thr Ile Leu Gly Met Val
          50          55          60
Gln Ala Gly Asp
65

```

(2) INFORMATION FOR SEQ ID NO:5062:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 218 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...218
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5062:

```

Asp Ser Met Val Lys Val Ala Thr Gln Thr Pro Ile Ile Ser Leu Phe
1          5          10          15
Leu Leu Ile Leu Ser Leu Glu Thr Ser Phe Ile Pro Ser Ile Ala Leu
          20          25          30
Asn Leu Ser Val Val Ala Phe Cys Ile Leu Phe Met Leu Tyr Tyr Arg
          35          40          45
Arg Phe Lys Met Leu Ala Trp Met Ile Ile Leu Ala Ile Leu Pro Ser
          50          55          60
Phe Ala Asn Tyr Trp Ala Val Gln Leu His Gly Asp Ala Ser Gln Ala
65          70          75          80
Val Met Leu Gly Thr Arg Ala Phe Val Thr Val Cys Ile Gly Leu Val

```


				85					90					95					
Phe	Val	Ser	Ser	Ile	Ser	Leu	Lys	Glu	Leu	Leu	Leu	Tyr	Leu	Ala	Gln				
			100					105					110						
Lys	Gly	Leu	Ser	Arg	Ser	Trp	Ser	Tyr	Ala	Leu	Ile	Val	Val	Phe	Asn				
		115					120					125							
Ser	Phe	Pro	Leu	Ile	Gln	Gln	Glu	Ile	Lys	Ser	Leu	Lys	Glu	Ala	Cys				
	130					135					140								
Leu	Leu	Arg	Gly	Gln	Glu	Leu	Tyr	Phe	Trp	Ser	Pro	Leu	Ile	Tyr	Ser				
145					150					155					160				
Lys	Val	Leu	Met	Thr	Val	Phe	Arg	Trp	Arg	His	Leu	Tyr	Leu	Arg	Ala				
				165					170						175				
Leu	Ser	Ala	His	Gly	Tyr	Asp	Glu	His	Ala	Gln	Leu	Lys	Asn	Ser	Tyr				
		180					185						190						
Arg	Thr	Phe	Tyr	Ile	Pro	Lys	Lys	Thr	Lys	Leu	Ile	Tyr	Leu	Leu	Phe				
	195					200						205							
Phe	Leu	Leu	Leu	Gln	Thr	Ser	Leu	Phe	Leu										
	210					215													

(2) INFORMATION FOR SEQ ID NO:5063:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 219 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5063:

Ser	Thr	Met	Val	Gly	Glu	Ile	Leu	Cys	His	Val	Gln	Asn	Ile	Leu	Gly
1			5					10					15		
Lys	Gln	Thr	Leu	Lys	Pro	Leu	Ser	Arg	Leu	Lys	Ile	Lys	Ser	Gln	Phe
		20					25					30			
Lys	Lys	Ala	Arg	Lys	Arg	Phe	Lys	Tyr	Ser	Arg	Arg	Phe	Arg	Lys	Val
	35					40					45				
Arg	Leu	Met	Tyr	Gln	Asp	Glu	Ala	Gly	Phe	Ser	Arg	Ile	Ser	Lys	Leu
	50				55					60					
Gly	Ser	Cys	Trp	Ser	Pro	Ile	Gly	Val	Asp	Pro	His	Val	His	Ser	His
65				70				75						80	
Tyr	Ile	Arg	Glu	Phe	Arg	Tyr	Cys	Tyr	Gly	Ala	Val	Asp	Ala	Tyr	Thr
		85					90					95			
Gly	Glu	Ser	Phe	Phe	Leu	Ile	Ala	Gly	Arg	Cys	Asn	Thr	Glu	Trp	Met
	100						105					110			
Asn	Ala	Phe	Leu	Glu	Glu	Leu	Ser	Gln	Ala	Tyr	Pro	Asp	Asp	Tyr	Leu
	115					120						125			
Leu	Leu	Val	Met	Asp	Asn	Ala	Ile	Trp	His	Lys	Ser	Ser	Ile	Leu	Lys
	130					135					140				
Ile	Pro	Thr	Asn	Ile	Gly	Phe	Ala	Phe	Ile	Pro	Pro	Tyr	Thr	Pro	Glu

145		150		155		160										
Met	Asn	Pro	Ile	Glu	Gln	Val	Trp	Lys	Glu	Ile	Arg	Lys	Arg	Gly	Phe	
		165				170								175		
Lys	Asn	Lys	Ala	Phe	Arg	Ile	Leu	Glu	Asp	Val	Met	Asn	Gln	Leu	Gln	
		180						185					190			
Asp	Val	Ile	Gln	Gly	Leu	Glu	Lys	Glu	Val	Ile	Lys	Ser	Ile	Val	Asn	
		195					200					205				
Arg	Arg	Trp	Thr	Arg	Met	Leu	Phe	Glu	Ser	Arg						
		210				215										

(2) INFORMATION FOR SEQ ID NO:5064:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 98 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...98
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5064:

Ser	Ala	Met	Val	Gly	Glu	Ile	Leu	Cys	His	Val	Gln	Asn	Ile	Leu	Gly
1				5				10						15	
Lys	Gln	Thr	Leu	Lys	Pro	Leu	Ser	Arg	Leu	Lys	Ile	Lys	Ser	Gln	Phe
			20					25					30		
Lys	Lys	Lys	Arg	Lys	Arg	Phe	Lys	Thr	Ser	Arg	Arg	Phe	His	Lys	Val
		35				40						45			
Arg	Leu	Met	Tyr	Gln	Asp	Glu	Ala	Gly	Phe	Gly	Arg	Ile	Ser	Lys	Leu
	50					55				60					
Gly	Ser	Cys	Trp	Ser	Pro	Ile	Gly	Val	Gly	Pro	His	Val	His	Ser	His
65				70					75					80	
Tyr	Ile	Arg	Glu	Phe	Arg	Tyr	Cys	Tyr	Gly	Pro	Ile	Gln	Ala	Asn	His
			85					90						95	
Phe	Ser														

(2) INFORMATION FOR SEQ ID NO:5065:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 219 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...219

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5065:

Ser	Ala	Met	Val	Gly	Glu	Ile	Leu	Cys	His	Val	Gln	Asn	Ile	Leu	Arg
1				5					10					15	
Lys	Gln	Thr	Leu	Lys	Pro	Leu	Ser	Arg	Leu	Lys	Ile	Lys	Ser	Gln	Phe
			20					25					30		
Lys	Lys	Lys	Arg	Lys	Arg	Phe	Lys	Thr	Ser	Arg	Arg	Phe	His	Lys	Val
		35				40						45			
Arg	Ser	Met	Tyr	Gln	Asp	Glu	Ala	Gly	Phe	Gly	Arg	Ile	Ser	Lys	Leu
	50				55					60					
Gly	Ser	Cys	Trp	Ser	Pro	Ile	Gly	Val	Gly	Pro	His	Val	His	Ser	His
65				70					75					80	
Tyr	Ile	Arg	Glu	Phe	Arg	Tyr	Cys	Tyr	Gly	Ala	Val	Asp	Ala	His	Thr
			85					90					95		
Gly	Glu	Ser	Phe	Phe	Leu	Arg	Ala	Gly	Gly	Cys	Asn	Thr	Glu	Trp	Met
		100					105					110			
Asn	Ala	Phe	Leu	Glu	Glu	Leu	Ser	Gln	Ala	Tyr	Pro	Asp	Asp	Tyr	Leu
	115					120					125				
Leu	Leu	Val	Met	Asp	Asn	Ala	Ile	Trp	His	Lys	Ser	Ser	Thr	Leu	Lys
	130				135					140					
Ile	Pro	Thr	Asn	Ile	Gly	Phe	Ala	Phe	Ile	Pro	Pro	Tyr	Thr	Pro	Glu
145				150					155					160	
Ile	Asn	Pro	Val	Glu	Gln	Val	Trp	Lys	Glu	Ile	Arg	Lys	Arg	Gly	Phe
			165					170					175		
Lys	Asn	Lys	Ala	Phe	Arg	Thr	Leu	Glu	Asp	Val	Met	Asn	Gln	Leu	Gln
		180					185					190			
Asp	Ile	Ile	Gln	Gly	Leu	Glu	Lys	Glu	Val	Ile	Lys	Pro	Ile	Val	Asn
	195				200						205				
Arg	Arg	Trp	Thr	Arg	Met	Leu	Phe	Glu	Ser	Arg					
	210				215										

(2) INFORMATION FOR SEQ ID NO:5066:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 62 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...62

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5066:

Ala	Leu	Met	Val	Pro	Leu	Gln	Ser	Leu	Ile	Phe	Val	Leu	Gly	Val	Gln
1			5					10					15		
Thr	Ile	Leu	Lys	Trp	Ala	Lys	Gly	Leu	Leu	Ser	Gln	Met	Lys	Asn	Phe
		20					25					30			
Lys	Arg	Trp	Trp	Met	Pro	Leu	Lys	Ala	Thr	Asn	Thr	Leu	Arg	Lys	Ser
	35					40					45				
Leu	Gln	Thr	Ala	Ser	Ala	Leu	Pro	Cys	Arg	Met	Tyr	Gly	Tyr		
	50					55				60					

(2) INFORMATION FOR SEQ ID NO:5067:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1262 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...1262

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5067:

Glu	Lys	Met	Val	Tyr	Ser	Ile	Arg	Ser	Leu	Lys	Asn	Gly	Thr	Gly	Ser
1			5					10					15		
Val	Leu	Ile	Gly	Ala	Ser	Leu	Val	Leu	Leu	Ala	Met	Ala	Thr	Pro	Thr
		20					25					30			
Ile	Ser	Ser	Asp	Glu	Ser	Thr	Pro	Thr	Thr	Asn	Glu	Pro	Asn	Asn	Arg
	35					40					45				
Asn	Thr	Thr	Ile	Leu	Ala	Gln	Pro	Leu	Thr	Asp	Thr	Ala	Ala	Gly	Ser
	50					55				60					
Gly	Lys	Asn	Glu	Ser	Asp	Ile	Ser	Ser	Pro	Arg	Asn	Ala	Asn	Ala	Ser
65				70					75					80	
Leu	Glu	Lys	Thr	Glu	Glu	Lys	Pro	Ala	Ala	Ser	Pro	Ala	Asp	Pro	Ala
		85						90					95		
Pro	Gln	Thr	Gly	Gln	Asp	Arg	Ser	Ser	Glu	Pro	Thr	Thr	Ser	Thr	Ser
	100						105					110			
Pro	Val	Thr	Thr	Glu	Thr	Lys	Ala	Glu	Glu	Pro	Ile	Glu	Asp	Asn	Tyr
	115					120					125				
Phe	Arg	Ile	His	Val	Lys	Lys	Leu	Pro	Glu	Glu	Asn	Lys	Asp	Ala	Gln
	130				135						140				
Gly	Leu	Trp	Thr	Trp	Asp	Asp	Val	Glu	Lys	Pro	Ser	Glu	Asn	Trp	Pro
145				150					155					160	
Asn	Gly	Ala	Leu	Ser	Phe	Lys	Asp	Ala	Lys	Lys	Asp	Asp	Tyr	Gly	Tyr
		165					170						175		
Tyr	Leu	Asp	Val	Lys	Leu	Lys	Gly	Glu	Gln	Ala	Lys	Lys	Ile	Ser	Phe
	180						185						190		
Leu	Ile	Asn	Asn	Thr	Ala	Gly	Lys	Asn	Leu	Thr	Gly	Asp	Lys	Ser	Val
	195					200					205				
Glu	Lys	Leu	Val	Pro	Lys	Met	Asn	Glu	Ala	Trp	Leu	Asp	Gln	Asp	Tyr

210					215					220					
Lys	Val	Phe	Ser	Tyr	Glu	Pro	Gln	Pro	Ala	Gly	Thr	Val	Arg	Val	Asn
225					230					235					240
Tyr	Tyr	Arg	Thr	Asp	Gly	Asn	Tyr	Asp	Lys	Lys	Ser	Leu	Trp	Tyr	Trp
				245					250					255	
Gly	Asp	Val	Lys	Asn	Pro	Ser	Ser	Ala	Gln	Trp	Pro	Asp	Gly	Thr	Asp
			260					265					270		
Phe	Thr	Ala	Thr	Gly	Lys	Tyr	Gly	Arg	Tyr	Ile	Asp	Ile	Pro	Leu	Asn
		275					280					285			
Glu	Ala	Ala	Arg	Glu	Phe	Gly	Phe	Leu	Leu	Leu	Asp	Glu	Ser	Lys	Gln
	290					295					300				
Gly	Asp	Asp	Val	Lys	Ile	Arg	Lys	Glu	Asn	Tyr	Lys	Phe	Thr	Asp	Leu
305				310					315					320	
Lys	Asn	His	Ser	Gln	Ile	Phe	Leu	Lys	Asp	Asp	Asp	Glu	Ser	Ile	Tyr
				325					330					335	
Thr	Asn	Pro	Tyr	Tyr	Val	His	Asp	Ile	Arg	Met	Thr	Gly	Ala	Gln	His
			340				345						350		
Val	Gly	Thr	Ser	Ser	Ile	Glu	Ser	Ser	Phe	Ser	Thr	Leu	Val	Gly	Ala
		355					360					365			
Lys	Lys	Glu	Asp	Ile	Leu	Lys	His	Ser	Asn	Ile	Thr	Asn	His	Leu	Gly
	370			375							380				
Asn	Lys	Val	Thr	Ile	Thr	Asp	Val	Ala	Ile	Asp	Glu	Ala	Gly	Lys	Lys
385				390					395					400	
Val	Thr	Tyr	Ser	Gly	Asp	Phe	Ser	Asp	Thr	Lys	His	Pro	Tyr	Thr	Val
			405					410					415		
Ser	Tyr	Asn	Ser	Asp	Gln	Phe	Thr	Thr	Lys	Thr	Ser	Trp	Arg	Leu	Lys
		420					425					430			
Asp	Glu	Thr	Tyr	Ser	Tyr	Asp	Gly	Lys	Leu	Gly	Ala	Asp	Leu	Lys	Glu
		435				440					445				
Glu	Gly	Lys	Gln	Val	Asp	Leu	Thr	Leu	Trp	Ser	Pro	Ser	Ala	Asp	Lys
	450			455					460						
Val	Ser	Val	Val	Val	Tyr	Asp	Lys	Asn	Asp	Pro	Asp	Lys	Val	Val	Gly
465				470					475					480	
Thr	Val	Ala	Leu	Glu	Lys	Gly	Glu	Arg	Gly	Thr	Trp	Lys	Gln	Thr	Leu
			485					490					495		
Asp	Ser	Thr	Asn	Lys	Leu	Gly	Ile	Thr	Asp	Phe	Thr	Gly	Tyr	Tyr	Tyr
		500					505					510			
Gln	Tyr	Gln	Ile	Glu	Arg	Gln	Gly	Lys	Thr	Val	Leu	Ala	Leu	Asp	Pro
	515			520					525						
Tyr	Ala	Lys	Ser	Leu	Ala	Ala	Trp	Asn	Ser	Asp	Asp	Ala	Lys	Ile	Asp
	530			535					540						
Asp	Ala	His	Lys	Val	Ala	Lys	Ala	Ala	Phe	Val	Asp	Pro	Ala	Lys	Leu
545				550					555					560	
Gly	Pro	Gln	Asp	Leu	Thr	Tyr	Gly	Lys	Ile	His	Asn	Phe	Lys	Thr	Arg
				565					570					575	
Glu	Asp	Ala	Val	Ile	Tyr	Glu	Ala	His	Val	Arg	Asp	Phe	Thr	Ser	Asp
		580						585				590			
Pro	Ala	Ile	Ala	Lys	Asp	Leu	Thr	Lys	Pro	Phe	Gly	Thr	Phe	Glu	Ala
	595					600					605				
Phe	Ile	Glu	Lys	Leu	Asp	Tyr	Leu	Lys	Asp	Leu	Gly	Val	Thr	His	Ile
	610			615					620						
Gln	Leu	Leu	Pro	Val	Leu	Ser	Tyr	Tyr	Phe	Val	Asn	Glu	Leu	Lys	Asn
625				630					635					640	
His	Glu	Arg	Leu	Ser	Asp	Tyr	Ala	Ser	Ser	Asn	Ser	Asn	Tyr	Asn	Trp
			645					650					655		

Gly	Tyr	Asp	Pro	Gln	Asn	Tyr	Phe	Ser	Leu	Thr	Gly	Met	Tyr	Ser	Ser
			660					665					670		
Asp	Pro	Lys	Asn	Pro	Glu	Lys	Arg	Ile	Ala	Glu	Phe	Lys	Asn	Leu	Ile
		675					680					685			
Asn	Glu	Ile	His	Lys	Arg	Gly	Met	Gly	Ala	Ile	Leu	Asp	Val	Val	Tyr
	690					695					700				
Asn	His	Thr	Ala	Lys	Val	Asp	Ile	Phe	Glu	Asp	Leu	Glu	Pro	Asn	Tyr
705					710						715				720
Tyr	His	Phe	Met	Asp	Ala	Asp	Gly	Thr	Pro	Arg	Thr	Ser	Phe	Gly	Gly
				725					730					735	
Gly	Arg	Leu	Gly	Thr	Thr	His	His	Met	Thr	Lys	Arg	Leu	Leu	Val	Asp
			740					745					750		
Ser	Ile	Lys	Tyr	Leu	Val	Asp	Thr	Tyr	Lys	Val	Asp	Gly	Phe	Arg	Phe
		755					760					765			
Asp	Met	Met	Gly	Asp	His	Asp	Ala	Ala	Ser	Ile	Glu	Glu	Ala	Tyr	Lys
	770					775					780				
Ala	Ala	Arg	Ala	Leu	Asn	Pro	Asn	Leu	Ile	Met	Leu	Gly	Glu	Gly	Trp
785					790					795					800
Arg	Thr	Tyr	Ala	Gly	Asp	Glu	Asn	Met	Pro	Thr	Lys	Ala	Ala	Asp	Gln
				805					810					815	
Asp	Trp	Met	Lys	His	Thr	Asp	Thr	Val	Ala	Val	Phe	Ser	Asp	Asp	Ile
		820						825					830		
Arg	Asn	Asn	Leu	Lys	Ser	Gly	Tyr	Pro	Asn	Glu	Gly	Gln	Pro	Ala	Phe
		835					840					845			
Ile	Thr	Gly	Gly	Lys	Arg	Asp	Val	Asn	Thr	Ile	Phe	Lys	Asn	Leu	Ile
	850					855					860				
Ala	Gln	Pro	Thr	Asn	Phe	Glu	Ala	Asp	Ser	Pro	Gly	Asp	Val	Ile	Gln
865					870					875					880
Tyr	Ile	Ala	Ala	His	Asp	Asn	Leu	Thr	Leu	Phe	Asp	Ile	Ile	Ala	Gln
				885					890					895	
Ser	Ile	Lys	Lys	Asp	Pro	Ser	Lys	Ala	Glu	Asn	Tyr	Ala	Glu	Ile	His
		900						905				910			
Arg	Arg	Leu	Arg	Leu	Gly	Asn	Leu	Met	Val	Leu	Thr	Ala	Gln	Gly	Thr
		915					920					925			
Pro	Phe	Ile	His	Ser	Gly	Gln	Glu	Tyr	Gly	Arg	Thr	Lys	Gln	Phe	Arg
	930					935					940				
Asp	Pro	Ala	Tyr	Lys	Thr	Pro	Val	Ala	Glu	Asp	Lys	Val	Pro	Asn	Lys
945					950					955					960
Ser	His	Leu	Leu	Arg	Asp	Lys	Asp	Gly	Asn	Pro	Phe	Asp	Tyr	Pro	Tyr
				965					970					975	
Phe	Ile	His	Asp	Ser	Tyr	Asp	Ser	Ser	Asp	Ala	Val	Asn	Lys	Phe	Asp
		980						985				990			
Trp	Thr	Lys	Ala	Thr	Asp	Gly	Lys	Thr	Tyr	Pro	Glu	Asn	Val	Lys	Ser
		995					1000					1005			
Arg	Asp	Tyr	Met	Lys	Gly	Leu	Ile	Ala	Leu	Arg	Gln	Ser	Thr	Asp	Ala
	1010					1015					1020				
Phe	Arg	Leu	Lys	Ser	Leu	Gln	Asp	Ile	Lys	Asp	Arg	Val	His	Leu	Ile
1025					1030					1035					1040
Thr	Val	Pro	Gly	Gln	Asn	Gly	Val	Glu	Lys	Glu	Asp	Val	Val	Ile	Gly
				1045					1050					1055	
Tyr	Gln	Ile	Thr	Ala	Pro	Asn	Gly	Asp	Ile	Tyr	Ala	Val	Phe	Val	Asn
		1060					1065					1070			
Ala	Asp	Glu	Lys	Ala	Arg	Glu	Phe	Asn	Leu	Gly	Thr	Ala	Phe	Ala	His
	1075						1080				1085				
Leu	Arg	Asn	Ala	Glu	Val	Leu	Ala	Asp	Glu	Asn	Gln	Ala	Gly	Ser	Val
	1090					1095					1100				
Gly	Ile	Ala	Asn	Pro	Lys	Gly	Leu	Glu	Trp	Thr	Glu	Lys	Gly	Leu	Lys

1105		1110		1115		1120
Leu	Asn	Ala	Leu	Thr	Ala	Thr
		1125		1130		1135
Ser	Pro	Glu	Ser	Thr	Ala	Glu
		1140		1145		1150
Pro	Glu	His	Gln	Asp	Pro	Ala
		1155		1160		1165
Pro	Asp	Ala	Lys	Val	Ala	Asp
		1170		1175		1180
Ala	Asp	Ser	Gln	Ala	Glu	Gln
		1185		1190		1195
Val	Lys	Glu	Ala	Val	Gln	Asn
		1205		1210		1215
Asn	Ile	Pro	Ala	Thr	Pro	Asp
		1220		1225		1230
Ile	Lys	Asn	Glu	Asn	Lys	Leu
		1235		1240		1245
Leu	Leu	Gly	Leu	Gly	Phe	Leu
		1250		1255		1260

(2) INFORMATION FOR SEQ ID NO:5068:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 231 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...231

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5068:

Gly	Glu	Met	Val	Glu	Ala	Met	Arg	Ala	Gly	Gln	Phe	Leu	His	Leu	Arg
1			5						10					15	
Val	Pro	Asp	Asp	Ala	His	Leu	Leu	Arg	Pro	Ile	Ser	Ile	Ser	Ser	
		20						25				30			
Ile	Asp	Lys	Ala	Asn	Lys	Gln	Cys	His	Leu	Ile	Tyr	Arg	Ile	Glu	Gly
		35				40					45				
Ala	Gly	Thr	Ala	Ile	Phe	Ser	Thr	Leu	Ser	Gln	Gly	Asp	Thr	Leu	Asp
		50				55				60					
Val	Met	Gly	Pro	Gln	Gly	Asn	Gly	Phe	Asp	Leu	Ser	Asp	Leu	Asp	Glu
65				70				75						80	
Gln	Asn	Gln	Val	Leu	Leu	Val	Gly	Gly	Gly	Ile	Gly	Val	Pro	Pro	Leu
			85					90					95		
Leu	Glu	Val	Ala	Lys	Glu	Leu	His	Glu	Arg	Gly	Val	Lys	Val	Val	Thr
		100						105					110		
Val	Leu	Gly	Phe	Ala	Asn	Lys	Asp	Ala	Val	Ile	Leu	Lys	Thr	Glu	Leu
		115				120						125			
Ala	Gln	Tyr	Gly	His	Val	Phe	Val	Thr	Thr	Asp	Asp	Gly	Ser	Tyr	Gly

130		135		140	
Ile	Lys	Gly	Asn	Val	Ser
145		150		155	
Asp	Ala	Val	Tyr	Ser	Cys
		165		170	
Gln	Thr	Phe	Asp	His	Pro
		180		185	
Met	Ala	Cys	Gly	Met	Gly
		195		200	
Glu	Asn	Glu	Thr	Val	Ser
		210		215	
Arg	Thr	Gly	Thr	Val	Val
225				230	

(2) INFORMATION FOR SEQ ID NO:5069:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 434 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...434
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5069:

Asn	Gln	Met	Val	Met	Trp	Ser	Tyr	Cys	Ile	Ala	Arg	Ile	Gly	Gly	Arg
1			5					10					15		
Met	Glu	Ser	Leu	Leu	Ile	Leu	Leu	Leu	Ile	Ala	Asn	Leu	Ala	Gly	Leu
		20					25					30			
Phe	Leu	Ile	Trp	Gln	Arg	Gln	Asp	Arg	Gln	Glu	Lys	His	Leu	Ser	Lys
	35				40						45				
Ser	Leu	Glu	Asp	Gln	Ala	Asp	His	Leu	Ser	Asp	Gln	Leu	Asp	Tyr	Arg
	50				55					60					
Phe	Asp	Gln	Ala	Arg	Gln	Ala	Ser	Gln	Leu	Asp	Gln	Lys	Asp	Leu	Glu
65			70					75						80	
Val	Ala	Val	Ser	Asp	Arg	Leu	Gln	Glu	Val	Arg	Ile	Glu	Leu	His	Gln
		85					90					95			
Gly	Leu	Thr	Gln	Val	Arg	Gln	Glu	Met	Thr	Asp	Asn	Leu	Leu	Gln	Thr
	100					105					110				
Arg	Asp	Lys	Thr	Asp	Gln	Arg	Leu	Gln	Ala	Leu	Gln	Glu	Ser	Asn	Glu
	115				120						125				
Gln	Arg	Leu	Glu	Gln	Met	Arg	Gln	Thr	Val	Glu	Glu	Lys	Leu	Glu	Lys
	130				135				140						
Thr	Leu	Gln	Thr	Arg	Leu	Gln	Ala	Ser	Phe	Glu	Thr	Val	Ser	Lys	Gln
145			150					155						160	
Leu	Glu	Ser	Val	Asn	Arg	Gly	Leu	Gly	Glu	Met	Gln	Thr	Val	Ala	Arg
		165				170						175			
Asp	Val	Gly	Ala	Leu	Asn	Lys	Val	Leu	Ser	Gly	Thr	Lys	Thr	Arg	Gly

			180					185				190			
Ile	Leu	Gly	Glu	Leu	Gln	Leu	Gly	Gln	Ile	Ile	Glu	Asp	Ile	Met	Thr
		195					200					205			
Pro	Ala	Gln	Tyr	Glu	Arg	Glu	Tyr	Ala	Thr	Val	Glu	Asn	Ser	Ser	Glu
	210					215					220				
Arg	Val	Glu	Tyr	Ala	Ile	Lys	Leu	Pro	Gly	Gln	Gly	Asp	Gln	Glu	Tyr
225					230				235						240
Val	Tyr	Leu	Pro	Ile	Asp	Ser	Lys	Phe	Pro	Leu	Ala	Asp	Tyr	Tyr	Arg
			245					250					255		
Leu	Glu	Glu	Ala	Tyr	Glu	Thr	Gly	Asp	Lys	Asp	Glu	Ile	Glu	Arg	Cys
		260					265					270			
Arg	Lys	Ser	Leu	Leu	Ala	Ser	Val	Lys	Arg	Phe	Ala	Lys	Asp	Ile	Lys
	275					280					285				
Ser	Lys	Tyr	Ile	Ala	Pro	Pro	Arg	Thr	Thr	Asn	Phe	Gly	Ile	Leu	Phe
	290					295				300					
Val	Pro	Thr	Glu	Gly	Leu	Tyr	Ser	Glu	Ile	Val	Arg	Asn	Pro	Val	Phe
305				310					315						320
Phe	Asp	Asp	Leu	Arg	Arg	Glu	Glu	Gln	Ile	Ile	Val	Ala	Gly	Pro	Ser
			325					330					335		
Thr	Leu	Ser	Ala	Leu	Leu	Asn	Ser	Leu	Ser	Val	Gly	Phe	Lys	Thr	Leu
		340					345					350			
Asn	Ile	Gln	Lys	Ser	Ala	Asp	His	Ile	Ser	Lys	Thr	Leu	Ala	Ser	Val
	355					360					365				
Tyr	Thr	Glu	Phe	Gly	Lys	Phe	Gly	Gly	Ile	Leu	Val	Gln	Ala	Gln	Lys
	370				375					380					
His	Leu	Gln	His	Ala	Ser	Gly	Asn	Ile	Asp	Glu	Leu	Leu	Asn	Arg	Arg
385				390					395						400
Thr	Ile	Ala	Ile	Glu	Arg	Thr	Leu	Arg	His	Ile	Glu	Leu	Ser	Glu	Gly
			405					410					415		
Glu	Pro	Ala	Leu	Asp	Leu	Leu	Tyr	Phe	Gln	Glu	Asn	Glu	Glu	Glu	Tyr
		420					425					430			
Glu	Asp														

(2) INFORMATION FOR SEQ ID NO:5070:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 88 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...88
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5070:

Asn	Arg	Met	Val	Lys	Trp	Leu	Ser	Met	Asn	Gly	Leu	Met	Val	Asp	Val
1			5					10					15		
Ile	Met	Leu	Ala	Leu	Thr	Glu	Phe	Gly	Arg	Lys	Val	Lys	Gln	Val	Gln

		20					25					30			
Phe	Leu	Leu	Val	Met	Ile	Ala	Ile	Val	Asn	Ile	Ser	Ala	Ala	Leu	Gly
		35					40					45			
Lys	Ala	Lys	Ser	Tyr	Asn	Ser	Leu	Phe	His	Met	Ser	Lys	Lys	Arg	Met
		50				55				60					
Tyr	Arg	Gln	Leu	Thr	Ser	Asp	Phe	Asp	Lys	Phe	Ser	Asn	Asp	Ala	Ala
65					70				75						80
Gln	Tyr	Ala	Ile	Asp	His	Leu	Asp								
				85											

(2) INFORMATION FOR SEQ ID NO:5071:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 377 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...377

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5071:

Lys	Arg	Met	Val	Pro	Arg	Val	Asn	Ala	Pro	Ser	Gly	Val	Phe	Gly	Met
1			5					10					15		
Trp	Phe	Ser	Phe	Tyr	Leu	Arg	Glu	Thr	Asp	Gly	Gly	Asn	Met	Ser	Thr
		20					25					30			
Ile	Glu	Glu	Gln	Leu	Lys	Ala	Leu	Arg	Glu	Glu	Thr	Leu	Ala	Ser	Leu
		35				40					45				
Lys	Gln	Ile	Thr	Ala	Gly	Asn	Glu	Lys	Glu	Met	Gln	Asp	Leu	Arg	Val
		50			55					60					
Ser	Val	Leu	Gly	Lys	Lys	Gly	Ser	Leu	Thr	Glu	Ile	Leu	Lys	Gly	Met
65				70				75							80
Lys	Asp	Val	Ser	Ala	Glu	Met	Arg	Pro	Ile	Ile	Gly	Lys	His	Val	Asn
			85					90					95		
Glu	Ala	Arg	Asp	Val	Leu	Thr	Ala	Ala	Phe	Glu	Glu	Thr	Ala	Lys	Leu
		100					105						110		
Leu	Glu	Glu	Lys	Lys	Val	Ala	Ala	Gln	Leu	Ala	Ser	Glu	Ser	Ile	Asp
		115				120						125			
Val	Thr	Leu	Pro	Gly	Arg	Pro	Val	Ala	Thr	Gly	His	Arg	His	Val	Leu
		130			135					140					
Thr	Gln	Thr	Ser	Glu	Glu	Ile	Glu	Asp	Ile	Phe	Ile	Gly	Met	Gly	Tyr
145				150				155							160
Gln	Val	Val	Asp	Gly	Phe	Glu	Val	Glu	Gln	Asp	Tyr	Tyr	Asn	Phe	Glu
			165				170						175		
Arg	Met	Asn	Leu	Pro	Lys	Asp	His	Pro	Ala	Arg	Asp	Met	Gln	Asp	Thr
		180				185						190			
Phe	Tyr	Ile	Thr	Glu	Glu	Ile	Leu	Leu	Arg	Thr	His	Thr	Ser	Pro	Val
		195				200					205				
Gln	Ala	Arg	Ala	Met	Asp	Ala	His	Asp	Phe	Ser	Lys	Gly	Pro	Leu	Lys

210	215	220
Met Ile Ser Pro Gly Arg Val Phe Arg Arg Asp Thr Asp Asp Ala Thr		
225	230	235
His Ser His Gln Phe His Gln Ile Glu Gly Leu Val Val Gly Lys Asn		240
	245	250
Ile Ser Met Ala Asp Leu Gln Gly Thr Leu Gln Leu Ile Val Gln Lys		255
	260	265
Met Phe Gly Glu Glu Arg Gln Ile Arg Leu Arg Pro Ser Tyr Phe Pro		270
	275	280
Phe Thr Glu Pro Ser Val Glu Val Asp Val Ser Cys Phe Lys Cys Gly		285
	290	295
Gly Glu Gly Cys Asn Ile Cys Lys Lys Thr Gly Trp Ile Glu Ile Met		300
305	310	315
Gly Ala Gly Met Val His Pro Arg Val Leu Glu Met Ser Gly Ile Asp		320
	325	330
Ala Thr Val Tyr Ser Gly Phe Ala Phe Gly Leu Gly Gln Glu Arg Val		335
	340	345
Ala Met Leu Arg Tyr Gly Ile Asn Asp Ile Arg Gly Phe Tyr Gln Gly		350
	355	360
Asp Val Arg Phe Ser Glu Gln Phe Lys		365
370	375	

(2) INFORMATION FOR SEQ ID NO:5072:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 117 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...117

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5072:

Thr Ile Val Val Asn Thr Ser His Leu Ser Asn Cys Pro Lys Cys Asn	
1	15
Ser Glu Tyr Val Tyr Glu Asp Gly Ala Leu Leu Val Cys Pro Glu Cys	
	30
Ala His Glu Trp Asn Pro Ala Glu Val Ala Glu Val Glu Glu Gly Leu	
	45
Val Ala Ile Asp Ala Asn Gly Asn Lys Leu Ala Asp Gly Asp Ile Val	
50	60
Thr Leu Ile Lys Asp Leu Lys Val Lys Gly Ala Pro Lys Asp Leu Lys	
65	80
Gln Gly Thr Arg Val Lys Asn Ile Arg Ile Val Glu Gly Asp His Asn	
	95
Ile Asp Cys Lys Ile Asp Gly Phe Gly Ala Met Lys Leu Lys Ser Glu	
	110
Phe Val Arg Lys Ile	

(2) INFORMATION FOR SEQ ID NO:5073:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5073:

```

Arg Phe Val Val Lys Arg Leu Gly Tyr Glu His Ser Met Ala Arg His
1          5          10          15
Leu Gly Ala Val Tyr Asn Leu Pro His Gly Val Cys Cys Ala Met Leu
          20          25          30
Leu Pro Val Ile Glu Arg Glu Asn Ala Lys Arg Val Pro Glu Ala Phe
          35          40          45
Arg Asn Val Ala Lys Ala Leu Gly Leu His Val Glu Gly Lys Ser Asp
          50          55          60
Gln Glu Cys Ala Asp Tyr Ala Ile Val Glu Ile Glu Lys Leu Ser Glu
65          70          75          80
Thr Val Gly Ile Pro Lys Lys Leu Thr Glu Leu Gly Ile Glu Glu Lys
          85          90          95
Asp Phe Asp Phe Glu Tyr Leu Ser Lys Asn Ala Leu Ile Asp Ala Cys
          100          105          110
Ala Pro Gly Asn Pro Phe Met Pro Thr Leu Glu Glu Thr Ile Ala Phe
          115          120          125
Tyr Lys Glu Leu Phe
          130

```

(2) INFORMATION FOR SEQ ID NO:5074:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 297 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...297

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5074:

Asn	Val	Val	Val	Gln	Glu	Lys	Ile	Ile	Val	Ile	Val	Gly	Pro	Thr	Ala	
1				5					10					15		
Val	Gly	Lys	Thr	Ala	Leu	Ala	Ile	Glu	Val	Ala	Lys	Arg	Phe	Asn	Gly	
			20					25					30			
Glu	Val	Val	Ser	Gly	Asp	Ser	Gln	Gln	Val	Tyr	Arg	Gly	Leu	Asp	Ile	
		35					40					45				
Gly	Thr	Ala	Lys	Ala	Ser	Pro	Glu	Glu	Gln	Ala	Ala	Val	Pro	His	His	
	50					55					60					
Leu	Ile	Asp	Val	Arg	Glu	Ile	Thr	Glu	Ser	Tyr	Ser	Ala	Phe	Asp	Phe	
65					70					75					80	
Val	Ser	Glu	Ala	Lys	Met	Thr	Ile	Glu	Gly	Ile	His	Asn	Arg	Gly	Lys	
				85					90					95		
Leu	Ala	Ile	Ile	Ala	Gly	Gly	Thr	Gly	Leu	Tyr	Ile	Gln	Ser	Leu	Leu	
			100					105					110			
Lys	Gly	Tyr	His	Leu	Gly	Gly	Glu	Thr	Pro	His	Glu	Glu	Ile	Leu	Ala	
		115					120					125				
Tyr	Arg	Ala	Ser	Leu	Glu	Pro	Tyr	Ser	Asp	Glu	Glu	Leu	Ala	His	Leu	
	130					135					140					
Val	Glu	Gln	Ala	Gly	Leu	Glu	Ile	Pro	Gln	Phe	Asn	Arg	Arg	Arg	Ala	
145					150					155					160	
Met	Arg	Ala	Leu	Glu	Ile	Ala	His	Phe	Gly	Gln	Asp	Leu	Glu	Asn	Gln	
				165					170					175		
Glu	Ile	Leu	Tyr	Glu	Pro	Leu	Ile	Ile	Cys	Leu	Asp	Asp	Glu	Arg	Ser	
		180					185					190				
Gln	Leu	Tyr	Glu	Arg	Ile	Asn	His	Arg	Val	Asp	Leu	Met	Phe	Glu	Ala	
		195					200					205				
Gly	Leu	Leu	Asp	Glu	Ala	Lys	Trp	Leu	Phe	Asp	His	Ser	Pro	Asn	Val	
	210					215				220						
Gln	Ala	Ala	Lys	Gly	Ile	Gly	Tyr	Lys	Glu	Leu	Phe	Pro	Tyr	Phe	Arg	
225				230						235					240	
Gly	Glu	Gln	Thr	Phe	Glu	Glu	Ala	Arg	Glu	Ser	Leu	Asn	Gln	Ala	Thr	
				245					250					255		
Arg	Arg	Phe	Ala	Lys	Arg	Gln	Leu	Thr	Trp	Phe	Arg	Asn	Arg	Met	Leu	
			260				265						270			
Val	Thr	Phe	Tyr	His	Ile	Gly	Glu	Ser	Gly	Val	Gln	Asp	Arg	Ile	Leu	
		275				280						285				
Ser	Gln	Ile	Glu	Glu	Ser	Leu	Asp	Asp								
	290					295										

(2) INFORMATION FOR SEQ ID NO:5075:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 60 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...60

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5075:

Phe	Leu	Val	Val	Lys	Leu	Phe	Asp	Leu	Cys	Tyr	Ser	Glu	Tyr	Ala	Trp
1				5					10					15	
Asp	Ser	Leu	Ser	Lys	Trp	Phe	Ile	Lys	Gln	Phe	Tyr	Phe	Thr	Lys	Thr
			20					25					30		
Ile	Val	Thr	Met	Gln	Lys	Ser	Asn	Gly	Lys	Ser	Val	Ala	Phe	Phe	Gly
		35					40					45			
Tyr	Lys	Arg	Leu	Leu	Ser	Gln	Thr	Leu	Phe	Phe	Val				
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:5076:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 336 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5076:

Glu	Ser	Ser	Val	Val	Ser	Ser	Leu	Ser	Tyr	Phe	Ser	Gly	Glu	Gly	Asp
1				5					10					15	
Glu	Lys	Met	Gln	Thr	Lys	Ser	Lys	His	Thr	Lys	Leu	Phe	Trp	Ile	Leu
			20					25					30		
Ile	Ile	Leu	Ala	Ile	Gly	Ala	Cys	Leu	Leu	Tyr	Phe	Trp	Pro	Ile	Thr
		35					40					45			
His	Leu	Ser	Ala	Phe	Ala	Trp	Lys	Leu	Arg	Ser	Gln	Lys	Ile	Ile	Val
	50					55					60				
Tyr	Leu	Leu	Val	Ala	Ile	Ala	Thr	Gly	Ile	Ser	Thr	Ile	Ser	Phe	Gln
65					70				75						80
Thr	Leu	Thr	Glu	Asn	Arg	Phe	Leu	Thr	Pro	Ser	Ile	Leu	Gly	Ile	Glu
			85					90					95		
Ser	Phe	Tyr	Val	Leu	Leu	Gln	Thr	Leu	Leu	Leu	Val	Phe	Glu	Ser	Lys
			100					105					110		
Phe	Leu	Gln	Leu	Gly	Lys	Ser	Pro	Ile	Leu	Glu	Phe	Leu	Val	Leu	Leu
		115					120					125			
Leu	Val	Gln	Ser	Leu	Phe	Phe	Leu	Ala	Leu	Gln	Gly	Tyr	Leu	Lys	Thr
	130					135					140				
Leu	Met	Lys	Gln	Asp	Leu	Val	Phe	Ile	Leu	Leu	Ile	Cys	Leu	Ala	Leu
145					150				155					160	
Arg	Ser	Leu	Phe	Arg	Asn	Ile	Ser	Thr	Phe	Leu	Gln	Val	Leu	Met	Asp
				165				170						175	

Pro	Asn	Glu	Tyr	Asp	Lys	Leu	Gln	Asn	Ser	Leu	Phe	Ala	Ser	Phe	Gln
			180					185					190		
His	Leu	Asn	Thr	Ser	Ile	Leu	Ala	Ile	Gly	Ser	Leu	Ile	Ile	Leu	Ala
		195					200					205			
Leu	Thr	Ile	Phe	Phe	Phe	Arg	Lys	Ala	Val	Val	Leu	Asp	Val	Leu	His
	210					215					220				
Leu	Gln	Arg	Glu	Thr	Ala	Gln	Ile	Leu	Gly	Leu	Asp	Val	Glu	Lys	Glu
225					230					235				240	
Gln	Lys	Glu	Leu	Leu	Trp	Gly	Ile	Val	Leu	Leu	Thr	Ser	Thr	Ala	Thr
			245						250					255	
Ala	Leu	Val	Gly	Pro	Met	Ala	Phe	Phe	Gly	Phe	Met	Leu	Ala	Asn	Leu
		260						265					270		
Thr	Tyr	Leu	Ile	Val	Lys	Asp	Tyr	Gln	His	Lys	Leu	Leu	Phe	Ile	Val
	275					280						285			
Ala	Ile	Leu	Ile	Gly	Phe	Ile	Ser	Leu	Thr	Leu	Gly	Gln	Ala	Leu	Ile
	290					295					300				
Glu	Arg	Val	Phe	Ala	Leu	Glu	Ile	Arg	Ile	Ser	Met	Ile	Ile	Glu	Ser
305					310					315				320	
Val	Gly	Gly	Phe	Leu	Phe	Phe	Ile	Leu	Leu	Tyr	Arg	Arg	Ala	Arg	Gln
			325					330						335	

(2) INFORMATION FOR SEQ ID NO:5077:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...61
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5077:

Cys	Ile	Pro	Val	Asn	Glu	Ser	Phe	Gly	Leu	Ile	Leu	Ser	Glu	Asn	Ala
1			5					10					15		
Leu	Gln	Thr	Asp	Val	Asn	Val	Ala	Leu	Pro	Cys	Val	Trp	Leu	Leu	Asn
		20					25					30			
Thr	Ser	Val	Leu	Ser	Thr	Thr	Ser	Lys	Gln	Cys	Phe	Glu	Gln	Ser	Ala
	35					40					45				
Ala	Ser	Phe	Leu	Val	Cys	Ser	Leu	Ile	Phe	Ile	Glu	Tyr			
	50				55						60				

(2) INFORMATION FOR SEQ ID NO:5078:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 148 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...148
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5078:

```

Val Glu Thr Val Lys Arg Leu Arg Lys Tyr Pro Lys Ile Glu Ile Val
1      5      10      15
Ser His Leu Ile Asn Gly Leu Pro Gly Glu Thr His Glu Met Met Val
      20      25      30
Glu Asn Val Arg Arg Cys Val Thr Asn Asn Asp Ile Gln Gly Ile Lys
      35      40      45
Leu His Leu Leu His Leu Met Thr Asn Thr Arg Met Gln Arg Asp Tyr
      50      55      60
His Glu Gly Arg Leu Gln Leu Met Ser Gln Asp Glu Tyr Val Arg Val
      65      70      75      80
Ile Cys Asp Gln Leu Glu Ile Ile Pro Lys His Ile Val Ile His Arg
      85      90      95
Ile Thr Gly Asp Ala Pro Arg Asp Met Leu Leu Gly Pro Met Trp Ser
      100     105     110
Leu Asn Lys Trp Glu Ala Leu Asn Ser Ile Glu Met Glu Met Arg Arg
      115     120     125
Arg Gly Ser Val Gln Gly Cys Lys Ala Val Lys Gln Glu Phe Glu Asn
      130     135     140
Glu Lys Thr Thr
145

```

(2) INFORMATION FOR SEQ ID NO:5079:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 94 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...94
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5079:

```

Glu Lys Thr Val Tyr Asp Gln Thr Ile His Arg Val Ala Glu Ile Val
1      5      10      15

```


Gln	Asn	Glu	Asp	Leu	Tyr	Lys	Lys	Gly	Leu	Asn	Val	Glu	Leu	Ala	His
			20					25					30		
Gln	Gln	Ile	Lys	Gly	Phe	Phe	Glu	Ala	Glu	Phe	Lys	Asn	Arg	Ile	Asn
		35					40					45			
Gly	Val	Leu	Asn	Thr	Lys	Ile	Lys	Asn	Ser	Thr	Leu	Asn	Arg	Val	Asn
	50					55					60				
Lys	Lys	Thr	Ile	His	Gln	Ser	Asn	Lys	Asn	Ser	Met	Ile	Asn	Leu	Lys
65					70					75					80
Gln	Lys	Gln	Arg	Lys	Met	Leu	Lys	Asn	Lys	Ala	Ile	Leu	Cys		
				85					90						

(2) INFORMATION FOR SEQ ID NO:5080:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 294 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5080:

Arg	Ser	Gln	Val	Arg	Leu	Leu	Pro	Ala	Ile	Gly	Leu	Ile	Ser	Gln	Glu
1				5					10					15	
Arg	Gln	Arg	Gln	Val	Ile	Ala	Leu	Leu	Leu	Val	Glu	Val	Met	Arg	Ile
			20					25					30		
Ile	Arg	Met	Leu	Gly	Leu	Val	Leu	Trp	Gly	Val	Tyr	Gln	Leu	His	Pro
		35					40					45			
Ala	Pro	Ala	Val	Gln	Val	Val	Val	Leu	Ala	Ile	Ala	Val	Thr	Gln	Val
	50					55					60				
Leu	His	Asp	Leu	Leu	Gln	Gly	Arg	Asp	Asp	Asn	Ser	Leu	Asn	Glu	Val
65					70					75					80
Ala	Asn	Gln	Trp	Ile	Ala	Thr	Phe	Phe	Leu	Ser	Cys	Tyr	Asn	Lys	Gly
			85					90						95	
Met	Asn	Gln	Tyr	Gln	Lys	Lys	Ile	Val	Asn	Gly	Lys	Ile	Tyr	Ser	Leu
			100					105					110		
Leu	Ser	Gly	Leu	Ile	Trp	Gly	Ile	Cys	Gly	Ile	Leu	Gly	Lys	Tyr	Phe
		115				120						125			
Phe	Thr	His	Tyr	Gln	Val	Ser	Ser	Gly	Trp	Ile	Thr	Ser	Met	Arg	Leu
	130					135					140				
Thr	Leu	Ala	Gly	Ser	Leu	Val	Leu	Ile	Trp	Ser	Ala	Ile	Gln	Leu	Lys
145					150					155					160
Ser	Gln	Val	Leu	Asp	Ile	Trp	Arg	Asp	Lys	Lys	Asn	Tyr	Leu	Pro	Phe
			165						170					175	
Leu	Ala	Tyr	Ala	Ile	Leu	Gly	Ile	Phe	Ser	Val	Gln	Tyr	Phe	Phe	Tyr
			180					185					190		
Leu	Cys	Val	Glu	Tyr	Ser	Asn	Ala	Thr	Thr	Ala	Thr	Ile	Leu	Gln	Phe
		195					200						205		

Ile	Ser	Pro	Val	Phe	Ile	Leu	Phe	Tyr	Asn	Arg	Leu	Val	Tyr	Gln	Lys
210						215					220				
Arg	Ala	Ser	Lys	Ser	Ala	Val	Phe	Tyr	Val	Leu	Val	Ala	Met	Leu	Gly
225					230					235					240
Val	Cys	Leu	Met	Ala	Thr	Lys	Gly	Asp	Leu	Ser	Gln	Leu	Ser	Met	Thr
				245					250					255	
Pro	Leu	Ala	Leu	Ile	Thr	Gly	Leu	Leu	Ser	Ala	Met	Gly	Val	Met	Phe
			260					265					270		
Asn	Val	Ile	Leu	Pro	Gln	Pro	Phe	Ala	Lys	Arg	Tyr	Gly	Phe	Val	Leu
	275						280					285			
Thr	Ser	Trp	Val	Gly	Gly										
290															

(2) INFORMATION FOR SEQ ID NO:5081:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 157 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...157

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5081:

Pro	Gly	Lys	Val	Cys	Ile	Thr	Lys	Val	Lys	Thr	Gly	Phe	Gly	Thr	Gly
1				5					10					15	
Gly	Trp	Gln	Leu	Ala	Ala	Leu	Arg	Trp	Cys	Ala	Lys	Ala	Ala	Arg	Lys
			20					25					30		
Pro	Ile	Ile	Ala	Asp	Gly	Gly	Ile	Arg	Thr	His	Gly	Asp	Ile	Ala	Lys
	35					40					45				
Ser	Ile	Arg	Phe	Gly	Ala	Ser	Met	Ile	Met	Ile	Gly	Ser	Leu	Phe	Ala
	50					55					60				
Gly	His	Ile	Glu	Ser	Pro	Gly	Lys	Thr	Ile	Glu	Val	Asp	Gly	Glu	Gln
65					70					75					80
Phe	Lys	Glu	Tyr	Tyr	Gly	Ser	Ala	Ser	Gln	Tyr	Gln	Lys	Gly	Ala	Tyr
				85					90					95	
Lys	Asn	Val	Glu	Gly	Lys	Arg	Ile	Leu	Leu	Pro	Ala	Lys	Gly	His	Leu
			100					105					110		
Gln	Asp	Thr	Leu	Thr	Glu	Met	Glu	Gln	Asp	Leu	Gln	Ser	Ala	Ile	Ser
		115					120					125			
Tyr	Ala	Gly	Gly	Arg	Gln	Val	Ala	Asp	Leu	Lys	His	Val	Asp	Tyr	Val
	130					135					140				
Ile	Val	Lys	Asn	Ser	Ile	Trp	Asn	Gly	Asp	Ala	Ser	His			
145					150					155					

(2) INFORMATION FOR SEQ ID NO:5082:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 72 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...72

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5082:

Glu	Ser	Lys	Val	Trp	Tyr	Cys	Phe	Thr	Lys	Ala	Phe	Leu	Gly	Ser	Phe
1				5					10					15	
Lys	Met	Arg	Thr	Lys	Ser	Ser	Thr	Val	Asn	Cys	Ser	Arg	Ala	Ala	Lys
			20					25					30		
Thr	Gly	Lys	Arg	Pro	Ile	Asn	Ser	Gly	Ile	Ile	Pro	Asn	Phe	Glu	Leu
		35					40					45			
Leu	Ser	Tyr	Gln	Gly	Glu	Arg	Trp	Gly	Arg	Gly	Thr	Asn	Val	Gln	Gly
	50					55					60				
Val	Gln	Leu	Arg	Met	Gly	Ser	Ala								
65					70										

(2) INFORMATION FOR SEQ ID NO:5083:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 331 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...331

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5083:

Ala	Arg	Lys	Val	Gly	Gly	Thr	Met	Lys	Thr	Arg	Ile	Thr	Glu	Leu	Leu
1				5					10					15	
Lys	Ile	Asp	Tyr	Pro	Ile	Phe	Gln	Gly	Gly	Met	Ala	Trp	Val	Ala	Asp
			20					25					30		
Gly	Asp	Leu	Ala	Gly	Ala	Val	Ser	Lys	Ala	Gly	Gly	Leu	Gly	Ile	Ile
		35					40					45			
Gly	Gly	Gly	Asn	Ala	Pro	Lys	Glu	Val	Val	Lys	Ala	Asn	Ile	Asp	Lys
	50					55					60				
Ile	Lys	Ser	Leu	Thr	Asp	Lys	Pro	Phe	Gly	Val	Asn	Ile	Met	Leu	Leu

65		70		75		80									
Ser	Pro	Phe	Val	Glu	Asp	Ile	Val	Asp	Leu	Val	Ile	Glu	Glu	Gly	Val
			85					90						95	
Lys	Val	Val	Thr	Thr	Gly	Ala	Gly	Asn	Pro	Ser	Lys	Tyr	Met	Glu	Arg
			100					105					110		
Phe	His	Glu	Ala	Gly	Ile	Ile	Val	Ile	Pro	Val	Val	Pro	Ser	Val	Ala
		115					120					125			
Leu	Ala	Lys	Arg	Met	Glu	Lys	Ile	Gly	Ala	Asp	Ala	Val	Ile	Ala	Glu
	130					135				140					
Gly	Met	Glu	Ala	Gly	Gly	His	Ile	Gly	Lys	Leu	Thr	Thr	Met	Thr	Leu
145					150					155					160
Val	Arg	Gln	Val	Ala	Thr	Ala	Ile	Ser	Ile	Pro	Val	Ile	Ala	Ala	Gly
			165						170					175	
Gly	Ile	Ala	Asp	Gly	Glu	Gly	Ala	Ala	Ala	Gly	Phe	Met	Leu	Gly	Ala
		180					185					190			
Glu	Ala	Val	Gln	Val	Gly	Thr	Arg	Phe	Val	Val	Ala	Lys	Glu	Ser	Asn
		195				200					205				
Ala	His	Pro	Asn	Tyr	Lys	Glu	Lys	Ile	Leu	Lys	Ala	Arg	Asp	Ile	Asp
	210				215						220				
Thr	Thr	Ile	Ser	Ala	Gln	His	Phe	Gly	His	Ala	Val	Arg	Ala	Ile	Lys
225				230						235					240
Asn	Gln	Leu	Thr	Arg	Asp	Phe	Glu	Leu	Ala	Glu	Lys	Asp	Ala	Phe	Lys
			245						250					255	
Gln	Glu	Asp	Pro	Asp	Leu	Glu	Ile	Phe	Glu	Gln	Met	Gly	Ala	Gly	Ala
		260					265					270			
Leu	Ala	Lys	Ala	Val	Val	His	Gly	Asp	Val	Glu	Gly	Gly	Ser	Val	Met
		275				280					285				
Ala	Gly	Gln	Ile	Ala	Gly	Leu	Val	Ser	Lys	Glu	Glu	Thr	Ala	Glu	Glu
	290				295						300				
Ile	Leu	Lys	Asp	Leu	Tyr	Tyr	Gly	Ala	Ala	Lys	Lys	Ile	Gln	Glu	Glu
305				310						315					320
Ala	Ser	Arg	Trp	Thr	Gly	Val	Val	Arg	Asn	Asp					
			325					330							

(2) INFORMATION FOR SEQ ID NO:5084:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 107 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...107

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5084:

Arg	Leu	Glu	Val	Ala	Gly	Phe	Thr	Trp	Ser	Leu	Cys	Leu	Arg	Ile	Tyr
1				5				10						15	

```

Leu His Gly Pro Leu Ile Thr Thr Val Ser Gln Asp Phe Thr Ser Leu
      20                25                30
Ser Asp Ile Ser Ala Thr His Phe Glu Gln Leu His Ile Val Ala Ile
      35                40                45
Val His Arg Asn Ile Gln Arg Asn Asn Ser Phe Leu Ala Gly Asp Asn
      50                55                60
Arg Leu Arg Phe His Arg Met Thr Phe Leu Phe Tyr Gln Asn Asn Trp
      65                70                75                80
Leu Val Asp Phe Phe Arg Thr Ile Tyr Phe Tyr Leu Cys Cys Ile His
      85                90                95
Asn His Arg Ile Leu Ser Thr Lys Met Ser Phe
      100                105

```

(2) INFORMATION FOR SEQ ID NO:5085:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 106 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...106
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5085:

```

Tyr Arg Glu Val Asn Phe Met Ala Asn Leu Asn Arg Phe Lys Phe Thr
1      5      10      15
Phe Gly Lys Lys Ser Leu Thr Leu Thr Ser Glu His Asp Asn Leu Phe
      20      25      30
Met Glu Glu Ile Ala Lys Val Ala Thr Glu Lys Tyr Gln Ala Ile Lys
      35      40      45
Glu Gln Met Pro Ser Ala Asp Asp Glu Thr Ile Ala Leu Leu Leu Ala
      50      55      60
Val Asn Cys Leu Ser Thr Gln Leu Ser Arg Glu Ile Glu Phe Asp Asp
      65      70      75      80
Lys Glu Gln Glu Leu Glu Glu Leu Arg His Lys Leu Val Thr Cys Lys
      85      90      95
Gln Glu Gln Ser Lys Ile Glu Asp Ser Leu
      100      105

```

(2) INFORMATION FOR SEQ ID NO:5086:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 63 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5086:

```
Arg Ser Glu Val Gln Thr Ile Tyr Lys Pro Met Phe Trp Lys Thr Gln
1          5          10          15
Asp Arg His Gly Lys Ala Leu Val Gly Asn Arg Val Gly Gln Trp Arg
          20          25          30
Tyr Arg Ile Gly Asn Tyr Arg Val Ile Val Gln Ile Val Asp Asp Glu
          35          40          45
Leu Val Val Ala Thr Leu Glu Val Gly His Arg Arg Asp Ile Tyr
          50          55          60
```

(2) INFORMATION FOR SEQ ID NO:5087:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 188 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5087:

```
Thr Val Glu Val Phe Met Asn Val Trp Thr Lys Leu Ala Met Phe Ser
1          5          10          15
Phe Phe Glu Thr Asp Arg Leu Tyr Leu Arg Pro Phe Phe Phe Ser Asp
          20          25          30
Ser Gln Asp Phe Arg Glu Ile Ala Ser Asn Pro Glu Asn Leu Gln Phe
          35          40          45
Ile Phe Pro Thr Gln Ala Ser Leu Glu Glu Ser Gln Tyr Ala Leu Ala
          50          55          60
Asn Tyr Phe Met Lys Ser Pro Leu Gly Val Trp Ala Ile Cys Asp Gln
65          70          75          80
Lys Asn Gln Gln Met Ile Gly Ser Ile Lys Phe Glu Lys Leu Asp Glu
          85          90          95
Ile Lys Lys Glu Ala Glu Leu Gly Tyr Phe Leu Arg Lys Asp Ala Trp
          100          105          110
Ser Gln Gly Phe Met Thr Glu Val Val Arg Lys Ile Cys Gln Leu Ser
```


210 215 220
Ser Arg Ser Ile
225

(2) INFORMATION FOR SEQ ID NO:5089:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 304 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc feature

(B) LOCATION 1...304

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5089:

Leu	Leu	Glu	Val	Arg	Met	Lys	Lys	Leu	Pro	Leu	Val	Phe	Ser	Gly	Cys
1				5					10					15	
Leu	Leu	Gly	Leu	Ala	Gly	Ala	Gly	Asn	Leu	Ile	Leu	Asp	Thr	Leu	Pro
			20					25					30		
Val	Leu	Ser	His	Leu	Phe	Ser	Leu	Thr	Gly	Leu	Val	Leu	Trp	Ile	Tyr
		35					40					45			
Phe	Leu	Ile	Leu	His	Leu	Phe	Asn	Trp	Lys	Glu	Thr	Lys	Gln	Glu	Leu
	50					55					60				
Thr	Lys	Pro	Pro	Leu	Leu	Ser	Gly	Met	Ala	Thr	Phe	Pro	Met	Ala	Gly
65					70					75				80	
Met	Ile	Leu	Ser	Thr	Tyr	Val	Phe	Arg	Val	Phe	Ser	Tyr	Leu	Pro	Leu
				85				90					95		
Val	Ala	Gln	Gly	Ile	Trp	Trp	Phe	Ser	Phe	Leu	Leu	Asp	Leu	Thr	Leu
			100					105					110		
Ile	Ala	Gly	Phe	Thr	Ile	Lys	Phe	Ala	Cys	Pro	Gly	Arg	Met	Val	His
		115					120					125			
Ala	Thr	Pro	Ser	Trp	Thr	Val	Leu	Tyr	Val	Gly	Ile	Ala	Val	Ala	Ala
		130				135					140				
Leu	Thr	Tyr	Pro	Leu	Val	Gly	Ile	Ile	Glu	Ile	Ala	Tyr	Ala	Thr	Leu
145					150					155				160	
Ser	Phe	Gly	Phe	Leu	Leu	Thr	Phe	Tyr	Leu	Tyr	Pro	Leu	Ile	Tyr	Ser
				165				170					175		
Asp	Leu	Lys	Lys	His	Pro	Leu	Pro	Leu	Ala	Leu	Leu	Gly	Gln	Glu	Gly
			180					185					190		
Ile	Tyr	Cys	Ala	Pro	Phe	Ser	Leu	Leu	Leu	Ala	Ser	Leu	Val	Arg	Val
		195					200					205			
Gly	Gly	Thr	Ser	Leu	Pro	Thr	Trp	Gly	Leu	Ile	Val	Met	Ile	Leu	Ala
		210				215					220				
Ser	Gln	Ser	Phe	Phe	Phe	Phe	Val	Leu	Thr	Arg	Met	Pro	Asn	Ile	Leu
225					230					235				240	
Lys	Gln	Gly	Phe	Gln	Pro	Ala	Phe	Ser	Ala	Leu	Thr	Phe	Pro	Thr	Ile
				245					250					255	
Ile	Thr	Ala	Thr	Ser	Leu	Lys	Met	Ala	Gln	Gly	Ile	Leu	Lys	Leu	Pro

		260				265				270					
Phe	Leu	Asp	Tyr	Leu	Val	Leu	Ala	Glu	Thr	Ile	Ile	Cys	Leu	Thr	Ile
		275					280					285			
Leu	Phe	Phe	Val	Leu	Gly	Ala	Tyr	Leu	Ile	Trp	Leu	Arg	Lys	Lys	Val
	290					295					300				

(2) INFORMATION FOR SEQ ID NO:5090:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 213 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...213

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5090:

Leu	Glu	Glu	Val	Lys	Leu	Met	Leu	Asn	Lys	Ile	Arg	Asp	Tyr	Leu	Asp
1				5					10					15	
Phe	Ser	Gly	Leu	Gln	Tyr	Arg	Ser	Pro	Asp	Lys	Ala	Gly	Ala	Glu	Arg
		20					25				30				
Glu	Lys	Met	Leu	Ala	Phe	Arg	His	Lys	Gly	Gln	Glu	Ala	Arg	Lys	Ala
		35				40					45				
Phe	Thr	Glu	Leu	Ala	Lys	Ala	Phe	Gln	Ala	Ser	His	Pro	Glu	Trp	Gln
	50				55				60						
Leu	Gln	Gln	Thr	Ser	Gln	Trp	Met	Asn	Gln	Ala	Gln	Arg	Leu	Arg	Pro
65				70				75					80		
His	Phe	Trp	Val	Tyr	Leu	Gln	Arg	Asp	Gly	Gln	Val	Thr	Glu	Pro	Met
			85				90				95				
Met	Ala	Leu	Arg	Leu	Tyr	Gly	Thr	Ser	Thr	Asp	Phe	Gly	Ile	Ser	Leu
		100				105					110				
Glu	Val	Ser	Phe	Ile	Glu	Arg	Lys	Lys	Asp	Glu	Gln	Thr	Leu	Gly	Lys
	115					120					125				
Gln	Ala	Lys	Val	Leu	Asp	Ile	Pro	Thr	Val	Lys	Gly	Ile	Tyr	Tyr	Leu
	130				135				140						
Thr	Tyr	Ser	Asn	Gly	Gln	Ser	Gln	Arg	Trp	Glu	Ala	Asn	Glu	Glu	Lys
145			150					155						160	
Arg	Arg	Thr	Leu	Arg	Glu	Lys	Val	Arg	Ser	Gln	Glu	Val	Arg	Lys	Val
			165					170					175		
Leu	Val	Lys	Val	Asp	Val	Pro	Met	Thr	Glu	Asn	Ser	Ser	Glu	Glu	Glu
		180					185				190				
Ile	Val	Glu	Gly	Leu	Leu	Lys	Ser	Tyr	Ser	Lys	Ile	Leu	Pro	Tyr	Tyr
	195					200					205				
Leu	Ala	Thr	Arg	Lys											
	210														

(2) INFORMATION FOR SEQ ID NO:5091:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 186 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...186
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5091:

```

Lys Leu Trp Val Glu Ala Ser Xaa Arg Val Leu Lys Gly Ile Asp Leu
1      5      10      15
Gly Leu Gly Glu Leu Arg Pro Asp Val Ile Val Met Asp Ile Val Met
      20      25      30
Pro Glu Met Asn Gly Ile Asp Ala Thr Leu Ala Ile Leu Lys Glu Trp
      35      40      45
Pro Glu Ala Lys Ile Leu Ile Val Thr Ser Tyr Leu Asp Asn Glu Lys
      50      55      60
Ile Met Pro Val Leu Asp Ala Gly Ala Lys Gly Tyr Met Leu Lys Thr
65      70      75      80
Ser Ser Ala Asp Glu Leu Leu His Ala Val Ser Lys Val Ala Ala Gly
      85      90      95
Glu Leu Ala Ile Glu Gln Glu Val Ser Lys Lys Val Glu Tyr His Arg
      100     105     110
Asn His Met Glu Leu His Glu Glu Leu Thr Ala Arg Glu Arg Asp Val
      115     120     125
Leu Gln Leu Ile Ala Lys Gly Tyr Glu Asn Gln Arg Ile Ala Asp Asp
      130     135     140
Leu Phe Ile Ser Leu Lys Thr Val Lys Thr His Val Ser Asn Ile Leu
145     150     155     160
Ala Lys Leu Glu Val Ser Asp Arg Thr Gln Ala Ala Val Tyr Ala Phe
      165     170     175
Gln His His Leu Val Gly Gln Glu Glu Phe
      180     185

```

(2) INFORMATION FOR SEQ ID NO:5092:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...64

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5092:

Ala	Ser	Trp	Val	Thr	Ile	Met	Thr	Val	Phe	Pro	Ser	Arg	Phe	Ile	Ser
1			5					10					15		
Lys	Arg	Asn	Phe	Lys	Thr	Lys	Ser	Leu	Phe	Ser	Gly	Ser	Ser	Glu	Pro
		20					25				30				
Val	Gly	Ser	Ser	Ala	Lys	Ile	Ser	Trp	Leu	Gly	Phe	Lys	Met	Ala	Leu
	35				40					45					
Ala	Thr	Ala	Ile	Arg	Cys	Cys	Ser	Pro	Pro	Asp	Asn	Ser	Glu	Thr	Leu
	50				55					60					

(2) INFORMATION FOR SEQ ID NO:5093:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 95 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5093:

Gly	Leu	Gly	Val	Lys	Lys	Gln	Lys	Ala	Cys	Phe	Ser	Ala	Ile	Glu	Glu
1			5				10					15			
Val	Ile	Met	Tyr	Lys	His	Leu	Phe	Phe	Leu	Asp	Ser	Lys	Thr	Leu	Asp
		20					25				30				
Arg	Leu	Thr	Pro	Tyr	Ile	Leu	Val	Leu	Ala	Ser	Asp	Thr	Ile	Ala	Phe
	35				40					45					
Asn	Val	Phe	Val	Leu	Thr	Phe	Val	Ser	Ala	Val	Val	Phe	Asn	Phe	Leu
	50				55					60					
Asn	Ser	Met	Leu	Ala	Leu	Met	Ala	Ile	Phe	Ile	Gly	Ala	Gly	Tyr	Val
65				70					75					80	
Val	Gly	Phe	Trp	Leu	Leu	Ile	Leu	Asn	Glu	Asn	Gln	Arg	Ala	Asn	
			85				90							95	

(2) INFORMATION FOR SEQ ID NO:5094:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 134 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...134

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5094:

```
Arg Phe Ser Leu Ala His Glu Leu Tyr His Leu Tyr Tyr Asp Glu Val
1      5      10      15
Lys Lys Ser Ser Val Ser Leu Ile Leu Ile Gly Glu Gly Asp Glu Thr
      20      25      30
Glu Arg Lys Ala Asp Gln Phe Ala Ser Tyr Phe Leu Ile Phe Pro Ser
      35      40      45
Ser Leu Tyr Arg Met Val Glu Glu Ile Arg Glu Asn Ala Asn Arg Thr
      50      55      60
His Leu Glu Val Glu Asp Ile Ile Lys Leu Gly Gln Phe Tyr Gly Ile
65      70      75      80
Ser His Lys Ala Met Leu Tyr Arg Leu Arg Asn Asp Gly Tyr Leu Asp
      85      90      95
Ala Glu Glu Ile Lys Asn Met Asp Ile Ser Val Ile Glu Thr Ala Ser
      100     105     110
Arg Leu Gly Tyr Asp Thr Ser Leu Tyr Arg Pro Leu Ser Glu Ser Lys
      115     120     125
Lys Glu Met Ala Leu Gly
130
```

(2) INFORMATION FOR SEQ ID NO:5095:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 222 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...222

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5095:

```
Gln Pro Leu Leu Val Gln Met Val Leu Glu Asn Arg Leu Phe Leu Ser
1      5      10      15
Ile Met Ser Arg Leu Thr Lys Lys Asp Gln Gly Val Leu Ser Ile Lys
      20      25      30
Gly Arg Glu Ile Glu Ser Trp Asn Ser Gln Glu Leu Ala Gln Glu Leu
      35      40      45
Thr Ile Leu Lys Gln Lys Ile Asn Tyr Gln Ala Lys Leu Thr Val Glu
```

50		55		60											
Glu	Leu	Val	Ser	Phe	Gly	Arg	Phe	Pro	Tyr	Ser	Arg	Gly	Arg	Leu	Arg
65					70					75				80	
Ser	Glu	Asp	Trp	Glu	Lys	Ile	Arg	Glu	Thr	Leu	Asn	Tyr	Leu	Glu	Leu
				85					90					95	
Thr	Asn	Leu	Lys	Asp	Arg	Tyr	Ile	Asn	Ser	Leu	Ser	Gly	Gly	Gln	Leu
			100					105					110		
Gln	Arg	Val	Phe	Ile	Ala	Met	Val	Leu	Ala	Gln	Asp	Thr	Asp	Phe	Ile
		115					120					125			
Leu	Leu	Asp	Glu	Pro	Leu	Asn	Asn	Leu	Asp	Ile	Lys	Gln	Ser	Val	Ser
	130					135					140				
Met	Met	Gln	Ile	Leu	Arg	Arg	Leu	Val	Glu	Glu	Leu	Gly	Lys	Thr	Ile
145					150					155					160
Ile	Ile	Val	Leu	His	Asp	Ile	Asn	Met	Ala	Ser	Gln	Tyr	Ala	Asp	Glu
				165					170					175	
Ile	Val	Ala	Phe	Lys	Asp	Gly	Gln	Val	Phe	Ser	Lys	Gly	Ser	Thr	Asp
		180						185					190		
Gln	Ile	Met	Gln	Ala	Asp	Leu	Leu	Ser	Gln	Leu	Tyr	Glu	Ile	Pro	Ile
		195					200					205			
Thr	Leu	Ala	Asp	Ile	Asn	Asp	Lys	Lys	Ile	Cys	Ile	Tyr	Ser		
	210					215					220				

(2) INFORMATION FOR SEQ ID NO:5096:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 617 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...617

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5096:

Ser	Asp	Leu	Phe	Arg	Lys	Cys	Val	Asn	Met	Glu	Phe	Ser	Lys	Lys	Thr
1			5						10					15	
Arg	Glu	Leu	Ser	Ile	Lys	Lys	Met	Gln	Glu	Arg	Thr	Leu	Asp	Leu	Leu
		20						25					30		
Ile	Ile	Gly	Gly	Gly	Ile	Thr	Gly	Ala	Gly	Val	Ala	Leu	Gln	Ala	Ala
		35				40						45			
Ala	Ser	Gly	Leu	Glu	Thr	Gly	Leu	Ile	Glu	Met	Gln	Asp	Phe	Ala	Glu
	50					55				60					
Gly	Thr	Ser	Ser	Arg	Ser	Thr	Lys	Leu	Val	His	Gly	Gly	Leu	Arg	Tyr
65				70					75					80	
Leu	Lys	Gln	Phe	Asp	Val	Glu	Val	Val	Ser	Asp	Thr	Val	Ser	Glu	Arg
			85					90					95		
Ala	Val	Val	Gln	Gln	Ile	Ala	Pro	His	Ile	Pro	Lys	Pro	Asp	Pro	Met
		100					105					110			
Leu	Leu	Pro	Val	Tyr	Asp	Glu	Asp	Gly	Ala	Thr	Phe	Ser	Pro	Phe	Arg

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Ile	Val	Glu	Pro	Val	Leu	Asp	Glu	Met	Gly	Arg	Phe	Tyr	Asp	Trp	Thr
			580					585					590		
Glu	Glu	Glu	Lys	Ala	Thr	Tyr	Arg	Ala	Asp	Val	Glu	Ala	Ala	Leu	Ala
		595					600					605			
Asn	Asn	Asp	Leu	Ala	Glu	Leu	Lys	Asn							
	610					615									

(2) INFORMATION FOR SEQ ID NO:5097:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 293 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5097:

Glu	Gly	Leu	Leu	Ser	Leu	Met	Asn	Thr	Leu	Ala	Glu	Lys	Phe	Arg	Leu
1				5					10					15	
Lys	Arg	Lys	Glu	Leu	Arg	Leu	Ser	Gln	Gln	Thr	Leu	Ala	Glu	Gly	Ile
		20					25					30			
Cys	Glu	Gln	Ser	Gln	Ile	Ser	Lys	Ile	Glu	Arg	Gly	His	Phe	Ile	Pro
	35					40					45				
Ser	Ala	Asp	Leu	Leu	Phe	Lys	Leu	Ser	Gln	Arg	Leu	Glu	Val	Pro	Leu
	50					55					60				
Asp	Tyr	Phe	Phe	Asn	Glu	Gln	Ile	Glu	Ile	Lys	Ser	Asn	Leu	Ser	Asn
65				70				75						80	
Phe	Lys	Gln	Leu	Ser	Ala	Arg	Leu	Leu	Asp	Asp	Arg	Asn	Tyr	Asp	Asp
		85					90						95		
Leu	Glu	Tyr	Ile	Tyr	Arg	Ile	Glu	Ile	Glu	Arg	Ser	Thr	Phe	Leu	Thr
	100						105						110		
Leu	Glu	Asp	Arg	Thr	Tyr	Leu	Glu	Trp	Ile	Lys	Ala	Ile	Ile	Asp	Phe
	115					120					125				
Tyr	Gln	Tyr	Asp	Ser	Lys	Cys	Glu	Ala	Ile	Ser	Ser	Leu	Glu	Asn	Ile
	130				135						140				
Leu	Leu	Lys	Val	Ser	Ser	Asn	Thr	Leu	Ile	Tyr	Leu	Lys	Ala	Leu	Asn
145				150						155					160
Thr	Leu	Ser	Asn	Phe	Tyr	Ser	Leu	Val	Gly	Arg	Glu	Gln	Glu	Tyr	Glu
			165						170					175	
Ala	Asn	Tyr	Ser	His	Leu	Ile	Glu	Leu	Tyr	Gln	Thr	Lys	Asn	Leu	Asp
	180						185						190		
His	Gln	Glu	Phe	Leu	Phe	Gly	Tyr	Ile	Arg	Val	Arg	Tyr	Asn	Tyr	Ala
	195					200					205				
His	Tyr	Leu	Val	Ser	Lys	Glu	Lys	Tyr	Asn	Glu	Ala	Ile	Gln	Glu	Ala
	210					215					220				
Leu	Glu	Thr	Ile	Glu	Leu	Cys	Lys	Gln	Arg	Gln	Thr	Ser	Tyr	Gln	Leu
225					230					235					240

Ala	Pro	Leu	Leu	Ile	Leu	Val	Gly	Asn	Ala	Gly	Ala	Lys	Phe	Leu	Asp
				245					250					255	
Arg	Glu	Gln	Val	Lys	Asn	Tyr	Tyr	Ile	Glu	Ala	Arg	Glu	Leu	Cys	Lys
			260					265					270		
Ile	Tyr	Asn	Asn	Pro	Leu	Met	Leu	Met	Lys	Ile	Glu	Asn	Tyr	Leu	Lys
		275					280					285			
Glu	Leu	Asp	Thr	Val											
		290													

(2) INFORMATION FOR SEQ ID NO:5098:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 64 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...64
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5098:

Pro	Ile	Leu	Leu	Glu	Gly	Val	Ser	Gly	Glu	Thr	Arg	Trp	His	Trp	His
1				5					10				15		
Phe	Pro	Arg	Thr	Lys	Arg	Asn	Pro	Gly	Gly	Val	Gln	Thr	Ile	Leu	Gly
			20					25				30			
Val	Ser	Lys	Lys	Phe	Leu	Val	Asn	Leu	Phe	Ile	Gly	Leu	Asn	Thr	Leu
		35				40					45				
Leu	Phe	Leu	Ile	Gln	Ile	Phe	Tyr	His	Gln	Met	Lys	Ser	Lys	Ile	Lys
		50				55				60					

(2) INFORMATION FOR SEQ ID NO:5099:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 503 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...503
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5099:

Pro	Gln	Leu	Phe	Thr	Pro	Asn	Leu	Lys	Thr	Ile	Gln	Asn	Pro	Cys	Leu
1				5					10					15	
Ser	Leu	Asp	Pro	Gly	Trp	Phe	Leu	Phe	Ser	Pro	Asn	Gly	Cys	Phe	Leu
			20					25					30		
Leu	Asp	Lys	Lys	Glu	Phe	Pro	Leu	Tyr	Gly	Ile	Ser	Val	Glu	Lys	Asn
		35					40					45			
Thr	Lys	Arg	Lys	Glu	Thr	His	Met	Asn	Ser	Leu	Pro	Asn	His	His	Phe
	50					55					60				
Gln	Asn	Lys	Ser	Phe	Tyr	Gln	Leu	Ser	Phe	Asp	Gly	Gly	His	Leu	Thr
65					70					75					80
Gln	Tyr	Gly	Gly	Leu	Ile	Phe	Phe	Gln	Glu	Leu	Phe	Ser	Gln	Leu	Lys
				85					90					95	
Leu	Lys	Glu	Arg	Ile	Ser	Lys	Tyr	Leu	Val	Thr	Asn	Asp	Gln	Arg	Arg
			100					105					110		
Tyr	Cys	Arg	Tyr	Ser	Asp	Ser	Asp	Ile	Leu	Val	Gln	Phe	Leu	Phe	Gln
		115					120					125			
Leu	Leu	Thr	Gly	Tyr	Gly	Thr	Asp	Tyr	Ala	Cys	Lys	Glu	Leu	Ser	Ala
	130					135					140				
Asp	Ala	Tyr	Phe	Pro	Lys	Leu	Leu	Glu	Gly	Gly	Gln	Leu	Ala	Ser	Gln
145					150					155					160
Pro	Thr	Leu	Ser	Arg	Phe	Leu	Ser	Arg	Thr	Asp	Glu	Glu	Thr	Val	His
				165					170					175	
Ser	Leu	Arg	Cys	Leu	Asn	Leu	Glu	Leu	Val	Glu	Phe	Phe	Leu	Gln	Phe
			180					185					190		
His	Gln	Leu	Asn	Gln	Leu	Ile	Val	Asp	Ile	Asp	Ser	Thr	His	Phe	Thr
		195					200					205			
Thr	Tyr	Gly	Lys	Gln	Glu	Gly	Val	Ala	Tyr	Asn	Ala	His	Tyr	Arg	Ala
	210					215					220				
His	Gly	Tyr	His	Pro	Leu	Tyr	Ala	Phe	Glu	Gly	Lys	Thr	Gly	Tyr	Cys
225					230					235					240
Phe	Asn	Ala	Gln	Leu	Arg	Pro	Gly	Asn	Arg	Tyr	Cys	Ser	Glu	Glu	Ala
				245					250					255	
Asp	Ser	Phe	Ile	Thr	Pro	Val	Leu	Glu	Arg	Phe	Asn	Gln	Leu	Leu	Phe
			260					265					270		
Arg	Met	Asp	Ser	Gly	Phe	Ala	Thr	Pro	Lys	Leu	Tyr	Asp	Leu	Ile	Glu
		275					280					285			
Lys	Thr	Gly	Gln	Tyr	Tyr	Leu	Ile	Lys	Leu	Lys	Lys	Asn	Thr	Val	Leu
	290					295						300			
Ser	Arg	Leu	Gly	Asp	Leu	Ser	Leu	Pro	Cys	Pro	Gln	Asp	Glu	Asp	Leu
305					310					315					320
Thr	Ile	Leu	Pro	His	Ser	Ala	Tyr	Ser	Glu	Thr	Leu	Tyr	Gln	Ala	Gly
				325					330					335	
Ser	Trp	Ser	His	Lys	Arg	Arg	Val	Cys	Gln	Phe	Ser	Glu	Arg	Lys	Glu
			340					345					350		
Gly	Asn	Leu	Phe	Tyr	Asp	Val	Ile	Ser	Leu	Val	Thr	Asn	Met	Thr	Ser
	355						360					365			
Gly	Thr	Ser	Gln	Asp	Gln	Phe	Gln	Leu	Tyr	Arg	Gly	Arg	Gly	Gln	Ala
	370					375					380				
Glu	Asn	Phe	Ile	Lys	Glu	Met	Lys	Glu	Gly	Phe	Phe	Gly	Asp	Lys	Thr
385					390					395					400
Asp	Ser	Ser	Thr	Leu	Ile	Lys	Asn	Glu	Val	Arg	Met	Met	Met	Ser	Cys
				405					410					415	
Ile	Ala	Tyr	Asn	Leu	Tyr	Leu	Phe	Phe	Lys	His	Leu	Ala	Gly	Gly	Asp
			420					425					430		
Phe	Gln	Thr	Leu	Thr	Ile	Lys	Arg	Phe	Arg	His	Leu	Phe	Leu	His	Val

(2) INFORMATION FOR SEQ ID NO:5100:

(A) LENGTH: 287 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Streptococcus pneumoniae*

(A) NAME/KEY: misc_feature
(B) LOCATION 1...287

3964

210	215	220
Tyr Ser Thr Trp Gln Gly Asn Tyr Tyr Leu Lys Ser Asp Gly Lys Met		
225	230	235
Ala Val Asn Glu Trp Val Asp Gly Gly Arg Tyr Tyr Val Gly Ala Asp		240
	245	250
Gly Val Trp Lys Glu Gly Gln Ala Ser Thr Val Ser Ser Ser Asn Asp		255
	260	265
Ser Asn Ser Glu Tyr Phe Cys Cys Phe Arg Lys Gly Lys Lys Leu		270
	275	280
		285

(2) INFORMATION FOR SEQ ID NO:5101:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 100 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...100

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5101:

Leu	Glu	Leu	Phe	Gly	Gly	Ile	Ile	Asn	Met	Ala	Asn	Lys	Gln	Asp	Leu
1				5				10						15	
Ile	Ala	Lys	Val	Ala	Glu	Ala	Thr	Glu	Leu	Thr	Lys	Lys	Asp	Ser	Ala
			20					25					30		
Ala	Ala	Val	Glu	Ala	Val	Phe	Ala	Ala	Val	Ala	Asp	Tyr	Leu	Ala	Ala
			35				40					45			
Gly	Glu	Lys	Val	Gln	Leu	Ile	Gly	Phe	Ser	Asn	Phe	Glu	Val	Arg	Glu
			50			55					60				
Arg	Ala	Glu	Arg	Lys	Gly	Arg	Asn	Pro	Gln	Thr	Gly	Lys	Glu	Met	Thr
65				70					75					80	
Ile	Ala	Ala	Ser	Lys	Val	Pro	Ala	Phe	Lys	Ala	Gly	Lys	Ala	Leu	Lys
				85				90						95	
Asp	Ala	Val	Lys												
			100												

(2) INFORMATION FOR SEQ ID NO:5102:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 95 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...95

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5102:

Cys	Pro	Phe	Leu	Phe	Gln	Tyr	Thr	Met	Ala	Pro	Met	Thr	Tyr	Lys	Asp
1				5					10					15	
Thr	Met	Thr	Ser	Asp	Phe	Phe	Glu	Ala	Cys	Phe	Gln	Lys	Phe	Leu	Leu
			20					25					30		
Pro	Thr	Leu	Asp	Thr	Pro	Ser	Leu	Ile	Ile	Met	Asp	Asn	Ala	Arg	Phe
			35				40					45			
His	Arg	Met	Asn	Met	Cys	Lys	Glu	Gln	Gly	Ile	Asp	Cys	Tyr	His	Phe
			50			55					60				
Leu	Pro	Ile	His	Leu	Ser	Ile	Ile	Pro	Leu	Arg	Lys	Tyr	Gly	Leu	Thr
65					70				75					80	
Ser	Lys	Thr	Ser	Gln	Asn	Asn	Ile	Val	Lys	Leu	Arg	Cys	Phe	Ser	
				85				90						95	

(2) INFORMATION FOR SEQ ID NO:5103:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 293 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...293

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5103:

Lys	Arg	Leu	Leu	His	Met	Ser	Arg	Gln	Thr	Pro	Ser	Leu	Ser	Phe	Glu
1				5					10					15	
Val	Phe	Pro	Pro	Asn	Pro	Ala	Val	Gly	Asn	Gly	Asn	Ile	Ile	Ser	Ala
			20					25					30		
Leu	Gln	Asp	Met	Gln	Glu	Leu	Ala	Pro	His	Phe	Ile	Ser	Val	Thr	Ala
			35				40					45			
Ser	Asn	Asn	Lys	Phe	Asn	Ile	Lys	Glu	Thr	Thr	Val	Arg	Leu	Ala	Asp
			50			55					60				
Phe	Ile	Gln	Asn	Asp	Leu	Ala	Ile	Pro	Thr	Ile	Ala	His	Leu	Pro	Ala
65					70				75					80	
Ile	Tyr	Leu	Thr	Lys	Asp	Lys	Val	Ala	Glu	Thr	Ile	Ala	Asp	Leu	Asp
				85				90					95		
Lys	Val	Gly	Val	Gln	Lys	Ile	Leu	Ala	Leu	Arg	Gly	Asp	Ile	Ile	Pro
			100				105					110			
Asp	Val	Glu	Pro	Gln	Lys	Asp	Phe	Arg	Tyr	Ala	Thr	Asp	Leu	Ile	Glu

(2) INFORMATION FOR SEO ID NO:5104:

(A) LENGTH: 194 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Streptococcus pneumoniae*

(A) NAME/KEY: misc_feature
(B) LOCATION 1...194

3967

		100					105				110				
Ile	Leu	Thr	Val	Ile	Ala	Pro	Gly	Ile	Gln	Gly	Glu	Lys	Thr	Val	Glu
		115					120					125			
Gln	Phe	Pro	Gln	Trp	Phe	Gln	Glu	Gln	Gly	Tyr	Lys	Asp	Ile	Pro	Val
		130					135					140			
Leu	Tyr	Asp	Thr	Lys	Ala	Thr	Thr	Phe	Gln	Ala	Tyr	Gln	Ile	Arg	Ser
145					150					155					160
Ile	Pro	Thr	Glu	Tyr	Leu	Ile	Asp	Ser	Gln	Gly	Lys	Ile	Gly	Lys	Ile
				165					170					175	
Gln	Phe	Gly	Ala	Ile	Ser	Asn	Ala	Asp	Ala	Glu	Ala	Ala	Phe	Lys	Glu
			180					185						190	
Met	Asn														

(2) INFORMATION FOR SEQ ID NO:5105:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 452 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...452

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5105:

Gly	Gly	Leu	Phe	Met	Asp	Gln	Gln	Asn	Gly	Leu	Phe	Gly	Phe	Leu	Glu
1				5				10						15	
Asn	His	Val	Met	Gly	Pro	Met	Gly	Lys	Leu	Ala	Gln	Phe	Lys	Val	Val
		20						25					30		
Arg	Ala	Ile	Thr	Ala	Ala	Gly	Met	Ala	Ala	Val	Pro	Phe	Thr	Ile	Val
		35					40					45			
Gly	Ser	Met	Phe	Leu	Val	Phe	Ser	Ile	Leu	Pro	Gln	Ala	Phe	Ser	Phe
	50					55					60				
Trp	Pro	Ile	Val	Ala	Asp	Ile	Phe	Ser	Ala	Ser	Phe	Asp	Lys	Phe	Arg
65					70					75					80
Ser	Leu	Tyr	Met	Val	Ala	Asn	Tyr	Ala	Thr	Met	Gly	Ser	Leu	Ser	Leu
				85					90					95	
Tyr	Phe	Val	Leu	Ser	Leu	Ala	Tyr	Glu	Leu	Thr	Lys	Ile	Tyr	Ala	Glu
			100					105					110		
Glu	Glu	Glu	Leu	Asn	Met	Asn	Pro	Leu	Asn	Gly	Ala	Leu	Leu	Ala	Leu
		115					120					125			
Met	Ala	Phe	Val	Met	Thr	Val	Pro	Gln	Ile	Ile	Phe	Asp	Gly	Gly	Met
	130					135					140				
Met	Lys	Thr	Val	Thr	Ser	Leu	Lys	Glu	Gly	Ala	Val	Ile	Ala	Asp	Gly
145					150					155					160
Trp	Ala	Met	Gly	Asn	Gly	Val	Ala	Arg	Phe	Gly	Thr	Thr	Gly	Ile	Phe
				165					170					175	

Ile	Arg	Leu	Phe	Phe	Gly	Ile	Ile	Lys	Val	Met	Glu	Ile	Glu	Lys	Thr
1			5					10						15	
Asn	Arg	Met	Asn	Ala	Leu	Phe	Glu	Phe	Tyr	Ala	Ala	Leu	Leu	Thr	Asp
		20					25						30		
Lys	Gln	Met	Asn	Tyr	Ile	Glu	Leu	Tyr	Tyr	Ala	Asp	Asp	Tyr	Ser	Leu
	35					40						45			
Ala	Glu	Ile	Ala	Glu	Glu	Phe	Gly	Val	Ser	Arg	Gln	Ala	Val	Tyr	Asp
	50				55						60				
Asn	Ile	Lys	Arg	Thr	Glu	Lys	Ile	Leu	Glu	Asp	Tyr	Glu	Met	Lys	Leu
65				70					75						80
His	Met	Tyr	Ser	Asp	Tyr	Ile	Val	Arg	Ser	Gln	Ile	Phe	Asp	Gln	Ile
			85					90						95	
Leu	Glu	Arg	Tyr	Pro	Lys	Asp	Asp	Phe	Leu	Gln	Glu	Gln	Ile	Glu	Ile
		100					105						110		
Leu	Thr	Ser	Ile	Asp	Asn	Arg	Glu								
		115				120									

(2) INFORMATION FOR SEQ ID NO:5107:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 169 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...169

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5107:

Arg	Arg	Leu	Phe	Ala	His	Trp	Asp	Leu	Ser	Thr	Trp	Lys	Leu	Leu	Thr
1			5					10						15	
Ser	Thr	Lys	Lys	Phe	Thr	Thr	Gly	Leu	Asp	Phe	Leu	Asn	Ser	Gln	Arg
		20					25						30		
Asp	Asp	Ile	Leu	Ser	Ala	Lys	Asn	Leu	Leu	Leu	Glu	Thr	Ile	Thr	Glu
	35					40						45			
Met	Asn	Asp	Glu	Val	Lys	Glu	Arg	Phe	Lys	Ser	Thr	Phe	Glu	Ala	Ile
	50				55						60				
Arg	Glu	Ser	Phe	Lys	Val	Thr	Phe	Lys	Gln	Met	Phe	Gly	Gly	Gly	Gln
65				70					75						80
Ala	Asp	Leu	Ile	Leu	Thr	Glu	Gly	Asp	Leu	Leu	Thr	Ala	Gly	Val	Glu
			85					90						95	
Ile	Ser	Val	His	Leu	Arg	Asp	Lys	Lys	Ile	Gln	Ser	Leu	Asn	Leu	Met
		100					105						110		
Ser	Gly	Gly	Glu	Lys	Ala	Leu	Arg	Leu	Leu	Pro	Cys	Phe	Ser	Pro	Leu
	115					120						125			
Phe	Val	Ser	Arg	Pro	Phe	Leu	Leu	Ser	Ser	Trp	Met	Arg	Trp	Lys	Leu
	130				135					140					
Arg	Trp	Met	Lys	Pro	Met	Leu	Asn	Val	Leu	Gly	Ile	Thr	Ser	Thr	Ala
145					150				155						160

Leu Thr Arg Thr Ala Ser Leu Ser Ser
165

(2) INFORMATION FOR SEQ ID NO:5108:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5108:

Met	Val	Ile	Phe	Leu	Leu	Lys	Met	Lys	His	Phe	Phe	Ala	Gly	Ile	Gly
1				5					10					15	
Glu	Ile	Asn	Phe	Val	Ser	Tyr	Leu	Leu	Tyr	Ile	Cys	Val	Gly	Ile	Ala
			20					25					30		
Pro	Phe	Phe	His	Val	Tyr	Ile	Ile	Gly	Ser	Glu	Met	Asn	Phe	Val	Lys
		35					40					45			
Ile	Val	Leu	Ser	Ile	Leu	Gly	Ile	Ile	Phe	Val	Cys	Ile	Leu	Thr	Ile
	50					55					60				
Ala	Arg	Ile	Tyr	Arg	Thr	Phe	Phe	Tyr	Lys	Glu					
65					70					75					

(2) INFORMATION FOR SEQ ID NO:5109:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 235 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...235

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5109:

Tyr	Tyr	Ile	Leu	Lys	Gly	Gly	Asp	Asn	Met	Val	Glu	Gln	Arg	Lys	Ser
1				5					10					15	
Ile	Thr	Met	Lys	Asp	Val	Ala	Leu	Glu	Ala	Gly	Val	Ser	Val	Gly	Thr

			20					25				30				
Val	Ser	Arg	Val	Ile	Asn	Lys	Glu	Lys	Gly	Ile	Lys	Glu	Val	Thr	Leu	
		35					40					45				
Lys	Lys	Val	Glu	Gln	Ala	Ile	Lys	Thr	Leu	Asn	Tyr	Ile	Pro	Asp	Tyr	
	50					55					60					
Tyr	Ala	Arg	Gly	Met	Lys	Lys	Asn	Arg	Thr	Glu	Thr	Ile	Ala	Ile	Ile	
65					70					75					80	
Val	Pro	Ser	Ile	Trp	His	Pro	Phe	Phe	Ser	Glu	Phe	Ala	Met	His	Val	
			85						90					95		
Glu	Asn	Glu	Val	Tyr	Lys	Arg	Asn	Asn	Lys	Leu	Leu	Leu	Cys	Ser	Ile	
			100					105					110			
Asn	Gly	Thr	Asn	Arg	Glu	Gln	Asp	Tyr	Leu	Glu	Met	Leu	Arg	His	Asn	
		115					120						125			
Lys	Val	Asp	Gly	Val	Val	Ala	Ile	Thr	Tyr	Ser	Pro	Ile	Glu	His	Tyr	
	130					135					140					
Leu	Thr	Ser	Gly	Ile	Pro	Phe	Val	Ser	Ile	Asp	Arg	Thr	Tyr	Ser	Asp	
145					150					155					160	
Ile	Ala	Ile	Pro	Cys	Val	Ser	Ser	Asp	Asn	Asp	Ala	Gly	Trp	Arg	Glu	
			165					170						175		
Ala	Ala	Lys	Gln	Leu	Ile	Ser	Lys	Gly	Cys	Gln	His	Leu	Ala	Phe	Val	
		180						185					190			
Gly	Gly	His	Asn	Thr	Thr	Ile	Asn	Glu	Thr	Lys	Arg	Arg	Arg	Ile	His	
		195					200					205				
Leu	Lys	Ser	Met	Ser	Lys	Ser	Ile	Lys	Tyr	Phe	Leu	Val	Phe	Leu	Ile	
	210					215					220					
Trp	Met	Arg	Gln	Leu	Leu	Thr	Ile	Met	Glu	Ser						
225					230					235						

(2) INFORMATION FOR SEQ ID NO:5110:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 69 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...69

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5110:

Pro	Val	Ser	Leu	Glu	Pro	Leu	Ser	Val	Ile	Leu	Asn	Thr	Val	Glu	Lys	
1			5					10					15			
Ser	Glu	Lys	Val	Trp	Arg	Gln	Ile	Ala	Leu	Asn	Ala	Leu	Thr	Gly	Ser	
		20					25					30				
Leu	Ser	Asp	Gly	Phe	Phe	Gly	Met	Asp	Val	Ala	Lys	Leu	Lys	Lys	Lys	
		35				40					45					
Ile	Thr	Lys	Asn	Phe	Ala	Lys	Asn	Ile	His	Ile	Lys	Ser	Leu	Phe	Phe	
	50					55					60					
Glu	Ile	Arg	Glu	Ser												

(2) INFORMATION FOR SEQ ID NO:5111:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 151 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...151

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5111:

Lys	Glu	Ile	Phe	Ile	Thr	Glu	Lys	Lys	Gly	Lys	Ser	Ser	Gln	Val	Pro
1				5					10					15	
Thr	Gly	Ser	Ser	Ile	Pro	Lys	Arg	Tyr	Leu	Leu	Asp	Gly	Lys	Thr	Pro
			20					25					30		
Arg	Ile	Ser	Ala	Thr	Asn	Ile	Asp	Asn	Gly	Ile	Leu	Gly	Tyr	Tyr	Glu
		35					40					45			
Asp	Ile	Asp	Asp	Lys	Asn	Tyr	Arg	Val	Phe	Glu	Asn	Phe	Ile	Ser	Val
	50					55					60				
Ser	Cys	Leu	Gly	Ala	Val	Phe	Tyr	His	Lys	Tyr	Lys	Ala	Ser	Leu	Asp
65					70					75				80	
Met	Lys	Ile	His	Cys	Leu	Lys	Leu	Lys	Asn	Lys	Glu	Leu	Asn	Lys	Glu
				85					90					95	
Val	Ala	Phe	Tyr	Leu	Thr	Ser	Ile	Ile	Arg	Gln	Ala	Leu	Lys	Asn	Thr
			100					105					110		
Glu	Tyr	Lys	Asp	Gln	Ile	Ser	Ser	Thr	Val	Leu	Pro	Asp	Ile	Lys	Ile
		115					120					125			
Lys	Leu	Pro	Ile	Asp	Ser	Arg	Gly	Thr	Pro	Asp	Trp	Asn	Tyr	Met	Glu
	130					135					140				
Arg	Tyr	Arg	Glu	Arg	Glu	Arg									
145					150										

(2) INFORMATION FOR SEQ ID NO:5112:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 110 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...110

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5112:

Asn	Arg	Ile	Phe	Asp	Asn	Asn	Cys	Leu	Ile	Gln	Val	Tyr	Lys	Phe	Ile
1			5						10					15	
Ser	Phe	Tyr	Asp	Ile	Cys	Glu	Met	Val	Phe	Ala	Phe	His	Leu	Pro	Pro
			20					25					30		
Asp	Glu	Leu	Ile	Thr	Asn	Val	Ile	Phe	Lys	Glu	Lys	Ile	Asn	Ser	Met
			35				40					45			
Leu	Lys	Cys	Tyr	Ile	Asp	Arg	Leu	Leu	Tyr	Val	Phe	Ile	Asn	Pro	Thr
	50					55					60				
His	Phe	Thr	Glu	Lys	Val	Asn	Leu	Gln	Phe	Tyr	Gly	Ser	Phe	Phe	Ser
65					70				75						80
Tyr	Glu	Phe	Ile	Cys	Arg	Glu	Val	Gly	Asn	Ile	Leu	Lys	Asn	Lys	Gly
				85				90					95		
Val	Lys	Cys	Asn	Leu	Asn	Phe	Phe	Glu	Gly	Glu	Glu	Tyr	Leu		
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:5113:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 233 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...233

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5113:

Lys	Gln	Ile	Leu	Val	Leu	Val	Lys	Lys	Gly	Lys	Ser	Met	Ser	Asp	Arg
1			5						10					15	
Thr	Ile	Gly	Ile	Leu	Gly	Leu	Gly	Ile	Phe	Gly	Ser	Ser	Val	Leu	Ala
			20					25					30		
Ala	Leu	Ala	Lys	Gln	Asp	Met	Asn	Ile	Ile	Ala	Ile	Asp	Asp	His	Ala
			35				40					45			
Glu	Arg	Ile	Asn	Gln	Phe	Glu	Pro	Val	Leu	Ala	Arg	Gly	Val	Ile	Gly
	50					55					60				
Asp	Ile	Thr	Asp	Glu	Glu	Leu	Leu	Arg	Ser	Ala	Gly	Ile	Asp	Thr	Cys
65				70					75						80
Asp	Thr	Val	Val	Val	Ala	Thr	Gly	Glu	Asn	Leu	Glu	Ser	Ser	Val	Leu
				85				90					95		
Ala	Val	Met	His	Cys	Lys	Ser	Leu	Gly	Val	Pro	Thr	Val	Ile	Ala	Lys
			100					105					110		
Val	Lys	Ser	Gln	Thr	Ala	Lys	Lys	Val	Leu	Glu	Lys	Ile	Gly	Ala	Asp
			115				120						125		

```

Ser Val Ile Ser Pro Glu Tyr Glu Met Gly Gln Ser Leu Ala Gln Thr
130          135          140
Ile Leu Phe His Asn Ser Val Asp Val Phe Gln Leu Asp Lys Asn Val
145          150          155          160
Ser Ile Val Glu Met Lys Ile Pro Gln Ser Trp Ala Gly Gln Ser Leu
          165          170          175
Ser Lys Leu Asp Leu Arg Gly Lys Tyr Asn Leu Asn Ile Leu Gly Phe
          180          185          190
Arg Glu Gln Glu Asn Ser Pro Leu Asp Val Glu Phe Gly Pro Asp Asp
          195          200          205
Leu Leu Lys Ala Asp Thr Tyr Ile Leu Ala Val Ile Asn Asn Gln Tyr
          210          215          220
Leu Asp Thr Leu Val Ala Leu Asn Ser
225          230

```

(2) INFORMATION FOR SEQ ID NO:5114:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 81 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...81
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5114:

```

Ile Lys Ile Leu Asp Lys Arg Lys Arg Met Thr Pro Asn Lys Glu Asp
1          5          10          15
Tyr Leu Lys Cys Ile Tyr Glu Ile Gly Ile Asp Leu His Lys Ile Thr
          20          25          30
Asn Lys Glu Ile Ala Ala Arg Met Gln Val Ser Pro Pro Ala Val Thr
          35          40          45
Glu Met Ile Lys Arg Met Lys Ser Glu Asn Leu Ile Leu Lys Asp Lys
          50          55          60
Glu Cys Gly Phe Leu Arg Thr Asp Leu Gly Leu Lys Leu Val Ser Glu
65          70          75          80
Leu

```

(2) INFORMATION FOR SEQ ID NO:5115:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 150 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...150

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5115:

```
Pro Phe Val Phe Ala Thr Glu Asn Asp Ser Leu Asn Gly Val Ser Met
1           5           10           15
Leu Phe Asn His Leu Leu Thr Asn Thr Pro Gln Ile Phe Ala Asp Val
20           25           30
Arg Thr Tyr Trp Ser Pro Glu Ala Val Glu Arg Val Thr Gly Tyr Thr
35           40           45
Leu Glu Gly Arg Ala Ala Ala Gly Phe Leu His Leu Ile Asn Ser Gly
50           55           60
Ser Cys Thr Leu Asp Gly Thr Gly Gln Ala Thr Arg Asp Gly Lys Pro
65           70           75           80
Val Met Lys Pro Phe Trp Glu Leu Asp Glu Ser Glu Val Gln Ala Met
85           90           95
Leu Glu Asn Thr Asp Val Pro Thr Ser Lys Pro Arg Ile Leu Pro Trp
100          105          110
Arg Arg Ile Leu Asn Ser Phe Leu Asp Glu Gly Gly Tyr Ala Ser Asn
115          120          125
Asn Gly Thr Ser Gln Ser Phe Lys Arg Gly Trp Ser Ser Ala Thr Asn
130          135          140
Cys Arg Arg Leu His Thr
145          150
```

(2) INFORMATION FOR SEQ ID NO:5116:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 295 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...295

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5116:

```
Thr His Val Phe Val Ile Arg Lys Glu Val Asn Val Met Lys Pro Met
1           5           10           15
Pro Leu Trp Lys Arg Asn Leu Lys Lys Phe Tyr Asn Asn Lys Leu Ala
20           25           30
```

Phe	Ile	Gly	Phe	Ile	Cys	Phe	Met	Leu	Ile	Leu	Leu	Ala	Cys	Ile	Leu
	35						40					45			
Ala	Pro	Leu	Leu	Thr	Thr	Tyr	Ser	Pro	Asp	Val	Val	Asp	Leu	Gly	Ser
	50					55					60				
Met	Asn	Arg	Pro	Pro	Ser	Ala	Lys	His	Ile	Leu	Gly	Thr	Asp	Lys	Leu
65					70					75					80
Gly	Arg	Asp	Val	Phe	Ala	Arg	Ile	Leu	Tyr	Gly	Gly	Arg	Val	Ser	Ile
			85						90					95	
Gln	Val	Gly	Met	Tyr	Gly	Ala	Ile	Cys	Gly	Ala	Val	Ile	Gly	Thr	Val
			100					105					110		
Leu	Gly	Gly	Ile	Ala	Gly	Tyr	Phe	Gly	Gly	Lys	Ile	Asp	Ala	Leu	Leu
		115					120					125			
Val	Arg	Leu	Ala	Glu	Leu	Phe	Leu	Thr	Phe	Pro	Asn	Met	Ile	Val	Ile
	130					135					140				
Leu	Leu	Leu	Ser	Ser	Ile	Phe	Gly	Gln	Gly	Val	Phe	Asn	Leu	Ile	Phe
145					150					155					160
Val	Phe	Ser	Val	Met	Gly	Trp	Met	Thr	Thr	Phe	Arg	Met	Val	Arg	Asn
			165						170					175	
Glu	Phe	Met	Ser	Leu	Lys	Gln	Glu	Thr	Tyr	Val	Asp	Val	Cys	Arg	Ala
		180						185					190		
Phe	Gly	Phe	Ser	Asp	Ser	Arg	Ile	Ile	Phe	Asn	Asn	Ile	Leu	Arg	Asn
	195					200						205			
Ala	Ile	Ser	Pro	Val	Ile	Val	Ser	Leu	Ser	Leu	Asn	Val	Ala	Gly	Phe
	210					215					220				
Ile	Leu	Ser	Glu	Ala	Gly	Leu	Ser	Phe	Leu	Gly	Val	Gly	Val	Pro	Ser
225					230					235					240
Asp	Ile	Pro	Thr	Trp	Gly	Asn	Ile	Ile	Asn	Ala	Ala	Lys	Thr	Ala	Asp
				245					250					255	
Val	Ile	Lys	Asn	Ser	Trp	Trp	Leu	Trp	Leu	Val	Pro	Gly	Ser	Ile	Ile
		260					265						270		
Thr	Leu	Phe	Val	Leu	Ser	Ile	Asn	Phe	Ile	Gly	Asp	Gly	Leu	Arg	Asp
	275					280						285			
Ile	Met	Asp	Pro	Lys	Gln	Gln									
	290					295									

(2) INFORMATION FOR SEQ ID NO:5117:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 75 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...75
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5117:

Val	Thr	Val	Phe	Ala	Tyr	Ser	Glu	Pro	Asn	Gly	Leu	Pro	Met	Ala	Ile
1			5					10						15	

Ala	Val	Ser	Pro	Thr	Val	Asn	Leu	Leu	Glu	Ser	Pro	Asn	Ser	Ala	Thr
			20					25					30		
Val	Val	Thr	Phe	Ser	Glu	Glu	Ile	Leu	Thr	Thr	Ala	Ile	Ser	Glu	Lys
		35					40					45			
Val	Ser	Ala	Pro	Thr	Ile	Ser	Pro	Gly	Thr	Leu	Val	Pro	Ser	Asp	Asn
	50					55					60				
Arg	Ile	Ser	Thr	Leu	Leu	Ala	Pro	Phe	Ile	Thr					
65					70					75					

(2) INFORMATION FOR SEQ ID NO:5118:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 188 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...188

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5118:

Asn	Lys	Val	Leu	Ser	Asn	Arg	Glu	Lys	Arg	Ile	Ser	Met	Arg	Lys	Glu
1				5					10					15	
Ile	Ala	Pro	Glu	Leu	Tyr	Asn	Tyr	Asn	Lys	Phe	Pro	Gly	Pro	Glu	Phe
			20					25					30		
His	Leu	His	Gly	Asp	Lys	Val	Glu	Thr	Glu	Gly	Ile	Ala	Phe	Ser	Leu
		35					40					45			
Val	Glu	Asn	Ile	Lys	Asp	Ala	Phe	Asp	Val	Thr	Thr	Phe	Asn	Gln	Arg
	50					55					60				
Phe	Ser	Glu	Val	Leu	Thr	Lys	Phe	Asp	Tyr	Ile	Val	Gly	Asp	Trp	Ser
65					70					75				80	
Asn	Glu	Gln	Leu	Arg	Leu	Arg	Gly	Phe	Tyr	Lys	Asp	Asp	Arg	Thr	Glu
			85					90						95	
Glu	Lys	Leu	Glu	Lys	Ile	Ser	Arg	Leu	Gln	Asp	Tyr	Leu	Leu	Glu	Tyr
		100						105					110		
Cys	Ser	Tyr	Gly	Cys	Ala	Tyr	Phe	Val	Leu	Glu	Asn	Glu	Ala	Pro	Lys
		115					120					125			
Arg	Ala	Ser	Phe	Asp	Lys	Lys	Met	Arg	Lys	Thr	Glu	Glu	Glu	Thr	Pro
	130					135					140				
Ser	Arg	Lys	Gly	Lys	Lys	Pro	Thr	Gln	Thr	Lys	Arg	Lys	Ser	Asn	Ala
145					150					155				160	
Asp	Lys	Lys	Asn	Arg	Arg	Arg	Gln	Lys	Asp	Gln	His	Ser	Gln	Lys	Glu
			165					170						175	
Asp	Lys	Gly	Gln	Arg	His	Phe	Val	Ile	Arg	Gln	Lys				
		180						185							

(2) INFORMATION FOR SEQ ID NO:5119:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 89 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...89

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5119:

Lys	Arg	Val	Phe	Val	Met	Asp	Thr	Lys	Ile	Met	Glu	Gln	Phe	His	Glu
1				5					10					15	
Met	Asp	Ile	Thr	Met	Leu	Ser	Ser	Ile	Glu	Gly	Gly	Lys	Asn	Asn	Trp
			20					25					30		
Gln	Thr	Asn	Val	Leu	Glu	Gly	Gly	Gly	Ala	Ala	Phe	Gly	Gly	Trp	Gly
		35					40					45			
Leu	Gly	Thr	Ala	Ile	Cys	Ala	Ala	Ser	Gly	Val	Gly	Ala	Pro	Phe	Met
	50					55					60				
Gly	Ala	Cys	Gly	Tyr	Ile	Gly	Ala	Lys	Phe	Gly	Val	Ala	Leu	Trp	Ala
65					70					75					80
Gly	Val	Thr	Gly	Ala	Thr	Ser	Gly	Phe							
					85										

(2) INFORMATION FOR SEQ ID NO:5120:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5120:

Val	Met	Val	Phe	Thr	Ala	Lys	Ser	Ser	Lys	Ile	Asn	Ile	Glu	Glu	Val
1				5					10					15	
Arg	Ala	Leu	Ser	Lys	Leu	Glu	Gly	Gln	Ala	Leu	Glu	Arg	Lys	Ser	Gln
			20					25					30		
Arg	Asp	Gln	Glu	Leu	Glu	Ala	Ile	Ile	Arg	Gly	Glu	Asp	Gln	Arg	Ile
		35					40					45			
Leu	Leu	Val	Ile	Gly	Pro	Cys	Ser	Ser	Asp	Asn	Glu	Glu	Ala	Val	Leu

50		55		60											
Glu	Tyr	Ala	Lys	Arg	Leu	Ala	Val	Leu	Gln	Glu	Glu	Val	Ala	Asp	Arg
65					70				75					80	
Ile	Phe	Met	Val	Met	Arg	Val	Tyr	Thr	Ala	Lys	Pro	Arg	Thr	Asn	Gly
			85						90					95	
Asp	Gly	Tyr	Lys	Gly	Leu	Ile	His	Gln	Pro	Asn	Ala	Thr	Glu	Ala	Pro
		100						105					110		
Ser	Leu	Ile	Asn	Gly	Ile	Lys	Ala	Val	Arg	His	Leu	His	Tyr	Arg	Val
	115					120					125				
Ile	Thr	Glu	Thr	Gly	Met	Thr	Thr	Ala	Asp	Glu	Met	Leu	Tyr	Pro	Glu
130					135					140					
Asn	Leu	Pro	Leu	Val	Asp	Asp	Leu	Ile	Ser	Tyr	Met	Ala	Val	Gly	Ala
145			150						155					160	
Arg	Ser	Val	Glu	Asp	Gln	Gln	His	Arg	Phe	Val	Ala	Ser	Gly	Ala	Gly
			165					170					175		
Phe	Ser	Thr	Gly	Phe	Lys	Asn	Pro	Thr	Ser	Gly	Asn	Leu	Asn	Val	Met
		180					185				190				
Phe	Asn	Gly	Ile	Tyr	Ala	Ala	Gln	Asn	Lys	Gln	Ser	Phe	Leu	Phe	Leu
	195				200				205						
Gly	Lys	Glu	Val	Glu	Thr	Thr	Gly	Asn	Pro	Leu	Ser	His	Ala	Ile	Leu
210					215				220						
Arg	Gly	Ala	Leu	Asn	Glu	Tyr	Gly	Lys	Asn	Ile	Pro	Asn	Tyr	Tyr	Tyr
225			230					235						240	
Asp	Asn	Leu	Ile	Asp	Thr	Ile	Ala	Gln	Tyr	Glu	Lys	Met	Gly	Leu	Glu
			245					250					255		
Asn	Pro	Phe	Ile	Ile	Asp	Thr	Asn	His	Asp	Asn	Ser	Gly	Lys	Gln	
	260				265						270				
Tyr	Ile	Glu	Gln	Ile	Arg	Ile	Val	Arg	Gln	Thr	Leu	Ile	Asn	Arg	Ala
	275				280					285					
Trp	Asn	Glu	Lys	Ile	Lys	Gln	Phe	Val	Arg	Gly	Phe	Met	Ile	Glu	Ser
290					295				300						
Tyr	Leu	Glu	Asp	Gly	Arg	Gln	Asn	Glu	Pro	Glu	Val	Phe	Gly	Lys	Ser
305			310					315						320	
Ile	Thr	Asp	Pro	Cys	Leu	Gly	Trp	Asp	Asn	Thr	Glu	Ala	Leu	Val	Arg
			325				330						335		
Glu	Ile	Tyr	Lys	Thr	Leu	Gly	Glu								
	340														

(2) INFORMATION FOR SEQ ID NO:5121:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 298 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...298

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5121:

```

Lys Glu Val Phe Met Thr Tyr Tyr Val Ala Ile Asp Ile Gly Gly Thr
1      5      10      15
Asn Ile Lys Tyr Gly Leu Val Asp Gln Glu Gly Gln Leu Leu Glu Ser
20      25      30
His Glu Met Pro Thr Glu Ala His Lys Gly Gly Pro His Ile Leu Gln
35      40      45
Lys Thr Lys Asp Ile Val Ala Ser Tyr Leu Glu Lys Gly Pro Val Ala
50      55      60
Gly Val Ala Ile Ser Ser Ala Gly Met Val Asp Pro Asp Lys Gly Glu
65      70      75      80
Ile Phe Tyr Ala Gly Pro Gln Ile Pro Asn Tyr Ala Gly Thr Gln Phe
85      90      95
Lys Lys Glu Ile Glu Glu Ser Phe Thr Ile Pro Cys Glu Ile Glu Asn
100     105     110
Asp Val Asn Cys Ala Gly Leu Ala Glu Ala Val Ser Gly Ser Gly Lys
115     120     125
Gly Ala Ser Val Thr Leu Cys Leu Thr Ile Gly Thr Gly Ile Gly Gly
130     135     140
Cys Leu Ile Met Asp Arg Lys Val Phe His Gly Phe Ser Asn Ser Ala
145     150     155     160
Cys Glu Val Gly Tyr Met His Met Gln Asp Gly Ala Phe Gln Asp Leu
165     170     175
Ala Ser Thr Thr Ala Leu Val Lys Tyr Val Ala Glu Ala His Gly Glu
180     185     190
Asp Val Asp Gln Trp Asn Gly Arg Ile Phe Lys Glu Ala Thr Glu
195     200     205
Gly Asn Lys Ile Cys Met Glu Gly Ile Asp Arg Met Val Asp Tyr Leu
210     215     220
Gly Lys Gly Leu Ala Asn Ile Cys Tyr Val Ala Asn Pro Glu Val Val
225     230     235     240
Ile Leu Gly Gly Gly Ile Met Gly Gln Glu Ala Ile Leu Lys Pro Lys
245     250     255
Ile Arg Thr Ala Leu Lys Glu Ala Leu Val Pro Ser Leu Ala Glu Lys
260     265     270
Thr Arg Leu Glu Phe Ala His His Gln Asn Thr Ala Gly Met Leu Gly
275     280     285
Ala Tyr Tyr His Phe Lys Thr Lys Gln Ser
290     295

```

(2) INFORMATION FOR SEQ ID NO:5122:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 512 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...512

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5122:

Arg	Arg	Phe	Leu	Met	Lys	Ser	Lys	Ile	Val	Leu	Gly	Ala	Ser	Leu	Ala
1			5					10						15	
Ile	Ala	Thr	Leu	Ser	Leu	Val	Ser	Leu	Val	Glu	Ile	Glu	Gly	Leu	Ser
		20						25					30		
Pro	Phe	Leu	Ile	Glu	Asn	Val	Ser	Ala	Asn	Thr	His	Ser	Ala	Asn	Lys
		35					40					45			
Val	Ile	Asn	His	Lys	Val	Ser	Ile	Tyr	Leu	Glu	Asn	Ala	Asp	Glu	Gly
	50					55					60				
Lys	Gly	Leu	Thr	Val	Asn	Phe	Ser	Thr	Asp	Ser	Val	Ser	Pro	Asn	Leu
65					70					75				80	
Phe	Asp	Glu	Phe	Glu	Lys	Lys	Ser	Gly	Ile	Thr	Ile	Thr	Thr	Met	Leu
			85					90						95	
Val	Asn	Ala	Lys	Thr	Gly	Glu	Val	Val	Glu	Lys	Arg	Leu	Thr	Pro	Ser
		100						105					110		
Val	Phe	Leu	Arg	Ser	Asn	Asp	Leu	Thr	Ser	Gly	Thr	Ile	Ser	Ser	Phe
	115						120					125			
Ile	Phe	Ser	Glu	Tyr	Pro	Asp	Gly	Glu	Tyr	Lys	Tyr	Val	Val	Ser	Lys
	130					135					140				
Gly	Asp	Phe	Ile	Asp	Pro	Lys	Thr	Gln	Phe	Lys	His	Gln	Tyr	Arg	Gly
145					150					155				160	
Glu	Ser	Pro	Val	Phe	Arg	Ile	Arg	Asn	Arg	Lys	Tyr	Val	Glu	Leu	Gly
			165					170						175	
Thr	Thr	Asp	Lys	Lys	Leu	Asp	Glu	Arg	Arg	Asp	Asn	Ser	Val	Tyr	Lys
		180						185					190		
Asp	Gly	Val	Val	Glu	His	Lys	Val	Asn	Leu	Ser	Leu	Thr	Ser	Tyr	Gln
	195						200						205		
Gly	Gly	Asn	Gly	Val	Thr	Ala	Ile	Phe	Ser	Thr	Asp	Ser	Val	Asn	Ser
	210					215					220				
Asn	Leu	Leu	Asn	Ser	Phe	Gly	Glu	Lys	Ala	Lys	Lys	Val	Leu	Ile	Arg
225					230					235				240	
Ser	Lys	Leu	Ile	Asn	Val	Lys	Thr	Gly	Glu	Val	Ile	Asp	Glu	Thr	Phe
			245					250						255	
Ser	Pro	Lys	Val	Ser	Leu	Thr	Ser	Lys	Ile	Leu	Lys	Ser	Gly	Ser	Thr
		260						265					270		
Ala	Val	Phe	Tyr	Phe	Ile	Asp	Leu	Thr	Asp	Gly	Glu	Tyr	Lys	Tyr	Val
	275					280						285			
Ala	Tyr	Glu	Ser	Gln	Gln	Tyr	Thr	Asp	Pro	Gln	Thr	Thr	Leu	Thr	His
	290					295				300					
Gln	Tyr	Arg	Gly	Glu	Ser	Pro	Ile	Phe	Ser	Ile	Lys	Asp	Gly	Lys	Phe
305					310					315				320	
Ser	Gly	Leu	Val	Ser	Ala	Ser	Lys	Pro	Asp	Glu	Asn	Pro	Lys	Pro	Thr
			325					330						335	
Pro	Lys	Pro	Asp	Glu	Lys	Pro	Lys	Pro	Ser	Ala	Pro	Gln	Gln	Glu	Lys
		340						345					350		
Pro	Lys	Pro	Thr	Val	Gln	Ser	Gly	Trp	Val	Gly	Ser	Ser	Tyr	Tyr	Gln
	355						360					365			
Asn	Gly	Lys	Lys	Val	Thr	Ser	Lys	Trp	Ile	Phe	Asp	Lys	Lys	Tyr	Asn
	370					375				380					
Ser	Tyr	Phe	Tyr	Leu	Asp	Ala	Ser	Gly	Asn	Tyr	Val	Gln	Asn	Ala	Trp
385					390					395				400	
Val	Gly	Asn	Tyr	Tyr	Leu	Lys	Ser	Gly	Gly	Tyr	Met	Ala	Lys	Ser	Glu
			405					410					415		
Trp	Ile	Tyr	Asp	Lys	Asn	Tyr	Gly	Ser	Tyr	Tyr	Tyr	Leu	Thr	Ser	Glu

			420					425					430			
Gly	Ser	Tyr	Ala	Arg	Asn	Thr	Trp	Ser	Gly	Asn	Tyr	Tyr	Leu	Lys	Ser	
		435						440					445			
Asn	Gly	Lys	Met	Ala	Lys	Ser	Glu	Trp	Val	Tyr	Asp	Ser	Asn	Tyr	Lys	
	450					455					460					
Ser	Tyr	Tyr	Tyr	Leu	Thr	Ser	Glu	Gly	Ser	Tyr	Ala	Arg	Asn	Thr	Trp	
465					470					475					480	
Val	Gly	Asn	Tyr	Tyr	Leu	Lys	Ser	Asn	Gly	Lys	Met	Ala	Val	Asn	Glu	
				485					490					495		
Arg	Thr	Pro	Asp	Gly	Tyr	Arg	Val	Asp	Gly	Ser	Gly	Lys	Trp	Val	Lys	
			500					505					510			

(2) INFORMATION FOR SEQ ID NO:5123:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 258 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...258

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5123:

Ile	Gln	Ser	Leu	Lys	Arg	Arg	Arg	Arg	Glu	Ile	Thr	Lys	Met	Lys	Arg
1				5					10					15	
Trp	Ile	Ala	Leu	Ser	Lys	Ile	Asp	Phe	Leu	Leu	Thr	Lys	Arg	Gln	Leu
		20						25					30		
Ile	Tyr	Tyr	Leu	Leu	Ser	Val	Gly	Met	Pro	Thr	Ala	Phe	Tyr	Leu	Phe
	35					40					45				
Phe	Ser	Gly	Ile	Tyr	Gln	Asp	Thr	Pro	Gly	Glu	Leu	Ala	Asn	Phe	Met
	50				55					60					
Arg	Asp	Tyr	Leu	Ile	Ser	Met	Thr	Ala	Phe	Ser	Met	Met	Ser	Thr	Ala
65				70					75					80	
Ile	Phe	Ser	Phe	Pro	Val	Val	Leu	His	Thr	Asp	Lys	Ile	Asn	Asn	Trp
			85					90					95		
Gln	Lys	Thr	Leu	Arg	His	Ser	Pro	Val	Asn	Met	Val	Glu	Tyr	Tyr	Leu
			100					105					110		
Ser	Lys	Ile	Thr	Ser	Met	Leu	Val	Asp	Tyr	Leu	Val	Ser	Ile	Leu	Val
		115				120						125			
Val	Phe	Ser	Val	Gly	His	Phe	Val	Arg	Gly	Val	Asp	Met	Ser	Leu	Gly
	130				135						140				
Asn	Trp	Ile	Gly	Ala	Ala	Leu	Leu	Leu	Ile	Val	Gly	Ser	Ile	Ala	Phe
145				150						155				160	
Val	Ala	Leu	Gly	Leu	Thr	Leu	Thr	Leu	Leu	Pro	Thr	Ser	Gln	Leu	Met
			165					170					175		
Ser	Val	Val	Gly	Asn	Leu	Leu	Tyr	Leu	Gly	Leu	Ala	Val	Leu	Gly	Gly
		180				185						190			
Leu	Trp	Met	Pro	Ile	Ser	Leu	Phe	Pro	Asp	Trp	Met	Gln	Val	Val	Gly

		195					200					205				
Lys	Cys	Leu	Pro	Thr	Tyr	Gln	Leu	Met	Glu	Leu	Leu	Lys	Thr	Phe	Leu	
	210					215					220					
Asn	Glu	Gly	Gly	Ile	Asn	Leu	Ser	Ala	Thr	Val	Tyr	Leu	Leu	Val	Phe	
225					230					235					240	
Ser	Val	Val	Leu	Phe	Gly	Leu	Thr	Ile	Tyr	Leu	Gln	Gly	His	Lys	Glu	
			245						250					255		
Asn	Ala															

(2) INFORMATION FOR SEQ ID NO:5124:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 79 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...79

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5124:

Val	His	Ser	Phe	Arg	Gly	Ile	Arg	Glu	Ile	Leu	Phe	Gln	Leu	Trp	Ser	
1			5					10					15			
Glu	Lys	Glu	Gly	Arg	Ala	Glu	Lys	Leu	Gly	Thr	Gly	Leu	Ile	Phe	Ser	
			20					25				30				
Asp	Ile	Leu	Leu	Arg	His	Asn	Ala	Lys	Gln	Ser	Leu	Ile	Asp	Ser	Asp	
		35				40					45					
Lys	Met	Val	Pro	Ile	Gln	Ser	Phe	Leu	Arg	Ser	Ser	Val	Asp	Ser	His	
	50				55					60						
Trp	Gln	Tyr	Leu	Ser	Ile	Ile	Gln	Pro	Lys	Ile	Glu	Tyr	Glu	Thr		
65				70					75							

(2) INFORMATION FOR SEQ ID NO:5125:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 159 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...159

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5125:

Thr	Asn	Ser	Leu	Arg	Met	Pro	Leu	Lys	Arg	Pro	Leu	Lys	Asn	Arg	Lys
1				5					10					15	
Lys	Glu	Lys	Asn	Met	Ser	Lys	Glu	Lys	Val	Ile	Leu	Ala	Tyr	Ser	Gly
			20					25					30		
Gly	Leu	Asp	Thr	Ser	Val	Ala	Ile	Thr	Trp	Leu	Lys	Lys	Asp	Tyr	Asp
		35					40					45			
Val	Val	Ala	Val	Cys	Met	Asp	Val	Gly	Glu	Gly	Lys	Asp	Leu	Asp	Phe
	50					55					60				
Ile	His	Asp	Lys	Ala	Leu	Lys	Val	Gly	Ala	Val	Glu	Ser	Tyr	Val	Ile
65					70				75						80
Asp	Val	Lys	Asp	Glu	Phe	Ala	Thr	Asp	Tyr	Val	Leu	Val	Ala	His	Gln
			85					90					95		
Ser	His	Ala	Tyr	Tyr	Glu	Gln	Lys	Tyr	Pro	Leu	Val	Ser	Ala	Leu	Ser
		100						105					110		
Arg	Pro	Leu	Ile	Ser	Lys	Lys	Leu	Val	Glu	Ile	Ala	His	Gln	Ile	Gly
		115					120					125			
Ala	Thr	Thr	Ile	Ala	His	Gly	Cys	Thr	Gly	Lys	Gly	Asn	Asp	Gln	Val
	130					135					140				
Glu	Tyr	Gln	Ile	Ala	Val	Ala	Lys	Lys	Ala	Asn	Glu	Ala	Lys	Lys	
145					150					155					

(2) INFORMATION FOR SEQ ID NO:5126:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 201 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...201

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5126:

Lys	Thr	Ser	Phe	Ser	Cys	Glu	Leu	Ala	Phe	Phe	Leu	Cys	Pro	His	Phe
1				5					10					15	
Arg	Ser	Asn	His	Trp	Lys	Ile	Leu	Thr	Val	Ser	Asp	Thr	Met	Glu	Glu
			20					25					30		
Lys	Arg	Leu	Glu	Tyr	Pro	Met	Val	Thr	Phe	Leu	Gly	Asn	Pro	Val	Ser
		35					40					45			
Phe	Thr	Gly	Lys	Gln	Leu	Gln	Val	Gly	Asp	Lys	Ala	Leu	Asp	Phe	Ser
	50					55					60				
Leu	Thr	Thr	Thr	Asp	Leu	Ser	Lys	Lys	Ser	Leu	Ala	Asp	Phe	Asp	Gly
65					70				75						80
Lys	Lys	Lys	Val	Leu	Ser	Val	Val	Pro	Ser	Ile	Asp	Thr	Gly	Ile	Cys
			85						90					95	

Ser	Thr	Gln	Thr	Arg	Arg	Phe	Asn	Glu	Glu	Leu	Ala	Gly	Leu	Asp	Asn
			100					105					110		
Thr	Val	Val	Leu	Thr	Val	Ser	Met	Asp	Leu	Pro	Phe	Ala	Gln	Lys	Arg
		115					120					125			
Trp	Cys	Gly	Ala	Glu	Gly	Leu	Asp	Asn	Ala	Ile	Met	Leu	Ser	Asp	Tyr
	130					135					140				
Phe	Asp	His	Ser	Phe	Gly	Arg	Asp	Tyr	Ala	Leu	Leu	Ile	Asn	Glu	Trp
145					150					155					160
His	Leu	Leu	Ala	Arg	Ala	Val	Phe	Val	Leu	Asp	Thr	Asp	Asn	Thr	Ile
				165					170					175	
His	Tyr	Val	Glu	Tyr	Val	Asp	Asn	Ile	Asn	Ser	Glu	Pro	Asn	Phe	Glu
			180				185						190		
Ala	Ala	Ile	Ala	Ala	Ala	Lys	Ala	Leu							
		195					200								

(2) INFORMATION FOR SEQ ID NO:5127:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 233 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...233
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5127:

Gly	Leu	Ser	Leu	Phe	His	Ser	Ile	Gly	Glu	Asn	Arg	Met	Lys	Lys	Ile
1				5				10					15		
Ile	Ser	His	Arg	Tyr	Phe	Ile	Ile	Val	Phe	Leu	Leu	Val	Ile	Ala	Asp
			20				25					30			
Gln	Lys	Phe	Ser	Val	Leu	Val	Leu	Arg	Ser	Asp	Leu	Val	Ala	Gly	Leu
		35				40					45				
Ser	Asp	Phe	Ala	Tyr	Tyr	Leu	Ser	Asp	Met	Met	Leu	Asn	Phe	Leu	Val
	50				55					60					
Val	Leu	Phe	Ala	Leu	Ile	Ala	Met	Ile	Trp	Ser	Gly	Lys	Trp	Gln	Lys
65				70				75						80	
Ile	Asn	Ser	Arg	Lys	Phe	Lys	Gly	Ser	Tyr	Leu	Phe	Tyr	Ser	Phe	Leu
			85				90						95		
Ala	Leu	Leu	Ala	Phe	Val	Ala	Trp	Asn	Phe	Val	Thr	Phe	Phe	Leu	Phe
			100				105					110			
Pro	Pro	Thr	Arg	Asn	Glu	Ile	Ser	Tyr	Gln	His	Ala	Ala	Pro	Thr	Phe
		115				120					125				
Thr	Gly	Ala	Thr	Ala	Phe	Leu	Met	Tyr	Phe	Phe	Tyr	Pro	Val	Ile	Ala
	130				135					140					
Gly	Pro	Ile	Phe	Glu	Asp	Met	Ile	Tyr	Arg	Gly	Leu	Val	Met	Thr	Ala
145				150					155					160	
Leu	Glu	Lys	Gly	Lys	Lys	Trp	Gly	Leu	Asp	Val	Leu	Gly	Ser	Ala	Val
			165				170						175		

Leu	Phe	Gly	Val	Ser	His	Ile	Ser	Asn	His	Gly	Trp	Val	Leu	Thr	Asp
			180					185					190		
Phe	Val	Phe	Tyr	Met	Gly	Gly	Gly	Leu	Ile	Phe	Ala	Val	Leu	Phe	Arg
		195					200					205			
Met	Thr	Lys	Ser	Ile	Tyr	Trp	Pro	Ile	Gly	Leu	His	Ile	Val	Tyr	Asn
	210					215					220				
Gly	Ile	Gly	Gln	Leu	Leu	Met	Leu	Leu							
225					230										

(2) INFORMATION FOR SEQ ID NO:5128:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 163 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...163

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5128:

Leu	Thr	Pro	Leu	Leu	Ser	Ala	Tyr	His	Leu	Ile	Lys	Arg	Pro	Val	Ile
1			5					10					15		
Asp	Lys	Cys	Gln	Ile	Ser	Lys	Ile	Ser	Thr	Ser	Ser	Val	Ser	Val	Phe
		20					25					30			
Phe	Ile	Ala	Ser	Ile	Thr	Thr	Leu	Thr	Ile	Asn	Met	Met	Ser	Lys	Lys
		35				40					45				
Tyr	Ser	Val	Gln	Ala	Glu	Pro	Gln	Val	Ile	Val	Ala	Ser	Gly	Ala	Gln
	50				55				60						
Pro	Thr	Ser	Val	Ile	Leu	Asn	Cys	Ile	Pro	Val	Phe	Ser	Thr	Asn	Phe
65				70				75						80	
Ala	Ser	Asp	Ala	Glu	Lys	Ala	Pro	Phe	Ser	Ile	Pro	Met	Ile	Ala	Pro
			85				90					95			
Ile	Pro	Val	Arg	Ala	Met	Ala	Ser	Leu	Ile	Pro	Pro	Ser	Ser	Ala	Leu
		100					105					110			
Glu	Asn	Phe	Thr	Pro	Lys	Ser	Lys	Ala	Asn	Thr	Val	Lys	Met	Ile	Asn
	115					120					125				
Met	Met	Thr	Gly	Pro	Pro	Ile	Ser	Lys	Met	Gly	Leu	Lys	Thr	Phe	Pro
	130					135				140					
Ile	Arg	Ser	Lys	Ile	Ala	Ser	Ile	Thr	Val	Pro	Pro	Phe	Phe	Met	Leu
145				150					155						160
Tyr	Glu	Cys													

(2) INFORMATION FOR SEQ ID NO:5129:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5129:

Phe	Glu	Pro	Phe	Tyr	Pro	Leu	Ser	Tyr	Ala	Lys	Ser	Glu	Thr	Glu	Ile
1				5					10					15	
Pro	Arg	Arg	Ala	Ala	Ile	Ser	Ser	Ala	Arg	Phe	Asn	Cys	Phe	Lys	Pro
			20					25					30		
Ser	Thr	Val	Ala	Arg	Thr	Met	Leu	Ile	Gly	Val	Leu	Glu	Pro	Ser	Asp
		35				40					45				
Leu	Asp	Val	Ile	Ser	Ala	Thr	Pro	Ala	Asn	Ser	Thr	Thr	Ala	Arg	Thr
50					55					60					
Ala	Pro	Pro	Ala	Ala	Thr	Pro	Glu	Pro	Ser	Thr	Ala	Gly	Phe	Asn	Asn
65				70					75					80	
Thr	Leu	Ala	Pro	Pro	Asn	Ser	Glu	Arg	Thr	Ser	Cys	Gly	Ile	Val	Val
			85					90					95		
Pro	Thr	Ile	Gly	Thr	Ser	Ile	Lys	Phe	Phe	Leu	Ala	Ser	Ser	Thr	Ala
			100					105					110		
Leu	Arg	Ile	Ala	Ser	Gly	Thr	Ser								
			115				120								

(2) INFORMATION FOR SEQ ID NO:5130:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 155 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...155

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5130:

Phe	Glu	Thr	Phe	Ala	Cys	Asn	Leu	Arg	Arg	Asn	Ile	Asn	Met	Asp	Gly
1				5					10					15	
Ile	Thr	Lys	Asp	Phe	Ile	Lys	Thr	Ala	Lys	Leu	Met	Lys	Gln	Leu	Trp
		20						25					30		

Pro	Gln	Leu	Thr	Asp	Lys	Glu	Ala	Ile	Asp	Glu	Val	Lys	Lys	Tyr	Thr
		35					40					45			
Asn	Gly	Lys	Asn	Thr	Ala	Ile	Phe	Thr	Glu	Val	Glu	Gly	Asp	Thr	Ile
	50					55					60				
Val	Gly	Leu	Ala	Leu	Cys	Ser	Leu	Arg	Phe	Asp	Tyr	Val	Glu	Gly	Cys
65					70					75					80
Lys	Tyr	Ser	Pro	Val	Gly	Phe	Leu	Glu	Gly	Ile	Ile	Val	Asp	Glu	Glu
				85					90					95	
Tyr	Arg	Leu	Lys	Asp	Ile	Ala	Lys	Asn	Leu	Cys	Thr	Lys	Cys	Glu	Glu
			100					105					110		
Trp	Ala	Lys	Asn	Lys	Gly	Cys	Lys	Glu	Phe	Ala	Ser	Asp	Cys	Thr	Leu
		115					120					125			
Thr	Asn	Thr	Asp	Ser	Ile	Arg	Phe	His	Leu	Asn	Ile	Gly	Phe	Gln	Glu
	130					135					140				
Ala	Asn	Arg	Ile	Ile	His	Phe	Lys	Lys	Lys	Leu					
145					150					155					

(2) INFORMATION FOR SEQ ID NO:5131:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5131:

Leu	Leu	Thr	Leu	Pro	Leu	Ala	Gln	Val	Val	Ile	Leu	Arg	Asp	Val	Ser
1				5				10						15	
Ser	Lys	Ser	Met	Ala	Gln	Ser	His	Leu	Val	Arg	Gln	Arg	Leu	Pro	Phe
		20						25					30		
Met	Gln	Leu	His	Lys	Arg	Lys	Lys	Val	Gly	Leu	Leu	Pro	Leu	Ser	
	35					40				45					
Met	Arg	Asn	Met	Pro	Leu	Ile	Gln	Leu	Met	Leu	Arg	Pro	Leu	Val	Ser
	50					55				60					
Ile	Leu	Thr	Asn	Cys	Ser	Cys	Leu	Asn	Gln	Thr	Gln	Glu	Ser	Lys	Val
65				70					75						80
Leu	Arg	Leu	Arg	Glu	Asn										
				85											

(2) INFORMATION FOR SEQ ID NO:5132:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 420 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
 (A) NAME/KEY: misc_feature
 (B) LOCATION 1...420

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5132:

```

Ile Met Thr Phe Ser Phe Asp Thr Ala Ala Ala Gln Gly Ala Val Ile
1      5      10      15
Lys Val Ile Gly Val Gly Gly Gly Gly Gly Asn Ala Ile Asn Arg Met
20      25      30
Val Asp Glu Gly Val Thr Gly Val Glu Phe Ile Ala Ala Asn Thr Asp
35      40      45
Val Gln Ala Leu Ser Ser Thr Lys Ala Glu Thr Val Ile Gln Leu Gly
50      55      60
Pro Lys Leu Thr Arg Gly Leu Gly Ala Gly Gly Gln Pro Glu Val Gly
65      70      75      80
Arg Lys Ala Ala Glu Glu Ser Glu Glu Thr Leu Thr Glu Ala Ile Ser
85      90      95
Gly Ala Asp Met Val Phe Ile Thr Ala Gly Met Gly Gly Gly Ser Gly
100     105     110
Thr Gly Ala Ala Pro Val Ile Ala Arg Ile Ala Lys Asp Leu Gly Ala
115     120     125
Leu Thr Val Gly Val Val Thr Arg Pro Phe Gly Phe Glu Gly Ser Lys
130     135     140
Arg Gly Gln Phe Ala Val Glu Gly Ile Asn Gln Leu Arg Glu His Val
145     150     155     160
Asp Thr Leu Leu Ile Ile Ser Asn Asn Asn Leu Leu Glu Ile Val Asp
165     170     175
Lys Lys Thr Pro Leu Leu Glu Ala Leu Ser Glu Ala Asp Asn Val Leu
180     185     190
Arg Gln Gly Val Gln Gly Ile Thr Asp Leu Ile Thr Asn Pro Gly Leu
195     200     205
Ile Asn Leu Asp Phe Ala Asp Val Lys Thr Val Met Ala Asn Lys Gly
210     215     220
Asn Ala Leu Met Gly Ile Gly Ile Gly Ser Gly Glu Glu Arg Val Val
225     230     235     240
Glu Ala Ala Arg Lys Ala Ile Tyr Ser Pro Leu Leu Glu Thr Thr Ile
245     250     255
Asp Gly Ala Glu Asp Val Ile Val Asn Val Thr Gly Gly Leu Asp Leu
260     265     270
Thr Leu Ile Glu Ala Glu Glu Ala Ser Gln Ile Val Asn Gln Ala Ala
275     280     285
Gly Gln Gly Val Asn Ile Trp Leu Gly Thr Ser Ile Asp Glu Ser Met
290     295     300
Arg Asp Glu Ile Arg Val Thr Val Val Ala Thr Gly Val Arg Gln Asp
305     310     315     320
Arg Val Glu Lys Val Val Ala Pro Gln Ala Arg Ser Ala Thr Asn Tyr
325     330     335
Arg Glu Thr Val Lys Pro Ala His Ser His Gly Phe Asp Arg His Phe

```

		340					345					350					
Asp	Met	Ala	Glu	Thr	Ala	Glu	Leu	Pro	Lys	Gln	Asn	Pro	Arg	Arg	Leu		
		355					360					365					
Glu	Pro	Thr	Gln	Ala	Ser	Ala	Phe	Gly	Asp	Trp	Asp	Leu	Arg	Arg	Glu		
		370					375					380					
Ser	Ile	Val	Arg	Thr	Thr	Asp	Ser	Val	Val	Ser	Pro	Val	Glu	Arg	Phe		
		385				390				395					400		
Glu	Ala	Pro	Ile	Ser	Gln	Asp	Glu	Asp	Glu	Leu	Asp	Thr	Pro	Pro	Phe		
				405					410						415		
Phe	Lys	Asn	Arg														
				420													

(2) INFORMATION FOR SEQ ID NO:5133:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 165 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...165

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5133:

Lys	Met	Ala	Phe	Lys	Asp	Asn	Ala	Val	Glu	Leu	Glu	Glu	Arg	Val	Val		
1				5					10					15			
Ala	Val	Asn	Arg	Val	Thr	Lys	Val	Val	Lys	Gly	Gly	Arg	Arg	Leu	Arg		
			20					25					30				
Phe	Ala	Ala	Leu	Val	Val	Val	Gly	Asp	His	Asn	Gly	Arg	Val	Gly	Phe		
		35					40				45						
Gly	Thr	Gly	Lys	Ala	Gln	Glu	Val	Pro	Glu	Ala	Ile	Arg	Lys	Ala	Val		
		50				55					60						
Asp	Asp	Ala	Lys	Lys	Asn	Leu	Ile	Glu	Val	Pro	Met	Val	Gly	Thr	Thr		
65				70					75					80			
Ile	Pro	His	Glu	Val	Leu	Ser	Glu	Phe	Gly	Gly	Ala	Lys	Val	Leu	Leu		
			85					90					95				
Lys	Pro	Ala	Val	Glu	Gly	Ser	Gly	Val	Ala	Ala	Gly	Gly	Ala	Val	Arg		
			100					105					110				
Ala	Val	Val	Glu	Leu	Ala	Gly	Val	Ala	Asp	Ile	Thr	Ser	Lys	Ser	Leu		
		115				120					125						
Gly	Ser	Asn	Thr	Pro	Ile	Asn	Ile	Val	Arg	Ala	Thr	Val	Glu	Gly	Leu		
		130				135				140							
Lys	Gln	Leu	Lys	Arg	Ala	Glu	Glu	Ile	Ala	Ala	Leu	Arg	Gly	Ile	Ser		
145				150					155					160			
Val	Ser	Asp	Leu	Ala													
				165													

(2) INFORMATION FOR SEQ ID NO:5134:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 66 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...66
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5134:

```

Arg Lys Ala Phe Asn Ile Thr Leu Gln Lys Ala Asn Thr Lys Leu Glu
1          5          10          15
Lys Pro Ile Asn Gln Pro Leu Ser Ser His Ile Phe Arg His Thr Leu
          20          25          30
Leu Ser Thr Leu Ala Glu Lys Asn Ala Ile Met Val Arg Val Glu His
          35          40          45
Lys Asn Ala Lys Thr Val Asn Asn Ile Tyr Thr His Val Ser Lys Arg
          50          55          60
Met Glu
65

```

(2) INFORMATION FOR SEQ ID NO:5135:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 410 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...410
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5135:

```

Lys Ala Pro Phe Gly Phe Asp Thr Ile Val Ser Lys Phe Glu Arg Ser
1          5          10          15
Phe Asn Met Asn Arg Tyr Ala Val Gln Leu Ile Ser Arg Gly Ala Ile
          20          25          30
Asn Lys Met Gly Asn Met Leu Tyr Asp Tyr Gly Asn Ser Val Trp Leu
          35          40          45
Ala Ser Met Gly Thr Ile Gly Gln Thr Val Leu Gly Met Tyr Gln Ile

```

50		55		60											
Ser	Glu	Leu	Val	Thr	Ser	Ile	Leu	Val	Asn	Pro	Phe	Gly	Gly	Val	Ile
65					70					75					80
Ser	Asp	Arg	Phe	Ser	Arg	Arg	Lys	Ile	Leu	Met	Thr	Ala	Asp	Leu	Val
				85						90					95
Cys	Gly	Ile	Leu	Cys	Leu	Ala	Ile	Ser	Phe	Ile	Arg	Asn	Asp	Ser	Trp
			100						105				110		
Met	Ile	Gly	Ala	Leu	Ile	Val	Ala	Asn	Ile	Val	Gln	Ala	Ile	Ala	Phe
		115					120					125			
Ala	Phe	Ser	Arg	Thr	Ala	Asn	Lys	Ala	Ile	Ile	Thr	Glu	Val	Val	Glu
		130					135				140				
Lys	Asp	Glu	Ile	Val	Ile	Tyr	Asn	Ser	Arg	Leu	Glu	Leu	Val	Leu	Gln
145					150					155					160
Val	Val	Gly	Val	Ser	Ser	Pro	Val	Leu	Ser	Phe	Leu	Val	Leu	Gln	Phe
				165					170					175	
Ala	Ser	Leu	His	Met	Thr	Leu	Leu	Leu	Asp	Ser	Leu	Thr	Phe	Phe	Ile
			180					185					190		
Ala	Phe	Val	Leu	Val	Ala	Phe	Leu	Pro	Lys	Glu	Glu	Ala	Glu	Val	Gln
		195					200					205			
Glu	Lys	Lys	Ala	Phe	Thr	Gly	Arg	Asp	Ile	Phe	Val	Asp	Ile	Lys	Asp
		210				215					220				
Gly	Leu	His	Tyr	Ile	Trp	His	Gln	Gln	Glu	Ile	Phe	Phe	Leu	Leu	Leu
225					230					235					240
Val	Ala	Ser	Ser	Val	Asn	Phe	Phe	Phe	Ala	Ala	Phe	Glu	Phe	Leu	Leu
				245					250					255	
Pro	Phe	Ser	Asn	Gln	Leu	Tyr	Gly	Ser	Glu	Gly	Ala	Tyr	Ala	Ser	Ile
			260					265					270		
Leu	Thr	Met	Gly	Ala	Ile	Gly	Ser	Ile	Ile	Gly	Ala	Leu	Leu	Ala	Ser
		275				280						285			
Lys	Ile	Lys	Ala	Asn	Ile	Tyr	Asn	Leu	Leu	Ile	Leu	Leu	Ala	Leu	Thr
		290				295					300				
Gly	Val	Gly	Val	Phe	Met	Met	Gly	Leu	Pro	Leu	Pro	Thr	Phe	Leu	Ser
305					310				315						320
Phe	Ser	Gly	Asn	Leu	Val	Cys	Glu	Leu	Phe	Met	Thr	Ile	Phe	Asn	Ile
			325						330					335	
His	Phe	Phe	Thr	Gln	Val	Gln	Thr	Lys	Val	Glu	Ser	Glu	Phe	Leu	Gly
			340					345					350		
Arg	Val	Leu	Ser	Thr	Ile	Phe	Thr	Leu	Ala	Ile	Leu	Phe	Met	Pro	Ile
		355					360					365			
Ala	Lys	Gly	Phe	Met	Thr	Val	Leu	Pro	Ser	Val	His	Leu	Ser	Ser	Phe
		370				375					380				
Leu	Ile	Ile	Gly	Ser	Gly	Val	Ile	Ile	Leu	Ser	Cys	Ile	Ser	Phe	Ile
385					390				395						400
Tyr	Val	Arg	Thr	His	Phe	Glu	Lys	Leu	Ile						
			405					410							

(2) INFORMATION FOR SEQ ID NO:5136:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 75 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5136:

```
Ile Tyr Pro Leu Gly Phe Ser Val Pro Ile Ile Arg Val Lys Thr Ala
1          5          10          15
Ile Pro Thr Pro Glu Lys Thr Lys Pro Ala Met Ala Gly Arg Lys Cys
          20          25          30
Ser Pro Asp Arg Ala Pro Arg Glu Gly Gly Lys Ile Lys Phe Pro Ala
          35          40          45
Pro Lys Asn Ile Pro Asn Arg Ser Lys Pro Val Arg Val Pro Phe Leu
          50          55          60
Ala Ile Lys Ile Ser Phe Ile Phe Ile Lys Tyr
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:5137:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 81 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...81

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5137:

```
Cys Leu Gln Leu Ile Lys Ile Cys Phe Phe Arg Val Val Ile Ser Glu
1          5          10          15
Cys Asn Ile Phe Pro Ile Cys Arg Thr Phe Ile His Thr Lys Arg Ser
          20          25          30
Ile Ile Trp Thr Thr Leu Tyr Ser Gly Leu Thr Ile Phe Ser Lys Lys
          35          40          45
Ile Met Phe Glu Ala Ile Lys Tyr Ile Pro Lys Ile Ser Thr Leu Asp
          50          55          60
Tyr Ile Phe Val Leu Asp Pro Ser Ala Lys Ser Asn Phe Leu Val Gln
65          70          75          80
Pro
```

(2) INFORMATION FOR SEQ ID NO:5138:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 76 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...76

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5138:

```
Met Val Gln Leu Leu Phe Thr Leu Ser Ser His Met Leu Phe Ile Tyr
1          5          10          15
Val Ser Phe Tyr Leu Leu Lys Asp Leu Val Arg Trp Glu Lys Val Leu
20          25          30
Lys Val Thr Asp Glu Asn Thr Arg Lys Val Arg Leu Leu Val Ala Phe
35          40          45
Phe Ser Ile Val Ile Gly Tyr Ile Leu Ser Ser Phe Phe Ile Ser Leu
50          55          60
Tyr His Leu Trp Gln Glu Ala Leu Arg Gly Leu Leu
65          70          75
```

(2) INFORMATION FOR SEQ ID NO:5139:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5139:

```
Met Ala Gln Leu Thr Ile Asn Gly Val Ala Val Lys Pro Pro Lys Ser
1          5          10          15
Phe Gln Val Gly Ile Gln Asp Ile Asp Gly Glu Thr Gly Arg Asn Ala
20          25          30
Asn Gly Asp Met Val Arg Asp Arg Ile Thr Thr Lys Arg Lys Leu Asp
35          40          45
Cys Glu Trp Gly Met Met Thr Gln Gly Glu Ile Ser Gln Leu Leu His
50          55          60
```

Ala	Val	Ser	Ser	Lys	Phe	Phe	Glu	Val	Ser	Tyr	Pro	Asp	Pro	Met	Asp
65					70				75					80	
Gly	Gln	Val	Thr	Lys	Thr	Phe	Tyr	Val	Gly	Asp	Arg	Thr	Ala	Pro	Ser
				85				90					95		
Tyr	Thr	Phe	Thr	Glu	Lys	Leu	Lys	Pro	Trp	Ser	Gly	Ala	Lys	Phe	Asn
			100					105					110		
Leu	Val	Glu	Arg												
			115												

(2) INFORMATION FOR SEQ ID NO:5140:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 67 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...67
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5140:

Lys	Lys	Gln	Leu	Met	Arg	Ser	Gly	Arg	Asp	Lys	Lys	Ile	Ala	Gly	Val
1			5				10		15						
Cys	Ala	Gly	Val	Ala	His	Tyr	Leu	Asp	Met	Asp	Pro	Thr	Ile	Val	Gln
			20				25					30			
Val	Ile	Trp	Gly	Val	Leu	Thr	Cys	Cys	Tyr	Gly	Ser	Gly	Ile	Val	Ala
		35				40					45				
Tyr	Ile	Ile	Leu	Trp	Ile	Ile	Ala	Pro	Val	Ala	Thr	Val	Phe	Thr	Thr
	50				55						60				
Gly	Phe	His													
65															

(2) INFORMATION FOR SEQ ID NO:5141:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 582 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...582

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5141:

Leu	Leu	Gln	Phe	Val	Val	Lys	Thr	Thr	Ala	Arg	Ile	Arg	Asn	Asn	Leu	1	5	10	15
Ser	Arg	Trp	Val	Gly	Arg	Arg	Arg	Asp	Leu	Gly	Gly	Leu	Ile	Phe	Ile	20	25	30	
Asp	Leu	Arg	Asp	Arg	Glu	Gly	Ile	Met	Gln	Leu	Val	Ile	Asn	Pro	Glu	35	40	45	
Lys	Val	Ser	Ala	Glu	Val	Met	Ala	Thr	Ala	Glu	Ser	Leu	Arg	Ser	Glu	50	55	60	
Phe	Val	Ile	Glu	Val	Thr	Gly	Gln	Val	Ala	Ala	Arg	Glu	Gln	Ala	Asn	65	70	75	80
Asp	Lys	Leu	Pro	Thr	Gly	Ala	Val	Glu	Leu	Asn	Val	Thr	Ala	Leu	Ile	85	90	95	
Val	Leu	Asn	Thr	Ala	Lys	Thr	Thr	Pro	Phe	Glu	Ile	Lys	Asp	Gly	Ile	100	105	110	
Glu	Ala	Asn	Asp	Asp	Thr	Arg	Leu	Arg	Tyr	Arg	Tyr	Leu	Asp	Leu	Arg	115	120	125	
Arg	Pro	Glu	Met	Leu	Glu	Asn	Leu	Lys	Leu	Arg	Ala	Lys	Val	Thr	His	130	135	140	
Ser	Ile	Arg	Asn	Tyr	Leu	Asp	Glu	Leu	Glu	Phe	Ile	Asp	Val	Glu	Thr	145	150	155	160
Pro	Phe	Leu	Ser	Lys	Ser	Thr	Pro	Glu	Gly	Ala	Arg	Asp	Tyr	Leu	Val	165	170	175	
Pro	Ser	Arg	Val	Asn	Lys	Gly	His	Phe	Tyr	Ala	Leu	Pro	Gln	Ser	Pro	180	185	190	
Gln	Ile	Thr	Lys	Gln	Leu	Leu	Met	Asn	Ala	Gly	Phe	Asp	Arg	Tyr	Tyr	195	200	205	
Gln	Ile	Val	Lys	Cys	Phe	Arg	Asp	Glu	Asp	Leu	Arg	Gly	Asp	Arg	Gln	210	215	220	
Pro	Glu	Phe	Thr	Gln	Val	Asp	Leu	Glu	Thr	Ser	Phe	Leu	Thr	Glu	Gln	225	230	235	240
Glu	Ile	Gln	Asp	Ile	Thr	Glu	Gly	Leu	Ile	Ala	Arg	Val	Met	Lys	Glu	245	250	255	
Thr	Lys	Gly	Ile	Glu	Val	Thr	Leu	Pro	Phe	Pro	Arg	Met	Lys	Tyr	Asp	260	265	270	
Asp	Ala	Met	Ala	Leu	Tyr	Gly	Ser	Asp	Lys	Pro	Asp	Thr	Arg	Phe	Asp	275	280	285	
Met	Leu	Leu	Gln	Asp	Leu	Thr	Glu	Val	Val	Lys	Gly	Val	Asp	Phe	Lys	290	295	300	
Val	Phe	Ser	Glu	Ala	Pro	Ala	Val	Lys	Ala	Ile	Val	Val	Lys	Glu	Ala	305	310	315	320
Ala	Asp	Asn	Tyr	Ser	Arg	Lys	Asp	Ile	Asp	Lys	Met	Thr	Glu	Val	Ala	325	330	335	
Lys	Gln	Tyr	Gly	Ala	Lys	Gly	Leu	Ala	Trp	Val	Lys	Val	Val	Asp	Gly	340	345	350	
Glu	Leu	Asn	Gly	Pro	Val	Ala	Lys	Phe	Leu	Thr	Gly	Ile	Gln	Glu	Glu	355	360	365	
Leu	Thr	Thr	Ala	Leu	Ala	Leu	Glu	Asp	Lys	Asp	Leu	Val	Leu	Phe	Val	370	375	380	
Ala	Asp	Thr	Leu	Glu	Val	Ala	Asn	Ala	Thr	Leu	Gly	Ala	Leu	Arg	Gly	385	390	395	400
Arg	Ile	Ala	Lys	Glu	Leu	Gly	Leu	Ile	Asp	Asn	Asp	Lys	Phe	Asn	Phe	405	410	415	
Leu	Trp	Val	Val	Asp	Trp	Pro	Met	Phe	Glu	Trp	Ser	Glu	Glu	Glu	Gly	420	425	430	

Arg	Tyr	Met	Ser	Ala	His	His	Pro	Phe	Thr	Leu	Pro	Gln	Glu	Glu	Thr
		435					440					445			
Val	His	Glu	Leu	Glu	Gly	Asp	Leu	Ala	Lys	Val	Arg	Ala	Ile	Ala	Tyr
	450					455				460					
Asp	Ile	Val	Leu	Asn	Gly	Tyr	Glu	Leu	Gly	Gly	Gly	Ser	Leu	Arg	Ile
465				470					475					480	
Asn	Gln	Lys	Asp	Leu	Gln	Glu	Arg	Met	Phe	Lys	Ala	Leu	Gly	Phe	Ser
			485						490					495	
Thr	Glu	Glu	Ala	Asn	Asp	Gln	Phe	Gly	Phe	Leu	Leu	Glu	Ala	Met	Asp
			500					505					510		
Tyr	Gly	Phe	Pro	Pro	His	Gly	Gly	Leu	Ala	Ile	Gly	Leu	Asp	Arg	Phe
	515					520						525			
Val	Met	Leu	Leu	Ala	Gly	Glu	Glu	Asn	Ile	Arg	Glu	Val	Ile	Ala	Phe
	530				535					540					
Pro	Lys	Asn	Asn	Lys	Ala	Thr	Asp	Pro	Met	Thr	Gln	Ala	Pro	Ser	Thr
545				550					555					560	
Val	Ala	Leu	Lys	Gln	Leu	Glu	Glu	Leu	Ser	Leu	Gln	Val	Glu	Glu	Asp
			565					570						575	
Glu	Thr	Asn	Lys	Thr	Asn										
			580												

(2) INFORMATION FOR SEQ ID NO:5142:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 437 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...437

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5142:

Pro	Met	Phe	Phe	Lys	Leu	Leu	Arg	Glu	Ala	Leu	Lys	Val	Lys	Gln	Val
1				5					10					15	
Arg	Ser	Lys	Ile	Leu	Phe	Thr	Ile	Phe	Ile	Val	Leu	Val	Phe	Arg	Ile
			20					25					30		
Gly	Thr	Ser	Ile	Thr	Val	Pro	Gly	Val	Asn	Ala	Asn	Ser	Leu	Asn	Ala
		35					40					45			
Leu	Ser	Gly	Leu	Ser	Phe	Leu	Asn	Met	Leu	Ser	Leu	Val	Ser	Gly	Asn
	50				55						60				
Ala	Leu	Lys	Asn	Phe	Ser	Ile	Phe	Ala	Leu	Gly	Val	Ser	Pro	Tyr	Ile
65				70					75					80	
Thr	Ala	Ser	Ile	Val	Val	Gln	Leu	Leu	Gln	Met	Asp	Ile	Leu	Pro	Lys
			85					90					95		
Phe	Val	Glu	Trp	Gly	Lys	Gln	Gly	Glu	Val	Gly	Arg	Arg	Lys	Leu	Asn
		100					105					110			
Gln	Ala	Thr	Arg	Tyr	Ile	Ala	Leu	Val	Leu	Ala	Phe	Val	Gln	Ser	Ile
		115					120					125			

Gly	Ile	Thr	Ala	Gly	Phe	Asn	Thr	Leu	Ala	Gly	Ala	Gln	Leu	Ile	Lys
130						135					140				
Thr	Ala	Leu	Thr	Pro	Gln	Val	Phe	Leu	Thr	Ile	Gly	Ile	Ile	Leu	Thr
145					150					155					160
Ala	Gly	Ser	Met	Ile	Val	Thr	Trp	Leu	Gly	Glu	Gln	Ile	Thr	Asp	Lys
				165					170					175	
Gly	Tyr	Gly	Asn	Gly	Val	Ser	Met	Ile	Ile	Phe	Ala	Gly	Ile	Val	Ser
			180					185					190		
Ser	Ile	Pro	Glu	Met	Ile	Gln	Gly	Ile	Tyr	Val	Asp	Tyr	Phe	Val	Asn
		195					200				205				
Val	Pro	Ser	Ser	Arg	Ile	Thr	Ser	Ser	Ile	Ile	Phe	Val	Ile	Ile	Leu
	210					215					220				
Ile	Ile	Thr	Val	Leu	Leu	Ile	Ile	Tyr	Phe	Thr	Thr	Tyr	Val	Gln	Gln
225				230						235					240
Ala	Glu	Tyr	Lys	Ile	Pro	Ile	Gln	Tyr	Thr	Lys	Val	Ala	Gln	Gly	Ala
			245						250					255	
Pro	Ser	Ser	Ser	Tyr	Leu	Pro	Leu	Lys	Val	Asn	Pro	Ala	Gly	Val	Ile
			260					265				270			
Pro	Val	Ile	Phe	Ala	Ser	Ser	Ile	Thr	Ala	Ala	Pro	Ala	Ala	Ile	Leu
	275						280				285				
Gln	Phe	Leu	Ser	Ala	Thr	Gly	His	Asp	Trp	Ala	Trp	Val	Arg	Val	Ala
	290					295					300				
Gln	Glu	Met	Leu	Ala	Thr	Ser	Pro	Thr	Gly	Ile	Ala	Met	Tyr	Ala	
305				310					315					320	
Leu	Leu	Ile	Ile	Leu	Phe	Thr	Phe	Phe	Tyr	Thr	Phe	Val	Gln	Ile	Asn
			325						330					335	
Pro	Glu	Lys	Ala	Ala	Glu	Ser	Leu	Gln	Lys	Ser	Gly	Ala	Tyr	Ile	His
		340						345					350		
Gly	Val	Arg	Pro	Gly	Lys	Gly	Thr	Glu	Glu	Tyr	Met	Ser	Lys	Leu	Leu
	355						360				365				
Arg	Arg	Leu	Ala	Thr	Val	Gly	Ser	Leu	Phe	Leu	Gly	Val	Ile	Ser	Ile
	370					375					380				
Leu	Pro	Ile	Ala	Ala	Lys	Asp	Val	Phe	Gly	Leu	Ser	Asp	Val	Val	Ala
385				390					395						400
Phe	Gly	Gly	Thr	Ser	Leu	Leu	Ile	Ile	Ile	Ser	Thr	Gly	Ile	Glu	Gly
			405						410					415	
Ile	Lys	Gln	Leu	Glu	Gly	Tyr	Leu	Leu	Lys	Arg	Lys	Tyr	Val	Gly	Phe
		420						425					430		
Met	Asp	Arg	Thr	Glu											
		435													

(2) INFORMATION FOR SEQ ID NO:5143:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 778 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature

(B) LOCATION 1...778

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5143:

Gln	Phe	Pro	Phe	Cys	Phe	Phe	Phe	Asp	Ile	Ile	Thr	Leu	Thr	Val	Ile
1				5					10					15	
Leu	Tyr	Gly	Gly	Ser	Met	Arg	Phe	Asn	Gln	Tyr	Ser	Tyr	Ile	Asn	Phe
			20					25					30		
Pro	Lys	Glu	Asn	Val	Leu	Ser	Glu	Leu	Lys	Lys	Cys	Gly	Phe	Asp	Leu
		35					40					45			
Gln	Asn	Thr	Ala	Asn	His	Lys	Asp	Ser	Leu	Glu	Thr	Phe	Leu	Arg	Arg
	50					55					60				
Phe	Phe	Phe	Thr	Tyr	Gln	Asp	Thr	Asn	Tyr	Pro	Leu	Ser	Ile	Leu	Ala
65					70				75						80
Ala	Asp	Lys	Lys	Thr	Asp	Leu	Leu	Thr	Phe	Phe	Gln	Ser	Glu	Asp	Glu
				85					90					95	
Leu	Thr	Ala	Asp	Ile	Phe	Tyr	Thr	Val	Ala	Phe	Gln	Leu	Leu	Gly	Phe
			100					105					110		
Ser	Tyr	Leu	Val	Asp	Phe	Glu	Asp	Ser	Asp	Val	Phe	Arg	Lys	Glu	Thr
	115						120					125			
Gly	Phe	Pro	Ile	Ile	Tyr	Gly	Asp	Leu	Ile	Glu	Asn	Leu	Tyr	Gln	Leu
	130					135					140				
Leu	Asn	Thr	Arg	Thr	Lys	Lys	Gly	Asn	Thr	Leu	Ile	Asp	Gln	Leu	Val
145					150					155					160
Ser	Asp	Gly	Leu	Ile	Pro	Glu	Asp	Asn	Asp	Tyr	His	Tyr	Phe	Asn	Gly
			165					170						175	
Lys	Ser	Leu	Ala	Thr	Phe	Ser	Asn	Gln	Asp	Val	Ile	Arg	Glu	Val	Val
		180						185					190		
Tyr	Val	Glu	Ser	Arg	Val	Asp	Thr	Asp	Gln	Lys	Gly	Leu	Ser	Asp	Leu
	195						200					205			
Val	Lys	Val	Ser	Ile	Ile	Arg	Pro	Arg	Phe	Asp	Gly	Lys	Ile	Pro	Ala
	210					215					220				
Ile	Met	Thr	Ala	Ser	Pro	Tyr	His	Gln	Gly	Thr	Asn	Asp	Lys	Ala	Ser
225					230					235					240
Asp	Lys	Ala	Leu	Tyr	Lys	Met	Glu	Gly	Glu	Leu	Glu	Val	Lys	Leu	Pro
			245					250						255	
His	Lys	Ile	Glu	Leu	Glu	Lys	Pro	Gln	Leu	Asn	Leu	Val	Gln	Pro	Gln
		260						265					270		
Gly	Lys	Ala	Glu	Leu	Ile	Ala	Glu	Ala	Glu	Glu	Lys	Leu	Thr	His	Ile
	275						280					285			
Asn	Ser	Ser	Tyr	Thr	Leu	Asn	Asp	Tyr	Phe	Leu	Pro	Arg	Gly	Phe	Ala
	290					295					300				
Asn	Leu	Tyr	Val	Ser	Gly	Val	Gly	Thr	Lys	Asp	Ser	Thr	Gly	Phe	Met
305					310					315					320
Thr	Asn	Gly	Asp	Tyr	Gln	Gln	Ile	Glu	Ala	Tyr	Lys	Asn	Val	Ile	Asp
			325						330					335	
Trp	Leu	Asn	Gly	Arg	Cys	Arg	Ala	Phe	Thr	Asp	His	Thr	Arg	Gln	Arg
		340						345					350		
Gln	Val	Lys	Ala	Asp	Trp	Ser	Asn	Gly	Lys	Val	Ala	Thr	Thr	Gly	Leu
	355						360					365			
Ser	Tyr	Leu	Gly	Thr	Met	Ser	Asn	Gly	Leu	Ala	Thr	Thr	Gly	Val	Asp
	370					375					380				
Gly	Leu	Glu	Val	Ile	Ile	Ala	Glu	Ala	Gly	Ile	Ser	Ser	Trp	Tyr	Asn
385					390					395					400
Tyr	Tyr	Arg	Glu	Asn	Gly	Leu	Val	Thr	Ser	Pro	Gly	Gly	Tyr	Pro	Gly
			405						410					415	
Glu	Asp	Phe	Asp	Ser	Leu	Ala	Glu	Leu	Thr	Tyr	Ser	Arg	Asn	Leu	Leu

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...246

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5144:

```
Asp Pro Lys Phe Gln Ile Leu Asp Ile Ile Asn Lys Asp Thr Gln Gln
1          5          10          15
Gly Ile Phe Gly Lys Leu Asp Tyr Glu Ala Pro Ser Cys Pro Glu Cys
          20          25          30

Gly Ser Gln Met Lys Lys Tyr Tyr Phe Gln Lys Pro Ser Lys Ile Pro
          35          40          45
Tyr Leu Glu Thr Thr Gly Met Pro Thr Arg Ile Leu Leu Arg Lys Arg
          50          55          60
Arg Phe Lys Cys Tyr His Cys Ser Lys Ile Met Val Ala Glu Thr Ser
65          70          75          80
Ile Val Lys Lys Asn His Gln Ile Pro Arg Ile Ile Asn Gln Lys Ile
          85          90          95
Ala Gln Lys Leu Ile Glu Lys Ile Ser Met Thr Asp Ile Ala His Gln
          100          105          110
Leu Ser Ile Ser Thr Ser Thr Val Ile Arg Lys Leu Asn Asp Phe His
          115          120          125
Phe Lys His Asp Phe Ser Cys Leu Ser Glu Ile Met Ser Trp Asp Glu
          130          135          140
Tyr Ala Phe Thr Lys Gly Lys Met Ser Phe Ile Ala Gln Asp Phe Asn
145          150          155          160
Lys Leu Asn Ile Ile Thr Val Leu Glu Gly Arg Thr Gln Ala Ile Ile
          165          170          175
Arg Asn His Phe Leu Arg Tyr Asp Arg Val Val Arg Cys Arg Val Lys
          180          185          190
Ile Ile Thr Met Asp Met Phe Ser Pro Tyr Tyr Asp Leu Ala Lys Gln
          195          200          205
Leu Arg Phe Gln Ile Ser Arg Leu Arg Leu Lys Gln Ser Pro Arg Leu
          210          215          220
Phe His Ser Arg Met Leu Lys Ser Cys Trp Ile Ala Phe Thr Leu Tyr
225          230          235          240
Asn Ile Leu Ala Val Leu
          245
```

(2) INFORMATION FOR SEQ ID NO:5145:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 203 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...203

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5145:

```
Tyr Thr Lys Leu Leu Glu Ala Asn Pro Gln Tyr Val Val Leu Asn Pro
1          5          10          15
Leu Glu Ala Lys Ala Lys Trp Arg Asp Leu Phe Gly Asn Asp Asn Pro
          20          25          30
Ile His Val Glu Val Gly Ser Gly Lys Gly Ala Phe Val Ser Gly Met
          35          40          45
Ala Lys Gln Asn Pro Asp Ile Asn Tyr Ile Gly Ile Asp Ile Gln Lys
          50          55          60
Ser Val Leu Ser Tyr Ala Leu Asp Lys Val Leu Glu Val Gly Val Pro
65          70          75          80
Asn Ile Lys Leu Leu Trp Val Asp Gly Ser Asp Leu Thr Asp Tyr Phe
          85          90          95
Glu Asp Gly Glu Ile Asp Arg Leu Tyr Leu Asn Phe Ser Asp Pro Trp
          100          105          110
Pro Lys Lys Arg His Glu Lys Arg Arg Leu Thr Tyr Lys Thr Phe Leu
          115          120          125
Asp Thr Phe Lys Arg Ile Leu Pro Glu Asn Gly Glu Ile His Phe Lys
130          135          140
Thr Asp Asn Arg Gly Leu Phe Glu Tyr Ser Leu Val Ser Phe Ser Gln
145          150          155          160
Tyr Gly Met Lys Leu Asn Gly Val Trp Leu Asp Leu His Ala Ser Asp
          165          170          175
Phe Glu Gly Asn Val Met Thr Glu Tyr Glu Gln Lys Phe Ser Asn Lys
          180          185          190
Gly Gln Val Ile Tyr Arg Val Glu Ala Glu Phe
          195          200
```

(2) INFORMATION FOR SEQ ID NO:5146:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 111 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...111

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5146:

```
Tyr Asn Lys Phe Glu Val Ile Phe Lys Glu Asn Gln Met Ile Tyr Glu
1          5          10          15
Phe Cys Ala Glu Asn Val Thr Leu Leu Glu Lys Ala Met Gln Ala Gly
```

		20					25				30				
Ala	Arg	Arg	Ile	Glu	Leu	Cys	Asp	Asn	Leu	Ala	Val	Gly	Gly	Thr	Thr
		35					40					45			
Pro	Ser	Tyr	Gly	Val	Thr	Lys	Ala	Ala	Val	Glu	Leu	Ala	Ala	Asn	Tyr
		50				55						60			
Asp	Thr	Thr	Ile	Met	Thr	Met	Ile	Arg	Pro	Arg	Gly	Gly	Asp	Phe	Val
65					70					75					80
Tyr	Asn	Asp	Leu	Glu	Ile	Ala	Ile	Met	Leu	Glu	Asp	Ile	Cys	Leu	Thr
			85						90				95		
Ala	Gln	Ala	Trp	Lys	Ser	Arg	Gly	Cys	Ile	Trp	Ser	Phe	Asn	Cys	
			100					105					110		

(2) INFORMATION FOR SEQ ID NO:5147:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 189 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...189

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5147:

Met	Thr	Lys	Leu	Leu	Val	Gly	Leu	Gly	Asn	Pro	Gly	Asp	Lys	Tyr	Phe
1			5						10					15	
Glu	Thr	Lys	His	Asn	Val	Gly	Phe	Met	Leu	Ile	Asp	Gln	Leu	Ala	Lys
			20					25				30			
Lys	Gln	Asn	Val	Thr	Phe	Thr	His	Asp	Lys	Ile	Phe	Gln	Ala	Asp	Leu
		35				40					45				
Ala	Ser	Phe	Phe	Leu	Asn	Gly	Glu	Lys	Ile	Tyr	Leu	Val	Lys	Pro	Thr
	50				55				60						
Thr	Phe	Met	Asn	Glu	Ser	Gly	Lys	Ala	Val	His	Ala	Leu	Leu	Thr	Tyr
65				70					75						80
Tyr	Gly	Leu	Asp	Ile	Asp	Asp	Leu	Leu	Ile	Ile	Tyr	Asp	Asp	Leu	Asp
			85					90					95		
Met	Glu	Val	Gly	Lys	Ile	Arg	Leu	Arg	Ala	Lys	Gly	Ser	Ala	Gly	Gly
			100					105					110		
His	Asn	Gly	Ile	Lys	Ser	Ile	Ile	Gln	His	Ile	Gly	Thr	Gln	Val	Phe
		115					120					125			
Asn	Arg	Val	Lys	Ile	Gly	Ile	Gly	Arg	Pro	Lys	Asn	Gly	Met	Ser	Val
	130				135						140				
Val	His	His	Val	Leu	Ser	Lys	Phe	Asp	Arg	Asp	Glu	Tyr	Ile	Gly	Ile
145				150					155						160
Leu	Gln	Ser	Val	Asp	Lys	Val	Asp	Asp	Ser	Val	Asn	Tyr	Tyr	Leu	Gln
			165					170						175	
Glu	Lys	Asn	Phe	Glu	Lys	Thr	Met	Gln	Arg	Tyr	Asn	Gly			
			180					185							

(2) INFORMATION FOR SEQ ID NO:5148:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 132 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...132
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5148:

Ile	Phe	Phe	Ser	Leu	Ser	Pro	Thr	Pro	Thr	Pro	Ile	Pro	Xaa	Ser	Ser
1				5					10					15	
Phe	Leu	Ser	Pro	Ser	Gln	Pro	Pro	Pro	Xaa	Pro	Xaa	Phe	Ser	Phe	Pro
			20					25					30		
Leu	Phe	Pro	Xaa	Thr	Ser	Xaa	Asn	Thr	Leu	Phe	Phe	Leu	Leu	Phe	Pro
			35				40					45			
Pro	Pro	Xaa	Xaa	Thr	Pro	Pro	Ser	Ser	Ser	Phe	Pro	Ser	Leu	Pro	Xaa
			50				55				60				
Phe	Ser	Pro	Pro	Phe	Xaa	Phe	Pro	Ser	Phe	Phe	Xaa	Phe	Pro	Phe	Xaa
65					70				75					80	
Xaa	Xaa	Xaa	Xaa	Phe	Phe	Phe	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Tyr	Xaa	Xaa
				85					90					95	
Xaa	Pro	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Tyr
			100					105					110		
Ser	Met	Lys	Ile	Lys	Glu	Gln	Thr	Arg	Lys	Leu	Ala	Ala	Gly	Cys	Ser
		115					120					125			
Lys	His	Cys	Phe												
															130

(2) INFORMATION FOR SEQ ID NO:5149:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 657 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...657

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5149:

Met	Lys	Lys	Phe	Tyr	Val	Ser	Pro	Ile	Phe	Pro	Ile	Leu	Val	Gly	Leu
1				5					10					15	
Ile	Ala	Phe	Gly	Val	Leu	Ser	Thr	Phe	Ile	Ile	Phe	Val	Asn	Asn	Asn
			20					25					30		
Leu	Leu	Thr	Val	Leu	Ile	Leu	Phe	Leu	Phe	Val	Gly	Gly	Tyr	Val	Phe
		35					40					45			
Leu	Phe	Lys	Lys	Leu	Arg	Val	His	Tyr	Thr	Arg	Ser	Asp	Val	Glu	Gln
	50					55					60				
Ile	Gln	Tyr	Val	Asn	His	Gln	Ala	Glu	Glu	Ser	Leu	Thr	Ser	Leu	Leu
65					70					75					80
Glu	Gln	Met	Pro	Val	Gly	Val	Met	Lys	Leu	Asn	Leu	Ser	Ser	Gly	Glu
				85					90					95	
Val	Glu	Trp	Phe	Asn	Pro	Tyr	Ala	Glu	Leu	Ile	Leu	Thr	Lys	Glu	Asp
			100					105					110		
Gly	Asp	Phe	Asp	Leu	Glu	Ala	Val	Gln	Thr	Ile	Ile	Lys	Ala	Ser	Val
	115						120					125			
Gly	Asn	Pro	Ser	Thr	Tyr	Ala	Lys	Leu	Gly	Glu	Lys	Arg	Tyr	Ala	Val
	130					135					140				
His	Met	Asp	Ala	Ser	Ser	Gly	Val	Leu	Tyr	Phe	Val	Asp	Val	Ser	Arg
145					150					155					160
Glu	Gln	Ala	Ile	Thr	Asp	Glu	Leu	Val	Thr	Ser	Arg	Pro	Val	Ile	Gly
				165					170					175	
Ile	Val	Ser	Val	Asp	Asn	Tyr	Asp	Asp	Leu	Glu	Asp	Ala	Thr	Ser	Glu
			180					185					190		
Ser	Asp	Ile	Ser	Gln	Ile	Asn	Ser	Phe	Val	Ala	Asn	Phe	Ile	Ser	Glu
	195					200						205			
Phe	Ser	Glu	Lys	Tyr	Met	Met	Phe	Ser	Arg	Arg	Val	Ser	Met	Asp	Arg
	210					215					220				
Phe	Tyr	Leu	Phe	Thr	Asp	Tyr	Thr	Val	Leu	Glu	Gly	Leu	Met	Asn	Asp
225					230					235					240
Lys	Phe	Ser	Val	Ile	Asp	Ala	Phe	Arg	Glu	Glu	Ser	Lys	Gln	Arg	Gln
				245					250				255		
Leu	Pro	Leu	Thr	Leu	Ser	Met	Gly	Phe	Ser	Tyr	Gly	Asp	Gly	Asn	His
			260				265						270		
Asp	Glu	Ile	Gly	Lys	Val	Ala	Leu	Leu	Asn	Leu	Asn	Leu	Ala	Glu	Val
	275						280					285			
Arg	Gly	Gly	Asp	Gln	Val	Val	Val	Lys	Glu	Asn	Asp	Glu	Thr	Lys	Asn
	290					295					300				
Pro	Val	Tyr	Phe	Gly	Gly	Gly	Ser	Ala	Ala	Ser	Ile	Lys	Arg	Thr	Arg
305					310					315					320
Thr	Arg	Thr	Arg	Ala	Met	Met	Thr	Ala	Ile	Ser	Asp	Lys	Ile	Arg	Ser
				325					330				335		
Val	Asp	Gln	Val	Phe	Val	Val	Gly	His	Lys	Asn	Leu	Asp	Met	Asp	Ala
			340					345					350		
Leu	Gly	Ser	Ala	Val	Gly	Met	Gln	Leu	Phe	Ala	Ser	Asn	Val	Ile	Glu
	355						360					365			
Asn	Ser	Tyr	Ala	Leu	Tyr	Asp	Glu	Glu	Gln	Met	Ser	Pro	Asp	Ile	Glu
	370					375					380				
Arg	Ala	Val	Ser	Phe	Ile	Glu	Lys	Glu	Gly	Val	Thr	Lys	Leu	Leu	Ser
385					390					395					400
Val	Lys	Asp	Ala	Met	Gly	Met	Val	Thr	Asn	Arg	Ser	Leu	Leu	Ile	Leu
				405					410					415	
Val	Asp	His	Ser	Lys	Thr	Ala	Leu	Thr	Leu	Ser	Lys	Glu	Phe	Tyr	Asp
			420					425					430		
Leu	Phe	Thr	Gln	Thr	Ile	Val	Ile	Asp	His	His	Arg	Arg	Asp	Gln	Asp

50		55		60	
Lys	Ile	Gly	Thr	Thr	Ile
65					70
Arg	Ser	Leu	Glu	Gln	Asn
					85
Val	Ser	Gln	Gly	Asn	Tyr
					100
Asn	Leu	Trp	Gln	Glu	Glu
					115
Phe	Tyr	Arg	Phe	Tyr	Gln
					130
Val	Gln	Ser	Ser	Ser	Leu
145					150
Ile	Gln	Gln	Tyr	Gln	Leu
					165
Arg	Asn	Phe	Leu	Lys	Ser
					180
Lys	Lys	Val	Ile	Leu	Met
					195
Asn	Gln	Leu	Leu	Gly	Lys
					210
Glu	Gln	Gln	Lys	Arg	Thr
225					230
Tyr	Glu	Gly	Asp	Trp	Ser
					245
Asn	Leu	Ser	Asn	Pro	Ile
					260
Trp	Asp	Glu	Lys	Ala	Ser
					275
Lys	Ile	Glu	Asn	Thr	Val
					290
Glu	Lys	Leu	Ser	Asp	Gly
305					310
Ile	Gln	Gln	Glu	Lys	Val
					325
Asn	Leu	Leu	Phe	Ala	Leu
					340
Phe	Leu	Leu	Val	Thr	Thr
					355
Lys	Lys	Phe	Met	Gly	Trp
					370
Val	Leu	Leu	Leu	Leu	Gly
385					390
Phe	Ala	His	Ala	Phe	Leu
					405
Leu	Asp	Ile	Leu	Phe	Val
					420
Ser	Leu	Val	Glu	Leu	Leu
					435
					440

(2) INFORMATION FOR SEQ ID NO:5151:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 128 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...128
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5151:

```

Leu Ser Phe Ser Ile Thr Asp Ile Lys Asp Ile Tyr Trp Phe Ile Arg
1          5          10          15
Lys Val Ser Asp Lys Leu Ala Ser Thr Leu His Leu Asn Gly Asp Ser
          20          25          30
Met Lys Lys Phe Ser Leu Leu Leu Ala Ile Leu Pro Phe Leu Val Ala
          35          40          45
Cys Glu Asn Gln Ala Thr Pro Lys Glu Thr Ser Ala Gln Lys Thr Ile
          50          55          60
Val Leu Ala Thr Ala Gly Asp Ser Ala Pro Phe Asp Tyr Glu Asp Lys
65          70          75          80
Gly Asn Leu Thr Gly Phe Asp Ile Glu Val Leu Lys Ala Val Asp Glu
          85          90          95
Lys Leu Ser Asp Tyr Glu Ile Gln Phe Gln Arg Thr Ala Trp Glu Ser
          100          105          110
Ile Phe Pro Gly Leu Asp Ser Gly His Tyr Gln Ala Ala Ala Ile Thr
          115          120          125

```

(2) INFORMATION FOR SEQ ID NO:5152:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 182 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...182
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5152:

```

Gly Asp Phe Ser Phe Trp Arg Phe Val Met Lys Thr Lys Glu Val Val
1          5          10          15
Asp Glu Leu Thr Val Lys Arg Ala Ile Thr Arg Ile Thr Tyr Glu Ile
          20          25          30
Ile Glu Arg Asn Lys Asp Leu Asn Lys Ile Val Leu Ala Gly Ile Lys
          35          40          45
Thr Arg Gly Val Phe Ile Ala His Arg Ile Gln Glu Arg Leu Lys Gln

```

50		55		60											
Leu	Glu	Asn	Leu	Ser	Val	Pro	Val	Val	Glu	Leu	Asp	Thr	Lys	Pro	Phe
65		70		75		80									
Arg	Asp	Asp	Val	Lys	Ser	Gly	Glu	Asp	Thr	Ser	Leu	Val	Ser	Val	Asp
		85		90		95									
Val	Thr	Asp	Arg	Glu	Val	Ile	Leu	Val	Asp	Asp	Val	Leu	Tyr	Thr	Gly
		100		105		110									
Arg	Thr	Ile	Arg	Ala	Ala	Ile	Asp	Asn	Ile	Val	Gly	His	Gly	Arg	Pro
		115		120		125									
Ala	Arg	Val	Ser	Leu	Ala	Val	Leu	Val	Asp	Arg	Gly	His	Arg	Glu	Leu
		130		135		140									
Pro	Ile	Arg	Pro	Asp	Tyr	Val	Gly	Lys	Asn	Ile	Pro	Thr	Ser	Arg	Ser
145		150		155		160									
Glu	Glu	Ile	Ile	Val	Glu	Met	Thr	Glu	Leu	Asp	Asp	Gln	Asp	Arg	Val
		165		170		175									
Leu	Ile	Thr	Glu	Glu	Ala										
		180													

(2) INFORMATION FOR SEQ ID NO:5153:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 404 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...404

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5153:

Arg	Leu	Phe	Ser	Thr	Asp	Phe	Thr	Asp	Ser	Ile	Ile	Thr	Ile	Ile	Phe
1		5		10		15									
Leu	Ile	Leu	Lys	Ile	Asn	Lys	Gly	Glu	Ser	Met	Ile	His	Phe	Ser	Ile
		20		25		30									
Asn	Lys	Asn	Leu	Phe	Leu	Gln	Ala	Leu	Asn	Thr	Thr	Lys	Arg	Ala	Ile
		35		40		45									
Ser	Ser	Lys	Asn	Ala	Ile	Pro	Ile	Leu	Ser	Thr	Val	Lys	Ile	Asp	Val
		50		55		60									
Thr	Asn	Glu	Gly	Ile	Thr	Leu	Ile	Gly	Ser	Asn	Gly	Gln	Ile	Ser	Ile
65		70		75		80									
Glu	Asn	Phe	Ile	Ser	Gln	Lys	Asn	Glu	Asp	Ala	Gly	Leu	Leu	Ile	Thr
		85		90		95									
Ser	Leu	Gly	Ser	Ile	Leu	Leu	Glu	Ala	Ser	Phe	Phe	Ile	Asn	Val	Val
		100		105		110									
Ser	Ser	Leu	Pro	Asp	Val	Thr	Leu	Asp	Phe	Lys	Glu	Ile	Glu	Gln	Asn
		115		120		125									
Gln	Ile	Val	Leu	Thr	Ser	Gly	Lys	Ser	Glu	Ile	Thr	Leu	Lys	Gly	Lys
		130		135		140									

Asp	Ser	Glu	Gln	Tyr	Pro	Arg	Ile	Gln	Glu	Ile	Ser	Ala	Ser	Thr	Pro
145					150					155					160
Leu	Ile	Leu	Glu	Thr	Lys	Leu	Leu	Lys	Lys	Ile	Ile	Asn	Glu	Thr	Ala
				165					170						175
Phe	Ala	Ala	Ser	Thr	Gln	Glu	Ser	Arg	Pro	Ile	Leu	Thr	Gly	Val	His
			180					185					190		
Phe	Val	Leu	Ser	Gln	His	Lys	Glu	Leu	Lys	Thr	Val	Ala	Thr	Asp	Ser
	195						200					205			
His	Arg	Leu	Ser	Gln	Lys	Lys	Leu	Thr	Leu	Glu	Lys	Asn	Ser	Asp	Asp
	210					215					220				
Phe	Asp	Val	Val	Ile	Pro	Ser	Arg	Ser	Leu	Arg	Glu	Phe	Ser	Ala	Val
225					230					235					240
Phe	Thr	Asp	Asp	Ile	Glu	Thr	Val	Glu	Ile	Phe	Phe	Ala	Asn	Asn	Gln
				245					250						255
Ile	Leu	Phe	Arg	Ser	Glu	Asn	Ile	Ser	Phe	Tyr	Thr	Arg	Leu	Leu	Glu
			260					265					270		
Gly	Asn	Tyr	Pro	Asp	Thr	Asp	Arg	Leu	Ile	Pro	Thr	Asp	Phe	Asn	Thr
	275						280					285			
Thr	Ile	Thr	Phe	Asn	Val	Val	Asn	Leu	Arg	Gln	Ser	Met	Glu	Arg	Ala
	290					295					300				
Arg	Leu	Leu	Ser	Ser	Ala	Thr	Gln	Asn	Gly	Thr	Val	Lys	Leu	Glu	Ile
305					310					315					320
Lys	Asp	Gly	Val	Val	Ser	Ala	His	Val	His	Ser	Pro	Glu	Val	Gly	Lys
				325					330					335	
Val	Asn	Glu	Glu	Ile	Asp	Thr	Asp	Gln	Val	Thr	Gly	Glu	Asp	Leu	Thr
		340						345				350			
Ile	Ser	Phe	Asn	Pro	Thr	Tyr	Leu	Ile	Asp	Ser	Leu	Lys	Ala	Leu	Asn
		355					360					365			
Ser	Glu	Lys	Val	Thr	Ile	Ser	Phe	Ile	Ser	Ala	Val	Arg	Pro	Phe	Thr
	370					375					380				
Leu	Val	Pro	Ala	Asp	Thr	Asp	Glu	Asp	Phe	Met	Gln	Leu	Ile	Thr	Pro
385					390					395					400
Val	Arg	Thr	Asn												

(2) INFORMATION FOR SEQ ID NO:5154:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 61 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...61
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5154:

Cys	Trp	Phe	Ser	Ser	Thr	Val	Tyr	Glu	Phe	Val	Lys	Ser	Gly	Arg	Tyr
1				5				10					15		

Pro	Arg	Asn	Gly	Trp	Phe	Arg	Arg	Leu	Asn	Ala	His	Asp	Glu	Glu	His
			20					25					30		
Ile	Thr	Ala	Ser	Leu	Asp	Ser	Val	Gly	Met	Trp	Asp	Ile	Glu	Thr	Asn
		35					40					45			
Ala	Trp	Val	Leu	Tyr	Leu	Gly	Asp	Lys	Ser	Ser	Glu	Arg			
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:5155:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 63 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...63

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5155:

Lys	Val	Lys	Phe	Lys	Ile	Lys	Gln	Asp	Phe	Tyr	Asp	Trp	Glu	Ser	Asn
1				5					10					15	
Val	Lys	Arg	Leu	Ala	Gly	Glu	Glu	Leu	Glu	Ile	Thr	Glu	Glu	Arg	Tyr
			20					25					30		
Ala	Glu	Leu	Ala	Asp	Asn	Ile	Ala	Ser	Asn	Gly	Val	Thr	Ile	Ser	Asp
		35				40					45				
Val	Leu	Glu	Lys	Ile	Leu	Pro	Glu	Pro	Glu	Phe	Leu	Glu	Glu	Asp	
	50					55					60				

(2) INFORMATION FOR SEQ ID NO:5156:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 135 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...135

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5156:

Cys Gln Leu Ser Lys Cys His Gly Ile Ser Gly Leu Glu Arg Asn Ile

1				5					10					15		
Asn	Ser	Lys	Met	Asn	Asp	Lys	Asp	Arg	Lys	Gly	Ala	Cys	Phe	Met	Asp	
			20					25					30			
Thr	Lys	Glu	Leu	Phe	Asp	Ala	Leu	Asp	Asp	Phe	Ser	Gln	Gln	Leu	Leu	
		35					40					45				
Val	Thr	Leu	Ala	Asp	Val	Glu	Ala	Ile	Lys	Lys	Asn	Leu	Lys	Ser	Leu	
	50					55					60					
Val	Glu	Glu	Asn	Thr	Ala	Leu	Arg	Leu	Glu	Asn	Ser	Lys	Leu	Arg	Glu	
65					70					75					80	
Arg	Leu	Gly	Glu	Val	Glu	Ala	Asp	Ala	Pro	Val	Lys	Ala	Lys	His	Val	
				85				90						95		
Arg	Glu	Ser	Val	Arg	Arg	Ile	Tyr	Arg	Asp	Gly	Phe	His	Val	Cys	Asn	
		100					105						110			
Asp	Phe	Tyr	Gly	Gln	Arg	Arg	Glu	Gln	Asp	Glu	Glu	Cys	Met	Phe	Cys	
	115					120						125				
Asp	Glu	Leu	Leu	Tyr	Arg	Glu										
	130					135										

(2) INFORMATION FOR SEQ ID NO:5157:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 294 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...294

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5157:

Lys	Glu	Leu	Ser	Lys	Gly	Glu	Gly	Leu	Gly	Asn	Lys	Phe	Leu	Ala	Asn	
1				5					10					15		
Ile	Arg	Glu	Val	Asp	Ala	Ile	Val	His	Val	Val	Arg	Ala	Phe	Asp	Asp	
		20					25					30				
Glu	Asn	Val	Met	Arg	Glu	Gln	Gly	Arg	Glu	Asp	Ala	Phe	Val	Asp	Pro	
	35					40					45					
Leu	Ala	Asp	Ile	Asp	Thr	Ile	Asn	Leu	Glu	Leu	Ile	Leu	Ala	Asp	Leu	
	50					55					60					
Glu	Ser	Val	Asn	Lys	Arg	Tyr	Ala	Arg	Val	Glu	Lys	Met	Ala	Arg	Thr	
65					70					75					80	
Gln	Lys	Asp	Lys	Glu	Ser	Val	Ala	Glu	Phe	Asn	Val	Leu	Gln	Lys	Ile	
		85					90						95			
Lys	Pro	Val	Leu	Glu	Asp	Gly	Lys	Ser	Ala	Arg	Thr	Ile	Glu	Phe	Thr	
	100					105						110				
Asp	Glu	Glu	Gln	Lys	Val	Val	Lys	Gly	Leu	Phe	Leu	Leu	Thr	Thr	Lys	
	115					120						125				
Pro	Val	Leu	Tyr	Val	Ala	Asn	Val	Asp	Glu	Asp	Val	Val	Ser	Glu	Pro	
	130					135						140				

(2) INFORMATION FOR SEO ID NO:5159:

(A) LENGTH: 271 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Streptococcus pneumoniae*

(A) NAME/KEY: misc_feature
(B) LOCATION 1...271

4015

50		55		60											
Val	Phe	Val	Gly	Ser	Gly	Ile	Phe	Lys	Ser	Gly	Asp	Pro	Val	Lys	Arg
65					70					75					80
Ala	Ser	Ala	Ile	Val	Lys	Ala	Val	Thr	Asn	Phe	Arg	Asn	Pro	Gln	Ile
				85					90					95	
Leu	Ala	Gln	Ile	Ser	Glu	Asp	Leu	Gly	Glu	Ala	Met	Val	Gly	Ile	Asn
			100					105					110		
Glu	Asn	Glu	Ile	Gln	Ile	Leu	Met	Ala	Glu	Arg	Gly	Lys			
		115				120						125			

(2) INFORMATION FOR SEQ ID NO:5161:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 224 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...224

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5161:

Arg	Arg	Lys	Phe	Pro	Met	Arg	Lys	Lys	Leu	Phe	Leu	Thr	Ser	Ala	Ala
1				5					10					15	
Val	Leu	Trp	Ala	Val	Thr	Ala	Met	Asn	Ser	Val	His	Ala	Ala	Thr	Asp
			20					25					30		
Val	Gln	Lys	Val	Ile	Asp	Glu	Thr	Tyr	Val	Gln	Pro	Glu	Tyr	Val	Leu
		35					40					45			
Gly	Ser	Ser	Leu	Ser	Glu	Asp	Gln	Lys	Asn	Gln	Thr	Leu	Lys	Lys	Leu
	50				55					60					
Gly	Tyr	Asn	Ala	Ser	Thr	Asp	Thr	Lys	Glu	Leu	Lys	Thr	Met	Thr	Pro
65				70					75						80
Asp	Val	Tyr	Ser	Lys	Ile	Met	Asn	Val	Ala	Asn	Asp	Ser	Ser	Leu	Gln
			85						90					95	
Leu	Tyr	Ser	Ser	Ala	Lys	Ile	Gln	Lys	Leu	Gly	Asp	Lys	Ser	Pro	Leu
		100					105					110			
Glu	Val	Lys	Ile	Glu	Thr	Pro	Glu	Asn	Ile	Thr	Lys	Val	Thr	Gln	Asp
	115					120					125				
Met	Tyr	Arg	Asn	Ala	Ala	Val	Thr	Leu	Gly	Met	Glu	His	Ala	Lys	Ile
	130				135					140					
Thr	Val	Ala	Ala	Pro	Ile	Pro	Val	Thr	Gly	Glu	Ser	Ala	Leu	Ala	Gly
145				150					155					160	
Ile	Tyr	Tyr	Ser	Leu	Glu	Ala	Asn	Gly	Ala	Lys	Val	Pro	Gln	Ala	Asn
			165				170						175		
Lys	Asp	Leu	Ala	Gln	Glu	Glu	Leu	Lys	Ala	Leu	Ser	Asp	Ile	Asn	Ala
		180					185					190			
Glu	Asn	Lys	Asp	Lys	Ser	Gly	Tyr	Asp	Ala	Asn	Lys	Leu	Asn	Val	Ala
	195					200					205				
Leu	Ala	Asp	Ile	Lys	Ser	Gly	Leu	Ala	Lys	Ala	Lys	Glu	Ser	Lys	Gly

210

215

220

(2) INFORMATION FOR SEQ ID NO:5162:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 84 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5162:

Arg	Glu	Ile	Ser	Phe	Tyr	Gln	Asn	His	Ser	Leu	Ile	Val	Phe	Leu	Gly
1				5					10					15	
Arg	Leu	Ile	Phe	Thr	Ser	Val	Ala	Ser	Ile	Ile	Ile	Val	Ser	Ser	Glu
			20					25					30		
Leu	Arg	Gly	Val	Leu	Glu	Ile	Val	Thr	Pro	Pro	Leu	Asn	Lys	Ser	Tyr
		35					40					45			
Phe	Asn	Pro	Leu	Ala	Pro	Thr	Asp	Lys	Glu	Asp	Leu	Ile	Arg	Thr	Leu
	50					55				60					
Glu	Leu	Ala	Pro	His	Val	Glu	Gly	Gly	Tyr	Phe	Arg	Gln	Thr	Lys	Lys
65					70				75						80
Leu	Gln	Thr	Leu												

(2) INFORMATION FOR SEQ ID NO:5163:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 407 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...407

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5163:

Lys	Glu	Ile	Ser	Gly	Thr	Ile	Phe	Ala	Val	Val	Thr	Leu	Asn	His	Tyr
1				5					10					15	

His	Trp	Ser	Leu	Thr	Val	Thr	Thr	Leu	Phe	Ser	Leu	Met	Ile	Met	Leu
			20					25					30		
Leu	Val	Pro	Lys	Ile	Phe	Ala	Leu	Lys	Met	Arg	Glu	Val	Ser	Leu	Asn
		35					40					45			
Leu	Thr	Asn	Gln	Asn	Glu	Ala	Phe	Leu	Lys	Phe	Ser	Glu	Thr	Ile	Leu
	50					55					60				
Asn	Gly	Phe	Asp	Val	Leu	Ala	Ser	Leu	Asn	Phe	Leu	Tyr	Val	Leu	Pro
65				70					75						80
Lys	Lys	Ile	Thr	Glu	Ala	Gly	Ile	Leu	Leu	Lys	Leu	Val	Ile	Gln	Ser
				85				90						95	
Lys	Thr	Thr	Val	Val	Thr	Leu	Ala	Gly	Asp	Ile	Ser	Phe	Phe	Leu	Asn
			100					105					110		
Ile	Phe	Phe	Gln	Ile	Ser	Phe	Val	Phe	Leu	Thr	Gly	Tyr	Leu	Ala	Ile
	115						120					125			
Lys	Gly	Ile	Val	Lys	Ile	Gly	Thr	Ile	Glu	Ala	Ile	Gly	Ala	Leu	Thr
	130					135					140				
Gly	Val	Ile	Phe	Thr	Ala	Leu	Gly	Glu	Leu	Gly	Gly	Gln	Leu	Ser	Phe
145					150				155						160
Ile	Ile	Gly	Thr	Lys	Pro	Ile	Phe	Leu	Lys	Leu	Tyr	Ser	Ile	Asn	Pro
				165				170						175	
Ile	Glu	Ser	Asn	Lys	Met	Asn	Asp	Ile	Glu	Pro	Asn	Glu	Val	Asn	Arg
		180					185						190		
Asp	Phe	Pro	Leu	Tyr	Glu	Ala	Lys	Asn	Ile	Cys	Tyr	Lys	Tyr	Gly	Asp
	195						200					205			
Lys	Glu	Ile	Leu	Lys	Asn	Leu	Asn	Phe	Cys	Phe	Gln	Arg	Asn	Glu	Lys
	210					215					220				
Tyr	Leu	Ile	Leu	Gly	Glu	Ser	Gly	Ser	Gly	Lys	Ser	Thr	Leu	Leu	Lys
225					230					235					240
Leu	Leu	Asn	Gly	Phe	Leu	Arg	Asp	Tyr	Ser	Gly	Glu	Leu	Arg	Phe	Cys
			245					250						255	
Gly	Asp	Asp	Ile	Lys	Lys	Thr	Ser	Tyr	Leu	Asn	Met	Val	Ser	Asn	Val
			260					265					270		
Leu	Tyr	Val	Asp	Gln	Lys	Ala	Tyr	Leu	Phe	Glu	Gly	Thr	Ile	Arg	Asp
		275					280					285			
Asn	Ile	Leu	Leu	Glu	Glu	Asn	Tyr	Thr	Asp	Glu	Glu	Ile	Leu	Gln	Ser
	290					295					300				
Leu	Glu	Gln	Val	Gly	Leu	Ser	Val	Lys	Asp	Phe	Pro	Asn	Asn	Ile	Leu
305					310					315					320
Asp	Tyr	Tyr	Val	Gly	Asp	Asp	Gly	Arg	Leu	Leu	Ser	Gly	Gly	Gln	Lys
			325					330						335	
Gln	Lys	Ile	Thr	Leu	Ala	Arg	Gly	Leu	Ile	Arg	Asn	Lys	Lys	Ile	Val
		340					345					350			
Leu	Ile	Asp	Glu	Gly	Thr	Ser	Ala	Ile	Asp	Arg	Arg	Thr	Ser	Leu	Ala
		355					360					365			
Ile	Glu	Arg	Lys	Ile	Leu	Asp	Arg	Glu	Asp	Leu	Thr	Val	Ile	Ile	Val
	370					375					380				
Thr	His	Ala	Pro	His	Pro	Glu	Leu	Lys	Gln	Tyr	Phe	Thr	Lys	Ile	Tyr
385					390					395					400
Gln	Phe	Pro	Lys	Asp	Phe	Ile									
				405											

(2) INFORMATION FOR SEQ ID NO:5164:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 66 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...66
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5164:

```

Leu Trp Ile Ser Val Leu Gly Met Glu Gln Trp Gly Phe Leu Leu Ala
1      5      10      15
Leu Val Leu Lys His Arg Tyr Cys Leu Leu Arg Phe Gln Glu Arg Leu
20      25      30
Ala Asp Met Ala Glu Arg Ser Val Arg Leu Asn Gly Leu Glu Glu Gln
35      40      45
Met Gln Val Ile Cys Asp Asp Leu Lys Asn Met Pro Ala His Ile Gln
50      55      60
Gly Lys
65

```

(2) INFORMATION FOR SEQ ID NO:5165:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 233 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...233
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5165:

```

Gly Arg Ile Ser Met Lys Lys Tyr Gln Leu Leu Phe Lys Ile Ser Ala
1      5      10      15
Val Phe Ser Tyr Leu Phe Phe Val Phe Gly Leu Ser Gln Leu Thr Leu
20      25      30
Ile Val Gln Asn Tyr Trp Gln Phe Ser Ser Gln Ile Gly Asn Phe Val
35      40      45
Trp Ile Gln Asn Ile Leu Ser Leu Leu Phe Ser Gly Val Met Ile Trp
50      55      60
Ile Leu Val Lys Thr Gly His Gly Tyr Leu Phe Arg Ile Pro Arg Lys
65      70      75      80
Lys Trp Leu Trp Tyr Ser Ile Leu Thr Val Leu Val Val Val Leu His

```


(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...196

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5167:

Arg	Ala	Val	Ser	Ser	Lys	Lys	Arg	Gly	Arg	Arg	Met	Ala	Arg	Thr	Glu
1				5				10						15	
Leu	Ser	Asp	Lys	Ile	Glu	Thr	Glu	Arg	Leu	Val	Leu	Arg	Val	Arg	Thr
			20					25					30		
Val	Ala	Asp	Ala	Glu	Asp	Ile	His	Ala	Tyr	Ala	Ser	Leu	Pro	Glu	Val
			35				40					45			
Ala	Tyr	Pro	Ala	Gly	Phe	Pro	Pro	Val	Lys	Thr	Leu	Glu	Asp	Glu	Ile
	50					55					60				
Tyr	Tyr	Leu	Glu	His	Ile	Leu	Pro	Glu	Arg	Asn	Gln	Lys	Glu	Asn	Leu
65					70					75				80	
Pro	Ala	Gly	Tyr	Gly	Ile	Val	Ile	Lys	Gly	Thr	Asp	Lys	Ile	Ala	Gly
				85					90					95	
Ser	Val	Asp	Phe	Asn	His	Arg	Tyr	Gly	Asp	Asp	Val	Leu	Glu	Leu	Gly
			100					105					110		
Tyr	Thr	Leu	His	Ser	Asp	Tyr	Trp	Gly	Arg	Gly	Tyr	Val	Pro	Glu	Ala
			115				120					125			
Ala	Arg	Ala	Leu	Ile	Asp	Leu	Ala	Phe	Lys	Asp	Leu	Gly	Leu	His	Lys
			130				135					140			
Ile	Glu	Leu	Thr	Cys	Phe	Gly	Tyr	Asn	Leu	Gln	Ser	Lys	Arg	Val	Ala
145					150					155				160	
Glu	Lys	Leu	Gly	Phe	Thr	Leu	Glu	Ala	Arg	Ile	Arg	Asp	Arg	Lys	Asp
				165					170					175	
Ala	Gln	Gly	Asn	Cys	Cys	Asp	Asp	Leu	Arg	Tyr	Ala	Leu	Leu	Lys	Ser
			180					185					190		
Glu	Trp	Glu	Glu												
			195												

(2) INFORMATION FOR SEQ ID NO:5168:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 344 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...344

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5168:

Asp	Met	Val	Ser	Thr	Ile	Gly	Ile	Val	Ser	Leu	Ser	Ser	Gly	Ile	Ile
1				5				10					15		
Gly	Glu	Asp	Phe	Val	Lys	His	Glu	Val	Asp	Leu	Gly	Ile	Gln	Arg	Leu
			20				25					30			
Lys	Val	Leu	Gly	Leu	Asn	Pro	Ile	Phe	Leu	Pro	His	Ser	Leu	Lys	Gly
		35				40					45				
Leu	Asp	Phe	Ile	Lys	Asp	His	Pro	Glu	Ala	Arg	Ala	Glu	Asp	Leu	Ile
	50				55					60					
His	Ala	Phe	Ser	Asp	Asp	Ser	Ile	Asp	Met	Ile	Leu	Cys	Ala	Ile	Gly
65				70				75						80	
Gly	Asp	Asp	Thr	Tyr	Arg	Leu	Leu	Pro	Tyr	Leu	Phe	Glu	Asn	Asp	Gln
			85					90					95		
Leu	Gln	Lys	Ala	Ile	Lys	Gln	Lys	Ile	Phe	Leu	Gly	Phe	Ser	Asp	Thr
		100					105					110			
Thr	Met	Asn	His	Leu	Met	Leu	His	Lys	Leu	Gly	Ile	Lys	Thr	Phe	Tyr
	115					120						125			
Gly	Gln	Ser	Phe	Leu	Ala	Asp	Ile	Cys	Glu	Leu	Asp	Lys	Glu	Met	Leu
	130				135						140				
Ala	Tyr	Ser	Leu	His	Tyr	Phe	Lys	Glu	Leu	Ile	Glu	Thr	Gly	Arg	Ile
145				150				155						160	
Ser	Glu	Ile	Arg	Pro	Ser	Asp	Val	Trp	Tyr	Glu	Glu	Arg	Thr	Asp	Phe
			165					170					175		
Ser	Pro	Thr	Ala	Leu	Gly	Thr	Pro	Arg	Val	Ser	His	Thr	Asn	Thr	Gly
		180					185						190		
Phe	Asp	Leu	Leu	Gln	Gly	Ser	Ala	Gln	Phe	Glu	Gly	Lys	Ile	Leu	Gly
	195					200						205			
Gly	Cys	Leu	Glu	Ser	Leu	Tyr	Asp	Ile	Phe	Asp	Asn	Ser	Arg	Tyr	Ala
	210				215					220					
Asp	Ser	Thr	Glu	Leu	Cys	Gln	Lys	Tyr	Lys	Leu	Phe	Pro	Asp	Leu	Ser
225				230						235				240	
Asp	Trp	Glu	Gly	Lys	Ile	Leu	Leu	Leu	Glu	Thr	Ser	Glu	Glu	Glu	Pro
			245						250				255		
Lys	Pro	Glu	Asp	Phe	Lys	Lys	Met	Leu	Leu	Thr	Leu	Lys	Asp	Thr	Gly
		260					265						270		
Ile	Phe	Ala	Val	Ile	Asn	Gly	Leu	Leu	Val	Gly	Lys	Pro	Met	Asp	Glu
	275				280							285			
Thr	Phe	His	Asp	Asp	Tyr	Lys	Glu	Ala	Leu	Leu	Asp	Ile	Ile	Asp	Asn
	290				295						300				
Asn	Ile	Pro	Ile	Val	Tyr	Asn	Leu	Asn	Val	Gly	His	Ala	Thr	Pro	Arg
305				310						315				320	
Ala	Ile	Val	Pro	Phe	Gly	Val	His	Ala	His	Val	Asp	Ala	Gln	Glu	Gln
			325					330					335		
Val	Ile	Arg	Phe	Asp	Tyr	Asn	Lys								
			340												

(2) INFORMATION FOR SEQ ID NO:5169:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 530 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...530

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5169:

Ser	Ser	Val	Ser	Val	Met	Ser	Trp	Lys	Val	Ser	Ile	Gly	Arg	Cys	Trp
1				5					10					15	
Met	Ala	Arg	Pro	Ser	Gln	Asn	Pro	Leu	Ser	Phe	Gly	Gln	Gly	Leu	Ile
			20					25					30		
Thr	Ser	Ser	Gly	Cys	Leu	Val	Lys	Leu	Ser	Ser	Ser	Ser	Tyr	Gln	Leu
			35				40					45			
Gly	Ile	Thr	Trp	Ser	Val	Ser	Arg	Lys	Met	Gly	Thr	Asn	Gln	Ile	Leu
	50					55				60					
Gly	Ile	Val	Leu	Gly	Ile	Cys	Leu	Val	Ser	Pro	Gln	Leu	Leu	Asn	Ala
65					70					75				80	
Tyr	Ala	Val	Ala	Ser	Thr	Pro	Ala	Ala	Asp	Ile	Ala	Ala	Asn	Trp	Val
				85					90					95	
Trp	Asn	Phe	Gly	Tyr	Phe	Thr	Val	Asn	Arg	Ile	Gly	Tyr	Gln	Ala	Gln
			100					105					110		
Val	Ile	Pro	Ala	Leu	Leu	Ala	Gly	Leu	Ser	Leu	Ser	Tyr	Leu	Glu	Ile
			115				120					125			
Phe	Trp	Arg	Lys	His	Ile	Pro	Glu	Val	Ile	Ser	Met	Ile	Phe	Val	Pro
	130					135					140				
Phe	Leu	Ser	Leu	Ile	Pro	Ala	Leu	Ile	Leu	Ala	His	Thr	Val	Leu	Gly
145					150					155				160	
Pro	Ile	Gly	Trp	Thr	Ile	Gly	Gln	Gly	Leu	Ser	Ser	Val	Val	Leu	Ala
				165					170					175	
Gly	Leu	Thr	Gly	Pro	Val	Lys	Trp	Leu	Phe	Gly	Ala	Ile	Phe	Gly	Ala
			180					185					190		
Leu	Tyr	Ala	Pro	Phe	Val	Ile	Thr	Gly	Leu	His	His	Met	Thr	Asn	Ala
	195						200					205			
Ile	Asp	Thr	Gln	Leu	Ile	Ala	Asp	Ala	Gly	Gly	Thr	Ala	Leu	Trp	Pro
	210					215					220				
Met	Ile	Ala	Leu	Ser	Asn	Ile	Ala	Gln	Gly	Ser	Ala	Val	Phe	Ala	Tyr
225					230					235				240	
Tyr	Phe	Met	His	Arg	His	Asp	Glu	Cys	Glu	Ala	Gln	Val	Ser	Leu	Pro
				245					250					255	
Ala	Thr	Ile	Ser	Ala	Tyr	Leu	Gly	Val	Thr	Glu	Pro	Ala	Leu	Phe	Gly
			260					265					270		
Val	Asn	Val	Lys	Tyr	Ile	Tyr	Pro	Phe	Val	Ala	Gly	Met	Thr	Gly	Ser
	275						280					285			
Ala	Leu	Ala	Gly	Met	Leu	Ser	Val	Thr	Phe	Asn	Val	Thr	Ala	Ala	Ser
	290						295					300			
Ile	Gly	Ile	Gly	Gly	Leu	Pro	Gly	Ile	Leu	Ser	Ile	Gln	Pro	Gln	Tyr
305					310					315				320	
Met	Leu	Pro	Phe	Ala	Gly	Thr	Met	Leu	Val	Ala	Ile	Val	Val	Pro	Met
				325					330					335	
Leu	Leu	Thr	Phe	Phe	Phe	Arg	Lys	Ala	Gly	Leu	Phe	Thr	Lys	Ile	Glu

Thr Thr Cys Thr Val Pro Phe Trp Ile Ser Ser Leu Asp His Lys Ala
85 90 95
Ile Asp Asp Thr Val Glu Gly Asn Thr Val Ile Val Ala Phe Phe Gly
100 105 110
Val Ser Glu Glu Ile Phe Asn Arg
115 120

(2) INFORMATION FOR SEQ ID NO:5171:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 347 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...347

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5171:

Leu Ala Ser Ser Val Tyr Ser Leu Phe Val Trp Tyr Asn Leu Phe Leu
1 5 10 15
Lys Lys Glu Arg Glu Val Ile Ser Met Arg Lys Trp Thr Lys Gly Phe
20 25 30
Leu Ile Phe Gly Val Val Thr Thr Val Ile Gly Phe Ile Leu Leu Phe
35 40 45
Val Gly Ile Gln Ser Asp Gly Ile Lys Ser Leu Leu Ser Met Ser Lys
50 55 60
Glu Pro Val Tyr Asp Ser Arg Thr Glu Lys Leu Thr Phe Gly Lys Glu
65 70 75 80
Val Glu Asn Leu Glu Ile Thr Leu His Gln His Ala Leu Thr Ile Thr
85 90 95
Asp Ser Phe Asp Asp Gln Ile His Ile Ser Tyr His Pro Ser Leu Ser
100 105 110
Ala His His Asp Leu Ile Thr Asn Gln Asn Asp Arg Thr Leu Ser Leu
115 120 125
Thr Asp Lys Lys Leu Ser Glu Thr Pro Phe Leu Ser Ser Gly Ile Gly
130 135 140
Gly Ile Leu His Ile Ala Ser Ser Tyr Ser Ser Arg Phe Glu Glu Val
145 150 155 160
Ile Leu Gln Leu Pro Lys Gly Arg Thr Leu Lys Gly Ile Asn Ile Ser
165 170 175
Ala Asn Arg Gly Gln Thr Thr Ile Ile Asn Ala Ser Leu Glu Asn Ala
180 185 190
Thr Leu Asn Thr Asn Ser Tyr Ile Leu Arg Ile Glu Gly Ser Arg Ile
195 200 205
Lys Asn Ser Lys Leu Thr Thr Pro Asn Ile Val Asn Ile Phe Asp Thr
210 215 220
Val Leu Thr Asp Ser Gln Leu Glu Ser Thr Glu Asn His Phe His Ala

225		230		235		240									
Glu	Asn	Ile	Gln	Val	His	Gly	Lys	Val	Glu	Leu	Thr	Ala	Lys	Asp	Tyr
		245		250		255									
Leu	Arg	Ile	Ile	Leu	Asp	Gln	Lys	Glu	Ser	Gln	Arg	Ile	Asn	Trp	Asp
		260		265		270									
Ile	Ser	Ser	Asn	Tyr	Gly	Ser	Ile	Phe	Gln	Phe	Thr	Arg	Glu	Lys	Pro
		275		280		285									
Glu	Ser	Arg	Gly	Thr	Glu	Leu	Ser	Asn	Pro	Tyr	Lys	Thr	Glu	Lys	Thr
		290		295		300									
Asp	Val	Lys	Asp	Gln	Leu	Ile	Ala	Arg	Ser	Asp	Asp	Asn	Ile	Asp	Leu
305				310		315									
Ile	Ser	Thr	Leu	Arg	Asp	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Thr	Lys	Gly	Xaa
				325		330									
Thr	Ser	Lys	Ala	Xaa	Xaa	Thr	Arg	Arg	Lys	Lys					
			340			345									

(2) INFORMATION FOR SEQ ID NO:5172:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 90 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...90
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5172:

Lys	His	Ser	Ser	Lys	Thr	Gln	Pro	Ser	Ile	Pro	Cys	Arg	Cys	Ser	Leu
1				5				10						15	
Tyr	Trp	Arg	Tyr	Gly	Leu	Leu	Ser	Cys	Glu	Asp	Leu	Arg	Leu	Gly	Ser
			20				25						30		
Val	Asp	Ser	Ser	Thr	Lys	Gln	Leu	Arg	Glu	Ile	Ser	Ser	Cys	Ser	Asn
		35				40						45			
Thr	Glu	Asp	Phe	Gln	Ala	Val	Arg	Ala	Gln	Ile	Arg	Tyr	Arg	Asp	Glu
		50				55					60				
Ala	Asp	Gly	Lys	Val	Lys	Leu	Pro	Ser	Tyr	Leu	Glu	Arg	Phe	Trp	Thr
65				70					75						80
Cys	Ser	Trp	Thr	Tyr	Ser	Gly	Cys	Asn	Ser						
				85				90							

(2) INFORMATION FOR SEQ ID NO:5173:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 80 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...80
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5173:

```

Arg Leu Glu Phe Ala Gly Phe Thr Trp Ser Leu Cys Leu Arg Ile Tyr
1      5      10      15
Leu His Glu Pro Leu Ile Thr Thr Val Ser Gln Asp Phe Thr Ser Leu
20     25     30
Ser Asp Ile Ser Ala Thr His Phe Glu Gln Leu His Ile Met Thr Ile
35     40     45
Val His Ser Asp Ile Gln Arg Asn Asn Ser Pro Leu Thr Cys Asp Asn
50     55     60
Arg Leu Ser Leu His Ser Val Ala Phe Leu Phe Thr Arg Ile Ile Arg
65     70     75     80

```

(2) INFORMATION FOR SEQ ID NO:5174:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 93 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...93
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5174:

```

Lys Ser Ser Ser Ala Leu Ala Leu Leu Phe Ser Ile Ile Arg Val Lys
1      5      10      15
Thr Ile Pro Phe Val Ile Leu Asp Glu Val Glu Ala Ala Leu Asp Glu
20     25     30
Ala Asn Val Lys Arg Phe Gly Asp Tyr Phe Asn Arg Phe Asp Lys Asp
35     40     45
Ser Gln Phe Ile Val Val Thr His Arg Lys Gly Thr Met Ala Ala Ala
50     55     60
Asp Ser Ile Tyr Gly Val Thr Met Gln Glu Ser Gly Val Ser Lys Ile
65     70     75     80
Val Ser Val Lys Leu Lys Asp Leu Glu Ser Ile Glu Gly
85     90

```

(2) INFORMATION FOR SEQ ID NO:5175:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 84 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...84

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5175:

Ala	Val	Pro	Ser	Ser	Ala	Ile	Phe	Pro	Trp	Ser	Arg	Lys	Ile	Ile	Arg
1				5					10					15	
Ser	Val	Met	Ala	Trp	Ala	Asn	Cys	Ile	Ser	Trp	Val	Thr	Lys	Ile	Met
		20					25						30		
Val	Arg	Pro	Ser	Trp	Val	Lys	Ser	Leu	Ile	Ser	Ser	Ser	Thr	Ser	Arg
		35				40						45			
Thr	Ile	Ser	Gly	Ser	Ser	Glu	Ala	Val	Thr	Ser	Ser	Lys	Arg	Met	Ile
	50					55				60					
Ser	Gly	Cys	Ile	Arg	Arg	Ala	Arg	Thr	Ile	Ala	Thr	Arg	Cys	Phe	Cys
65				70					75						80
Pro	Pro	Asp	Asn												

(2) INFORMATION FOR SEQ ID NO:5176:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 336 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...336

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5176:

Gln	Met	Pro	Ser	His	Tyr	Thr	Arg	Asn	Lys	Thr	Phe	Met	Asp	Ile	Tyr
1				5					10					15	
Ile	Lys	Lys	Ala	Ile	Ile	His	Gln	Phe	Ser	Pro	Asp	Asp	Thr	Glu	Leu
		20					25						30		

Phe	Leu	Ala	Asp	Lys	Phe	Leu	Asn	Ile	Thr	Pro	Lys	Ile	Glu	Glu	Tyr	35	40	45
Leu	Arg	Lys	Lys	Ile	Glu	His	Val	Tyr	Ser	Asp	Glu	Ala	Lys	Thr	Gly	50	55	60
Ile	Phe	Glu	Glu	Glu	Asn	Pro	Phe	Phe	Asn	His	Ile	Thr	Asp	Asp	Leu	65	70	75
Leu	Glu	Thr	Ser	Val	Thr	Leu	Ala	Asn	Leu	Trp	Lys	Glu	Glu	Phe	Ser	85	90	95
Ile	Ser	Glu	Asn	Leu	Lys	Thr	Asn	Asp	Leu	Ile	Phe	Val	Gln	Phe	Ser	100	105	110
Lys	Glu	Gly	Val	Glu	His	Phe	Ala	Phe	Leu	Arg	Ile	Ala	Leu	Arg	Glu	115	120	125
Thr	Leu	Thr	His	Leu	Gly	Gly	Glu	Val	Asp	Asn	Pro	Ile	Lys	Leu	Thr	130	135	140
Gln	Asn	Asn	Leu	Pro	Gly	Phe	Gly	Thr	Gly	Ala	Asp	Glu	Ala	Leu	Val	145	150	155
Val	Asn	Leu	Gln	Ser	Arg	Lys	Tyr	His	Leu	Ile	Glu	Lys	Arg	Ile	Lys	165	170	175
Tyr	Asn	Gly	Thr	Phe	Leu	Asn	Tyr	Phe	Ser	Asp	Asn	Leu	Leu	Ala	Val	180	185	190
Ala	Pro	Lys	Ile	Ser	Pro	Lys	Lys	Ser	Ile	Lys	Glu	Leu	Glu	Lys	Thr	195	200	205
Ala	Gln	Arg	Ile	Ala	Glu	Ser	Phe	Asn	Thr	Asp	Asp	Phe	Gln	Phe	Gln	210	215	220
Ser	Lys	Val	Lys	Ser	Ala	Ile	Phe	Asn	Asn	Leu	Glu	Glu	Ser	Asn	Glu	225	230	235
Leu	Ser	Pro	Glu	Lys	Leu	Ala	Asn	Asp	Leu	Phe	Asp	Asn	Asn	Leu	Thr	245	250	255
Ala	Arg	Leu	Ser	Phe	Ile	Asp	Gln	Val	Lys	Glu	Ala	Val	Pro	Glu	Pro	260	265	270
Val	Gln	Phe	Asp	Glu	Ile	Asp	Ala	Ser	Arg	Gln	Leu	Lys	Lys	Phe	Glu	275	280	285
Asn	Gln	Lys	Leu	Ser	Leu	Ser	Asn	Gly	Ile	Glu	Leu	Ile	Val	Pro	Asn	290	295	300
Asn	Val	Tyr	Gln	Asp	Ala	Glu	Ser	Val	Glu	Phe	Ile	Gln	Asn	Glu	Asn	305	310	315
Gly	Thr	Tyr	Ser	Ile	Leu	Ile	Lys	Asn	Ile	Glu	Asp	Ile	Gln	Ser	Lys	325	330	335

(2) INFORMATION FOR SEQ ID NO:5177:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 175 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...175

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5177:

Gln	Thr	Pro	Ser	Lys	Val	Phe	Gln	Thr	Asn	Cys	Cys	Gln	Val	His	Ser
1				5					10					15	
Gln	Arg	Leu	Thr	Leu	Gln	Leu	Leu	Met	Asp	Leu	Val	Leu	Gln	Met	Leu
			20					25					30		
Ser	Cys	Gln	Asp	Leu	Pro	Leu	Val	Leu	Ile	Gly	Gln	Leu	Ile	Thr	Ile
		35					40					45			
Val	Leu	Leu	Ile	Val	Phe	Lys	Asn	Pro	Ile	Leu	Ile	Ile	Thr	Gly	Phe
	50					55					60				
Val	Pro	Val	Phe	Phe	Asp	Asn	Ala	Ala	Ile	Ala	Val	Tyr	Ala	Asp	Lys
65					70					75					80
Arg	Gly	Gly	Trp	Lys	Ala	Ala	Val	Ile	Leu	Ser	Phe	Ile	Ser	Gly	Val
				85					90					95	
Leu	Gln	Val	Ala	Leu	Gly	Ala	Leu	Cys	Val	Ala	Leu	Leu	Asp	Leu	Ala
			100					105					110		
Ser	Tyr	Gly	Gly	Tyr	His	Gly	Asn	Ile	Asp	Phe	Glu	Phe	Pro	Trp	Leu
		115					120					125			
Gly	Phe	Gly	Tyr	Ile	Phe	Lys	Tyr	Leu	Gly	Ile	Val	Gly	Tyr	Val	Leu
	130					135					140				
Val	Cys	Leu	Phe	Leu	Leu	Val	Ile	Pro	Gln	Leu	Gln	Phe	Ala	Lys	Ala
145					150					155					160
Lys	Asp	Lys	Glu	Lys	Tyr	Tyr	Asn	Gly	Glu	Val	Gln	Glu	Glu	Ala	
				165					170					175	

(2) INFORMATION FOR SEQ ID NO:5178:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 360 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...360

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5178:

Gly	Gly	Thr	Ser	Ser	Arg	Thr	Asn	Glu	Asp	Gly	Ser	Leu	Ser	Arg	Ser
1				5					10					15	
Lys	Val	Lys	Asp	Ile	Thr	Gln	Gln	Leu	Ala	Met	Leu	His	Glu	Ala	Gly
			20					25					30		
His	Glu	Leu	Ile	Leu	Gly	Ser	Ser	Gly	Ala	Ile	Ala	Ala	Gly	Phe	Gly
		35				40						45			
Ala	Leu	Gly	Phe	Lys	Lys	Arg	Pro	Thr	Lys	Ile	Ala	Asp	Lys	Gln	Ala
	50					55					60				
Ser	Ala	Ala	Val	Gly	Gln	Gly	Leu	Leu	Leu	Glu	Glu	Tyr	Thr	Thr	Asn
65					70					75					80
Leu	Leu	Leu	Arg	Gln	Ile	Val	Ser	Ala	Gln	Ile	Leu	Leu	Thr	Gln	Asp

1				5					10					15			
Tyr	Ile	Asn	Val	Ile	Gly	Ala	Gly	Leu	Ala	Gly	Ser	Glu	Ala	Ala	Tyr		
			20					25					30				
Gln	Ile	Ala	Glu	Arg	Gly	Ile	Pro	Val	Lys	Leu	Tyr	Glu	Met	Arg	Gly		
		35					40					45					
Val	Lys	Ser	Thr	Pro	Gln	His	Lys	Thr	Asp	Asn	Phe	Ala	Glu	Leu	Val		
	50					55				60							
Cys	Ser	Asn	Ser	Leu	Arg	Gly	Asp	Ala	Leu	Thr	Asn	Ala	Val	Gly	Leu		
65					70					75					80		
Leu	Lys	Glu	Glu	Met	Arg	Arg	Leu	Gly	Ser	Val	Ile	Leu	Glu	Ser	Ala		
				85				90					95				
Glu	Ala	Thr	Arg	Val	Pro	Ala	Gly	Gly	Ala	Leu	Ala	Val	Asp	Arg	Asp		
		100					105						110				
Gly	Phe	Ser	Gln	Met	Val	Thr	Glu	Lys	Val	Val	Asn	His	Pro	Leu	Ile		
	115						120					125					
Glu	Val	Val	Arg	Asp	Glu	Ile	Thr	Glu	Leu	Pro	Thr	Asp	Val	Ile	Thr		
	130					135					140						
Val	Val	Ala	Thr	Gly	Pro	Leu	Thr	Ser	Asp	Ala	Leu	Ala	Glu	Lys	Ile		
145					150				155						160		
His	Ala	Leu	Asn	Asn	Gly	Asp	Gly	Phe	Tyr	Phe	Tyr	Asp	Ala	Ala	Ala		
			165					170					175				
Pro	Ile	Ile	Asp	Val	Asn	Thr	Ile	Asp	Met	Ser	Lys	Val	Tyr	Leu	Asn		
			180					185					190				
Asn	Leu	Arg															
	195																

(2) INFORMATION FOR SEQ ID NO:5180:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...77

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5180:

Tyr	Leu	Thr	Ser	Phe	Ser	Val	Pro	Lys	Ile	Ala	Ser	Ser	Lys	Val	Lys
1				5				10					15		
Leu	Thr	Arg	Tyr	Trp	Arg	Ser	Ser	Pro	Trp	Arg	Gly	Ala	Phe	Gly	Leu
		20					25					30			
Arg	Glu	Glu	Pro	Pro	Pro	Pro	Lys	Lys	Leu	Glu	Lys	Ile	Ser	Ser	Lys
		35					40					45			
Pro	Pro	Lys	Pro	Pro	Ala	Pro	Leu	Lys	Pro	Pro	Lys	Pro	Pro	Ala	Pro
	50					55					60				
Pro	Lys	Pro	Pro	Leu	Ala	Pro	Ala	Ala	Pro	Tyr	Trp	Ser			
65				70						75					

(2) INFORMATION FOR SEQ ID NO:5181:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 86 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...86

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5181:

```
Leu Pro Thr Ser Met Ile Phe Pro Trp Ser Arg Thr Met Thr Arg Leu
1          5          10          15
Val Arg Ser Ala Ile Leu Arg Arg Trp Ala Thr Lys Arg Met Val Leu
          20          25          30
Ser Val Arg Asp Ile Arg Leu Ser Ile Thr Phe Phe Ser Val Lys Thr
          35          40          45
Ser Arg Pro Leu Val Ala Ser Ser Ser Ile Lys Thr Gly Ala Leu Val
          50          55          60
Lys Arg Ala Arg Ala Arg Ala Ile Arg Cys Phe Cys Pro Pro Asp Arg
65          70          75          80
Pro Ala Pro Ser Glu Ser
          85
```

(2) INFORMATION FOR SEQ ID NO:5182:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 253 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...253

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5182:

```
Ile Arg Thr Ser Phe Leu Glu Arg Ser Glu Phe Met Ser Gln Asp Glu
1          5          10          15
Lys Leu Ile Arg Glu Gln Ile Cys Asp Val Cys His Lys Met Trp Gln
          20          25          30
```



```

Leu Gly Trp Val Ala Ala Asn Asp Gly Asn Val Ser Val Arg Leu Asp
   35           40           45
Glu Asp Thr Ile Leu Ala Thr Pro Thr Gly Ile Ser Lys Ser Phe Ile
   50           55           60
Thr Pro Glu Lys Leu Val Lys Leu Asn Leu Lys Gly Glu Ile Leu Glu
   65           70           75           80
Ala Glu Gly Asp Tyr Cys Pro Ser Ser Glu Ile Lys Met His Ile Arg
           85           90           95
Cys Tyr Glu Glu Arg Glu Asp Val Arg Ser Val Val His Ala His Pro
           100           105           110
Pro Ile Ala Thr Gly Phe Ala Leu Ala His Ile Pro Leu Asp Thr Tyr
           115           120           125
Ser Leu Ile Glu Ser Ala Ile Val Val Gly Ala Ile Pro Ile Thr Pro
           130           135           140
Phe Gly Val Pro Ser Thr Met Glu Val Pro Glu Ala Ile Thr Pro Tyr
   145           150           155           160
Leu Pro Asp His Asp Val Met Leu Leu Glu Asn His Gly Ala Leu Thr
           165           170           175
Val Gly Ser Asp Val Ile Thr Ala Tyr Tyr Arg Met Glu Thr Leu Glu
           180           185           190
Leu Val Ala Lys Thr Thr Phe His Gly Arg Met Leu Leu Ser Thr Lys
           195           200           205
Gly Ile Glu Glu Gln Glu Ile Ala Arg Pro Thr Leu Glu Arg Leu Phe
           210           215           220
Ser Met Arg Glu Asn Tyr Lys Val Thr Gly Arg His Pro Gly Tyr Arg
   225           230           235           240
Lys Tyr Asn Gly Asp Gly Ser Ile Lys Glu Thr Lys Lys
           245           250

```

(2) INFORMATION FOR SEQ ID NO:5183:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 143 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...143

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5183:

```

Leu Leu Thr Ser Ser Val Ser Ser Thr Thr Ser Lys Pro Cys Phe Glu
1           5           10           15
Leu Thr Ser Ser Val Leu Ser Thr Thr Ser Lys Leu Cys Phe Glu Gln
           20           25           30
Pro Ala Ala Ser Phe Leu Val Cys Ser Leu Ile Phe Ile Glu Phe Ile
           35           40           45
Phe Tyr Arg Ser Ala Leu Phe Cys Phe Cys Cys Val Leu Phe Val Thr

```

50					55					60					
Phe	Asp	His	Leu	Phe	Ser	Val	Pro	Ser	Lys	Asp	Thr	Asp	Ile	Glu	Tyr
65					70					75					80
Lys	Glu	Gly	Tyr	Cys	Thr	Lys	Asp	Cys	Phe	Asp	Ile	Thr	Ser	Cys	Ser
				85					90					95	
Val	Thr	Asn	Cys	Pro	Thr	Lys	Lys	Phe	Phe	Asp	Trp	Ser	Phe	Lys	Ser
			100					105					110		
Arg	Val	Ser	Asn	Gln	Leu	Ser	Leu	Ala	His	Thr	Phe	Trp	Glu	Gly	Thr
			115				120					125			
Tyr	Thr	Phe	Ser	Lys	Phe	Cys	Cys	Lys	Trp	Cys	Asn	Lys	Cys	Thr	
130						135					140				

(2) INFORMATION FOR SEQ ID NO:5184:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 435 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...435

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5184:

Gln	Val	Thr	Ser	Pro	Ser	Lys	Phe	Cys	Ser	Asn	Gly	Ala	Ile	Arg	Asn
1				5					10					15	
Pro	Leu	Ser	Leu	Phe	Gly	Ala	Pro	Val	Thr	Pro	Ala	Ser	Tyr	Gly	Ser
			20					25					30		
Ser	Val	Val	Pro	Ile	Leu	Ile	Met	Val	Trp	Leu	Met	Lys	Tyr	Ile	Glu
		35				40					45				
Lys	Met	Ile	Ala	Lys	Leu	Thr	Pro	Ala	Val	Thr	Lys	Ser	Phe	Leu	Gln
	50				55				60						
Pro	Thr	Leu	Val	Leu	Val	Ser	Ser	Cys	Ile	Ala	Leu	Val	Val	Val	
65				70					75					80	
Gly	Pro	Ile	Gly	Val	Ile	Val	Gly	Glu	Gly	Leu	Ser	Asn	Leu	Val	Gly
			85					90					95		
Gln	Met	Tyr	Gly	Val	Ala	Gly	Trp	Leu	Thr	Leu	Ala	Ile	Leu	Gly	Ala
		100					105						110		
Ile	Met	Pro	Phe	Ile	Val	Met	Thr	Gly	Met	His	Trp	Ala	Phe	Ala	Pro
	115					120						125			
Ile	Phe	Leu	Ala	Ala	Ser	Ile	Ala	Thr	Pro	Asp	Val	Leu	Ile	Leu	Pro
	130				135				140						
Ala	Met	Leu	Gly	Ser	Asn	Leu	Ala	Gln	Gly	Ala	Ala	Ser	Met	Ala	Val
145				150					155					160	
Ala	Leu	Lys	Ser	Lys	Asn	Asn	Asn	Thr	Lys	Gln	Ile	Ala	Phe	Ala	Ala
			165					170					175		
Gly	Phe	Ser	Ala	Leu	Leu	Ala	Gly	Ile	Thr	Glu	Pro	Ala	Leu	Tyr	Gly
		180				185					190				
Val	Thr	Leu	Lys	Tyr	Lys	Lys	Pro	Leu	Tyr	Ala	Ala	Met	Ile	Gly	Gly

	195					200					205				
Gly	Leu	Ala	Gly	Leu	Phe	Ala	Gly	Leu	Thr	Ser	Val	Lys	Ala	Tyr	Leu
	210					215					220				
Phe	Ala	Val	Pro	Ser	Leu	Ile	Ala	Leu	Pro	Gln	Phe	Ile	Tyr	Ser	Asp
225					230					235					240
Val	Pro	Ser	Asn	Ile	Val	Asn	Ala	Leu	Ile	Val	Ala	Val	Ile	Ser	Val
			245						250					255	
Val	Ile	Thr	Phe	Val	Leu	Ala	Tyr	Ile	Phe	Gly	Ile	Asp	Glu	Glu	Glu
		260						265				270			
Ser	Ser	Ser	Asn	Leu	Glu	Val	Lys	Ala	Gly	Val	Ser	Asn	Lys	Lys	Met
	275					280					285				
Ile	Phe	Ser	Pro	Ile	Ser	Gly	Glu	Ile	Ile	Pro	Leu	Ser	Asp	Val	Gln
	290					295				300					
Asp	Lys	Thr	Phe	Ser	Asp	Lys	Leu	Ile	Gly	Asp	Gly	Val	Ala	Ile	Ile
305					310					315					320
Pro	Ser	Glu	Gly	Lys	Val	Tyr	Ala	Pro	Phe	Asp	Gly	Lys	Ile	Thr	Asn
			325						330					335	
Ile	Phe	Pro	Thr	Lys	His	Ala	Ile	Gly	Leu	Lys	Ser	Asp	Glu	Gly	Val
		340						345				350			
Glu	Leu	Leu	Ile	His	Ile	Gly	Leu	Asp	Thr	Val	Glu	Leu	Lys	Gly	Gln
	355					360				365					
Gly	Phe	Ile	Ser	His	Val	Glu	Glu	Gly	Asp	Arg	Val	Phe	Lys	Asn	Gln
	370					375				380					
Leu	Ile	Phe	Glu	Met	Asp	Leu	Asn	Leu	Ile	Lys	Thr	Lys	Gly	Tyr	Glu
385					390					395					400
Thr	Val	Thr	Pro	Val	Ile	Val	Thr	Asn	Thr	Asn	Asp	Phe	Leu	Asp	Val
			405						410					415	
Leu	Val	Leu	Pro	Asn	Asn	Gln	Thr	Ile	Glu	His	Ser	Lys	Glu	Leu	Leu
		420						425					430		
Val	Ile	Leu													
	435														

(2) INFORMATION FOR SEQ ID NO:5185:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 394 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...394
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5185:

Ile	Gly	Ala	Ser	Ile	Phe	Asn	Leu	Val	Phe	Ile	Val	Tyr	Ala	Ser	Thr
1				5					10					15	
Leu	Ser	Gln	Ala	Ser	Phe	Ala	Val	Ala	Met	Ala	Asn	Ile	Val	Met	Leu
		20						25					30		
Leu	Ser	Asp	Leu	Phe	Thr	Val	Phe	Ala	Gly	Ile	Arg	Ala	Asp	Tyr	Thr

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...207

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5186:

Ala	Ile	Ala	Ser	Leu	Leu	Ala	Thr	Gly	Met	Ala	Leu	Phe	Phe	Lys	Ala
1				5					10					15	
Ser	Thr	Ala	Ala	Ala	Thr	Ala	Val	Ser	Ile	Pro	Arg	Arg	Ile	Pro	Ile
			20					25					30		
Gly	Phe	Ala	Pro	Ala	Val	Thr	Phe	Leu	Ile	Pro	Ser	Arg	Thr	Ile	Ala
		35					40					45			
Trp	Val	Lys	Thr	Val	Ala	Val	Val	Val	Pro	Ser	Pro	Ala	Ile	Ser	Leu
	50					55					60				
Val	Leu	Glu	Ala	Thr	Ser	Asp	Thr	Asn	Leu	Ala	Pro	Ile	Phe	Ser	Lys
65					70				75					80	
Trp	Ser	Ser	Asn	Ser	Ile	Ser	Leu	Ala	Met	Val	Thr	Pro	Ser	Leu	Val
			85						90					95	
Ile	Lys	Gly	Glu	Pro	Asn	Asp	Phe	Ser	Arg	Thr	Thr	Leu	Arg	Pro	Phe
		100						105					110		
Gly	Pro	Lys	Val	Thr	Leu	Thr	Val	Ser	Ala	Arg	Ile	Ser	Thr	Pro	Arg
		115					120					125			
Thr	Met	Ala	Glu	Arg	Ala	Ser	Asp	Glu	Asn	Leu	Ile	Ser	Phe	Asp	Ile
	130					135					140				
Leu	Thr	Phe	Ser	Phe	Tyr	Ser	Ser	Met	Ile	Ala	Lys	Met	Leu	Ala	Ser
145					150					155					160
Pro	Thr	Met	Met	Tyr	Phe	Ser	Ser	Pro	Ser	Leu	Thr	Ser	Arg	Pro	Ala
			165						170					175	
Trp	Ala	Ser	Thr	Lys	Thr	Arg	Ser	Pro	Val	Leu	Thr	Leu	Gly	Ala	Thr
			180					185					190		
Lys	Ser	Pro	Phe	Lys	Val	Arg	Thr	Pro	Cys	Pro	Val	Ala	Thr	Thr	
		195					200					205			

(2) INFORMATION FOR SEQ ID NO:5187:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 491 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:
(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:
(A) NAME/KEY: misc_feature
(B) LOCATION 1...491

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5187:

Asp Leu Ala Ser Ile Arg Lys Arg Arg Val Met Met Pro Ile Gln Asn

1			5					10				15			
Lys	Thr	Met	Leu	Ile	Thr	Tyr	Ser	Asp	Ser	Leu	Gly	Asn	Asn	Leu	Lys
			20					25					30		
Asp	Leu	Tyr	Asp	Asn	Leu	Glu	Glu	His	Phe	Arg	Asp	Ala	Ile	Gly	Gly
		35					40					45			
Val	His	Leu	Leu	Pro	Phe	Phe	Pro	Ser	Thr	Gly	Asp	Arg	Gly	Phe	Ala
	50					55					60				
Pro	Val	Asp	Tyr	Asp	Glu	Val	Asp	Ser	Ala	Phe	Gly	Asp	Trp	Glu	Asp
65					70					75				80	
Val	Lys	Arg	Leu	Gly	Glu	Arg	Tyr	Tyr	Leu	Met	Phe	Asp	Phe	Met	Ile
				85					90					95	
Asn	His	Ile	Ser	Arg	Gln	Ser	Lys	Tyr	Tyr	Lys	Asp	Tyr	Gln	Glu	Lys
			100					105					110		
His	Glu	Ala	Ser	Glu	Phe	Lys	Ala	Leu	Phe	Leu	Asn	Trp	Asp	Lys	Phe
		115					120					125			
Trp	Pro	Glu	Asn	Arg	Pro	Thr	Gln	Ser	Asp	Val	Asp	Leu	Ile	Tyr	Lys
	130					135					140				
Arg	Lys	Asp	Arg	Ala	Pro	Lys	Gln	Glu	Ile	Val	Phe	Glu	Asp	Gly	Ser
145					150					155					160
Val	Glu	His	Leu	Trp	Asn	Thr	Phe	Gly	Glu	Glu	Gln	Ile	Asp	Leu	Asp
			165					170						175	
Val	Thr	Lys	Glu	Val	Thr	Met	Glu	Phe	Ile	Arg	Lys	Thr	Ile	Gln	His
		180					185						190		
Leu	Ala	Ser	Asn	Gly	Cys	Asp	Leu	Ile	Arg	Leu	Asp	Ala	Phe	Ala	Tyr
		195					200					205			
Ala	Val	Lys	Lys	Leu	Asp	Thr	Asn	Asp	Phe	Phe	Val	Glu	Pro	Asp	Ile
	210					215					220				
Trp	Asp	Leu	Leu	Asp	Lys	Val	Arg	Asp	Ile	Ala	Thr	Glu	Tyr	Gly	Thr
225					230					235					240
Glu	Phe	Leu	Pro	Glu	Ile	His	Glu	His	Tyr	Ser	Ile	Gln	Phe	Lys	Ile
				245					250					255	

Ala	Asp	His	Asp	Tyr	Tyr	Val	Tyr	Asp	Phe	Ala	Leu	Pro	Met	Val	Thr
			260					265					270		
Leu	Tyr	Thr	Leu	Tyr	Ser	Ser	Arg	Thr	Glu	Arg	Leu	Ala	Lys	Trp	Leu
		275					280					285			
Lys	Met	Ser	Pro	Met	Lys	Gln	Phe	Thr	Thr	Leu	Asp	Thr	His	Asp	Gly
	290					295					300				
Ile	Gly	Val	Val	Asp	Val	Lys	Asp	Ile	Leu	Thr	Asp	Glu	Glu	Ile	Asp
305					310					315					320
Tyr	Ala	Ser	Asn	Glu	Leu	Tyr	Lys	Val	Gly	Ala	Asn	Val	Lys	Arg	Lys
			325						330					335	
Tyr	Ser	Ser	Ala	Glu	Tyr	Asn	Asn	Leu	Asp	Ile	Tyr	Gln	Ile	Asn	Ser
			340					345					350		
Thr	Tyr	Tyr	Ser	Ala	Leu	Gly	Asp	Glu	Val	Lys	Tyr	Phe	Leu	Ala	
		355					360					365			
Arg	Leu	Ile	Gln	Ala	Phe	Ala	Pro	Gly	Ile	Pro	Gln	Val	Tyr	Tyr	Val
	370					375					380				
Gly	Leu	Leu	Ala	Gly	Lys	Asn	Asp	Leu	Lys	Leu	Leu	Glu	Glu	Thr	Lys
385					390					395					400
Glu	Gly	Arg	Asn	Ile	Asn	Arg	His	Tyr	Tyr	Ser	Asn	Glu	Glu	Ile	Ala
			405						410					415	
Lys	Glu	Val	Gln	Arg	Pro	Val	Val	Lys	Ala	Leu	Leu	Asn	Leu	Phe	Ser
			420					425					430		
Phe	Arg	Asn	Arg	Ser	Glu	Ala	Phe	Asp	Leu	Glu	Gly	Thr	Thr	Glu	Ile
		435					440					445			
Glu	Thr	Pro	Thr	Ala	His	Ser	Ile	Val	Ile	Lys	Arg	Gln	Asn	Lys	Asp

450		455		460											
Lys	Ser	Val	Thr	Ala	Val	Ala	Glu	Ile	Asp	Leu	Gln	Asn	Gln	Thr	Tyr
465				470						475					480
Arg	Val	Ile	Glu	Asn	Gly	Val	Glu	Val	Thr	Phe					
				485					490						

(2) INFORMATION FOR SEQ ID NO:5188:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 100 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...100
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5188:

Thr	Ala	Tyr	Ser	Cys	Ser	Ala	Ala	Ser	Ser	Val	Ala	Ser	Ala	Phe	Val
1				5					10					15	
Ala	Phe	Ser	Ala	Ser	Ser	Ala	Ser	Lys	Ala	Ala	Leu	Ala	Ser	Trp	Ala
			20					25					30		
Ala	Phe	Ser	Arg	Ala	Phe	Ser	Arg	Ser	Ser	Thr	Trp	Met	Thr	Ser	Ser
		35				40					45				
Ser	Ile	Pro	Ser	Ser	Lys	Ser	Arg	Ser	Ser	Thr	Ser	Trp	Ser	Ser	Ser
	50				55					60					
Ser	Arg	Thr	Arg	Met	Ser	Arg	Pro	Arg	Asp	Cys	Asn	Ser	Leu	Thr	Arg
65				70					75					80	
Thr	Arg	Lys	Asp	Ser	Gly	Thr	Pro	Gly	Phe	Gly	Ile	Gly	Leu	Pro	Phe
			85					90						95	
Val	Ile	Ala	Ser												
			100												

(2) INFORMATION FOR SEQ ID NO:5189:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 142 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature

(B) LOCATION 1...142

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5189:

Asn	Gly	Glu	Leu	Asn	Met	Leu	Ala	Asn	Gly	Ile	Thr	Leu	Ser	Tyr	Gly
1				5				10					15		
Glu	Thr	Lys	Asp	Ser	Tyr	Thr	Lys	Leu	Val	Gly	Leu	Lys	Glu	Val	Pro
		20						25				30			
Glu	Phe	Gly	Ile	Glu	Leu	Glu	Lys	Val	Glu	Asn	Thr	Thr	Leu	Glu	Asp
		35					40					45			
Thr	Val	Lys	Lys	Tyr	Glu	Phe	Gly	Ile	Gly	Asp	Ile	Gly	Glu	Leu	Glu
	50					55				60					
Tyr	Lys	Phe	Ser	Tyr	Asn	Asn	Ser	Ser	Ala	Thr	Ala	Pro	Tyr	Arg	Val
65					70				75					80	
Leu	Arg	Lys	Ala	Ala	Asp	Asp	Lys	Lys	Lys	Leu	Tyr	Phe	Glu	Gln	Ala
			85					90					95		
Tyr	Pro	Asp	Gly	Thr	Lys	Val	Ile	Phe	Glu	Gly	Gln	Val	Ser	Val	Lys
		100						105				110			
Leu	Gly	Gly	Gly	Gly	Val	Asn	Ala	Val	Ile	Asp	Phe	Thr	Leu	Lys	Ile
		115					120					125			
Ala	Leu	Gln	Ser	Asn	Leu	Thr	Phe	Thr	Asp	Gly	Ile	Gly	Gly		
	130					135					140				

(2) INFORMATION FOR SEQ ID NO:5190:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 116 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...116

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5190:

Phe	Ala	Tyr	Ser	Ala	Thr	Ser	Ser	Ile	Lys	Cys	Val	Thr	Lys	Thr	Met
1				5				10					15		
Val	Ile	Pro	Asp	Trp	Trp	Ser	Phe	Leu	Asn	Arg	Val	Ile	Asn	Ser	Phe
		20						25				30			
Leu	Pro	Arg	Gly	Ser	Arg	Pro	Ala	Val	Gly	Ser	Ser	Lys	Thr	Asn	Ile
		35					40					45			
Ala	Gly	Ser	Met	Ala	Ser	Met	Pro	Ala	Met	Ala	Thr	Arg	Leu	Ile	Cys
	50					55				60					
Pro	Pro	Asp	Ser	Ser	Asn	Gly	Leu	Arg	Ser	Lys	Ser	Asp	Ser	Ser	Ile
65					70				75					80	
Pro	Thr	Arg	Ala	Ser	Phe	Ser	Arg	Ala	Val	Phe	Thr	Ala	Ser	Ser	Ser
			85					90				95			
Glu	Thr	Pro	Lys	Phe	Cys	Gly	Pro	Lys	Ala	Thr	Ser	Phe	Lys	Thr	Val
		100						105				110			

Ser Ser Lys Ile
115

(2) INFORMATION FOR SEQ ID NO:5191:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 133 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...133

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5191:

Lys	Cys	His	Ser	Met	Glu	Pro	Gln	Ala	Ile	Val	Thr	Ser	Gln	Glu	Arg
1				5					10					15	
Ile	Val	Ser	Leu	Asn	Ile	Ala	Val	Asn	Tyr	Cys	His	Asp	Met	Lys	Leu
			20					25					30		
Phe	Lys	Met	Ser	Arg	Arg	Asn	Ile	Gly	Gln	Ala	Gly	Lys	Ile	Leu	Ala
		35					40					45			
Asp	Ser	Gly	Tyr	Gln	Gly	Pro	Met	Lys	Ile	Tyr	Pro	Gln	Ala	Gln	Thr
	50					55				60					
Pro	Arg	Lys	Ser	Ser	Asn	Leu	Lys	Pro	Leu	Ile	Ala	Glu	Asp	Lys	Ala
65					70					75					80
Tyr	Asn	His	Ala	Leu	Ser	Lys	Glu	Arg	Ser	Lys	Val	Glu	Asn	Ile	Phe
			85						90					95	
Ala	Lys	Val	Lys	Thr	Phe	Lys	Met	Phe	Ser	Thr	Thr	Tyr	Arg	Asn	His
			100					105					110		
Arg	Lys	Arg	Phe	Gly	Leu	Arg	Met	Asn	Leu	Ile	Val	Gly	Ile	Ile	Asn
			115				120					125			
His	Glu	Leu	Gly	Phe											
															130

(2) INFORMATION FOR SEQ ID NO:5192:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 212 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...212

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5192:

```
Ile Met Glu Phe Arg Thr Ile Lys Glu Asp Gly Gln Val Gln Glu Glu
1      5      10      15
Ile Lys Lys Ser Arg Phe Ile Cys His Ala Lys Arg Val Tyr Ser Glu
      20      25      30
Glu Glu Ala Arg Asp Phe Ile Thr Ala Ile Lys Lys Glu His Tyr Lys
      35      40      45
Ala Thr His Asn Cys Ser Ala Phe Ile Ile Gly Glu Arg Ser Glu Ile
      50      55      60
Lys Arg Thr Ser Asp Asp Gly Glu Pro Ser Gly Thr Ala Gly Val Pro
65      70      75      80
Met Leu Gly Val Leu Glu Asn His Asn Leu Thr Asn Val Cys Val Val
      85      90      95
Val Thr Arg Tyr Phe Gly Gly Ile Lys Leu Gly Ala Gly Gly Leu Ile
      100     105     110
Arg Ala Tyr Ala Gly Ser Val Ala Leu Ala Val Lys Glu Ile Gly Ile
      115     120     125
Ile Glu Ile Lys Glu Gln Ala Gly Ile Ala Ile Gln Met Ser Tyr Ala
      130     135     140
Gln Tyr Gln Glu Tyr Ser Asn Phe Leu Lys Glu His Asp Leu Met Glu
145     150     155     160
Leu Asp Thr Asn Phe Thr Asp Gln Val Asp Thr Met Ile Tyr Val Asp
      165     170     175
Lys Glu Glu Lys Glu Thr Ile Lys Ala Ala Leu Val Glu Phe Phe Asn
      180     185     190
Gly Lys Val Thr Leu Thr Asp Gln Gly Leu Arg Glu Val Glu Val Pro
      195     200     205
Val Asn Leu Val
      210
```

(2) INFORMATION FOR SEQ ID NO:5193:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 120 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature
(B) LOCATION 1...120

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5193:

```
Val Met Glu Leu Met Asn Lys Thr Arg Val Thr Asp Ser Leu Ala Val
1      5      10      15
Val Ile Gly Pro Glu Ser Ile Glu Val Leu Val Thr Glu Gly Phe Leu
```

		20					25				30				
Phe	Asp	Val	Ala	Ile	Arg	Phe	Val	Lys	Val	Asp	Glu	Thr	Asn	Leu	Asp
		35					40				45				
Gln	Gly	Asn	Glu	Lys	Pro	Val	Phe	Thr	Pro	Glu	Tyr	Lys	Leu	Val	Thr
		50					55				60				
Val	Ala	Lys	Tyr	Lys	Glu	Lys	Pro	Ile	Phe	Glu	Ser	Glu	Glu	Asp	Ile
65					70					75					80
Arg	Lys	Phe	Glu	Lys	Gln	Ala	Lys	Glu	Val	Lys	Ser	Leu	Phe	Ala	Phe
				85					90					95	
Ala	Lys	Val	Asn	Lys	Gln	Asn	Trp	Phe	Asn	Thr	Ala	Leu	Tyr	Pro	Gly
			100					105					110		
Val	Leu	Thr	Glu	Lys	Val	Gly	Val								
			115				120								

(2) INFORMATION FOR SEQ ID NO:5194:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 270 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...270
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5194:

Gln	Met	Glu	Leu	Thr	Lys	Tyr	Ala	Ser	Ser	Met	Leu	Leu	Asp	Pro	Glu
1				5					10					15	
Tyr	Gly	Leu	Pro	Ala	Thr	Lys	Ala	Leu	Asp	Glu	Lys	Ala	Gly	Leu	Leu
			20					25					30		
Leu	Ala	Tyr	Glu	Lys	Thr	Gly	Tyr	Asp	Thr	Thr	Ser	Thr	Lys	Arg	Leu
		35				40					45				
Pro	Asp	Cys	Leu	Asp	Val	Trp	Ser	Ala	Lys	Arg	Ile	Lys	Glu	Glu	Gly
	50					55					60				
Ala	Asp	Ala	Val	Lys	Phe	Leu	Leu	Tyr	Tyr	Asp	Val	Asp	Ser	Ser	Asp
65					70					75					80
Glu	Leu	Asn	Gln	Glu	Lys	Gln	Ala	Tyr	Ile	Glu	Arg	Ile	Gly	Ser	Glu
				85					90					95	
Cys	Val	Ala	Glu	Asp	Ile	Pro	Phe	Phe	Leu	Glu	Ile	Leu	Ala	Tyr	Asp
			100					105					110		
Glu	Lys	Ile	Ala	Asp	Ala	Gly	Ser	Val	Glu	Tyr	Ala	Lys	Val	Lys	Pro
		115				120						125			
His	Lys	Val	Ile	Gly	Ala	Met	Lys	Val	Phe	Ser	Asp	Pro	Arg	Phe	Asn
	130					135					140				
Ile	Asp	Val	Leu	Lys	Val	Glu	Val	Pro	Val	Asn	Ile	Lys	Tyr	Val	Glu
145					150					155					160
Gly	Phe	Ala	Glu	Gly	Glu	Val	Val	Tyr	Thr	Arg	Glu	Glu	Ala	Ala	Ala
			165						170				175		
Phe	Phe	Lys	Ala	Gln	Asp	Glu	Ala	Thr	Asn	Leu	Pro	Tyr	Ile	Tyr	Leu

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...75

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5196:

Gly	Gly	His	Ser	Phe	Ile	Lys	His	Lys	Thr	Gly	Trp	Phe	Asp	Gly	Met
1				5					10					15	
Met	Thr	Thr	Gly	Cys	Ser	Met	Gly	Ala	Tyr	His	Ala	Leu	Asn	Phe	Phe
			20					25					30		
Leu	Gln	His	Pro	Asp	Val	Phe	Thr	Lys	Val	Ile	Ala	Leu	Ser	Gly	Val
		35					40					45			
Tyr	Asp	Ala	Arg	Phe	Phe	Val	Gly	Asp	Tyr	Tyr	Asn	Asp	Asp	Ala	Ile
	50					55					60				
Tyr	Gln	Asn	Ser	Pro	Val	Asp	Tyr	Ile	Trp	Asn					
65					70					75					

(2) INFORMATION FOR SEQ ID NO:5197:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 378 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Streptococcus pneumoniae

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...378

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5197:

Met	Lys	His	Ser	Val	His	Phe	Gly	Ala	Gly	Asn	Ile	Gly	Arg	Gly	Phe
1				5					10					15	
Ile	Gly	Glu	Ile	Leu	Phe	Lys	Asn	Gly	Phe	His	Ile	Asp	Phe	Val	Asp
			20					25					30		
Val	Asn	Asn	Gln	Ile	Ile	Tyr	Ala	Leu	Asn	Glu	Lys	Gly	Lys	Tyr	Glu
		35					40					45			
Ile	Glu	Ile	Ala	Gln	Lys	Gly	Gln	Ser	Arg	Ile	Glu	Val	Thr	Asn	Val
	50					55					60				
Ala	Gly	Ile	Asn	Ser	Lys	Glu	His	Pro	Glu	Gln	Val	Ile	Glu	Ala	Ile
65					70					75					80
Gln	Lys	Thr	Asp	Ile	Ile	Thr	Thr	Ala	Ile	Gly	Pro	Asn	Ile	Leu	Pro
			85						90					95	
Phe	Ile	Ala	Glu	Leu	Leu	Ala	Lys	Gly	Ile	Glu	Ala	Arg	Arg	Val	Ala
		100						105					110		
Gly	Asn	Thr	Gln	Ala	Leu	Asp	Val	Met	Ala	Cys	Glu	Asn	Met	Ile	Gly
	115						120					125			
Gly	Ser	Gln	Phe	Leu	Tyr	Gln	Glu	Val	Lys	Lys	Tyr	Leu	Ser	Pro	Glu
	130					135					140				
Gly	Leu	Thr	Phe	Ala	Asp	Asn	Tyr	Ile	Gly	Phe	Pro	Asn	Ala	Ala	Val
145					150					155					160

```

Asp Arg Ile Val Pro Thr Gln Ser His Glu Asp Ser Leu Phe Val Met
      165                      170                      175
Val Glu Pro Phe Asn Glu Trp Val Val Glu Thr Lys Arg Leu Lys Asn
      180                      185                      190
Pro Asp Leu Arg Leu Lys Asp Val His Tyr Glu Glu Asp Leu Glu Pro
      195                      200                      205
Phe Ile Glu Arg Lys Leu Phe Ser Val Asn Ser Gly His Ala Thr Ser
      210                      215                      220
Ala Tyr Ile Gly Ala His Tyr Gly Ala Lys Thr Ile Leu Glu Ala Leu

225                      230                      235                      240
Gln Asn Pro Asn Ile Lys Ser Arg Ile Glu Ser Val Leu Ala Glu Ile
      245                      250                      255
Arg Ser Leu Leu Ile Ala Lys Trp Asn Phe Asp Lys Lys Glu Leu Glu
      260                      265                      270
Asn Tyr His Lys Val Ile Ile Glu Arg Phe Glu Asn Pro Phe Ile Val
      275                      280                      285
Asp Glu Val Ser Arg Val Ala Arg Thr Pro Ile Arg Lys Leu Gly Tyr
      290                      295                      300
Asn Glu Arg Phe Ile Arg Pro Ile Arg Glu Leu Lys Glu Leu Ser Leu
305                      310                      315                      320
Ser Tyr Lys Asn Leu Leu Lys Thr Val Gly Tyr Ala Phe Asp Tyr Arg
      325                      330                      335
Asp Val Asn Asp Glu Glu Ser Ile Arg Leu Gly Glu Leu Leu Ala Lys
      340                      345                      350
Gln Ser Val Lys Asp Val Val Ile Gln Val Thr Gly Leu Asp Asp Gln
      355                      360                      365
Glu Leu Ile Glu Gln Ile Val Glu Tyr Ile
370                      375

```

(2) INFORMATION FOR SEQ ID NO:5198:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 291 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: *Streptococcus pneumoniae*
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...291
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5198:

```

Lys Glu Glu Leu Lys Met Glu Lys Leu Val Ala Tyr Lys Arg Met Pro
1      5      10      15
Leu Trp Asn Lys Gln Thr Met Pro Glu Ala Val Gln Gln Lys His Asn
      20      25      30
Thr Lys Val Gly Thr Trp Gly Lys Ile Thr Val Leu Lys Gly Ala Leu
      35      40      45
Lys Phe Ile Glu Leu Thr Glu Glu Gly Glu Val Leu Ala Glu His Leu

```

50		55		60															
Phe	Glu	Ala	Gly	Ala	Asp	Asn	Pro	Met	Ala	Gln	Pro	Gln	Ala	Trp	His				
65					70					75					80				
Arg	Val	Glu	Ala	Ala	Thr	Asp	Asp	Val	Glu	Trp	Tyr	Leu	Glu	Phe	Tyr				
				85						90					95				
Cys	Lys	Pro	Glu	Asp	Tyr	Phe	Ala	Lys	Lys	Tyr	Asn	Thr	Asn	Pro	Val				
			100					105					110						
His	Ser	Glu	Val	Leu	Glu	Ala	Met	Gln	Thr	Val	Lys	Gln	Gly	Lys	Ala				
			115				120					125							
Leu	Asp	Leu	Gly	Cys	Gly	Gln	Gly	Arg	Asn	Ser	Leu	Phe	Leu	Ala	Gln				
			130			135					140								
Gln	Asp	Phe	Asp	Val	Thr	Ala	Val	Asp	Gln	Asn	Gly	Leu	Ala	Leu	Glu				
145					150					155					160				
Ile	Leu	Gln	Ser	Ile	Val	Glu	Gln	Glu	Asp	Leu	Asp	Met	Pro	Val	Asp				
			165					170						175					
Leu	Tyr	Asp	Ile	Asn	Ser	Ala	Ser	Ile	Glu	Gln	Glu	Tyr	Asp	Phe	Ile				
			180				185						190						
Val	Ser	Thr	Val	Val	Leu	Met	Phe	Leu	Gln	Ala	Asp	Arg	Ile	Pro	Ala				
			195				200					205							
Ile	Ile	Gln	Asn	Met	Gln	Glu	Lys	Thr	Ser	Val	Gly	Gly	Tyr	Asn	Leu				
			210			215					220								
Ile	Val	Cys	Ala	Met	Asp	Thr	Glu	Asp	Tyr	Pro	Cys	Ser	Val	Asn	Phe				
225					230					235					240				
Pro	Phe	Thr	Phe	Lys	Glu	Gly	Glu	Leu	Ala	Asp	Tyr	Tyr	Lys	Asp	Trp				
			245						250					255					
Glu	Leu	Val	Lys	Tyr	Asn	Glu	Asn	Pro	Gly	His	Leu	His	Arg	Arg	Asp				
			260				265						270						
Glu	Asn	Gly	Asn	Arg	Ile	Gln	Leu	Arg	Phe	Ala	Thr	Leu	Leu	Ala	Lys				
			275			280						285							
Lys	Ile	Lys																	
290																			

(2) INFORMATION FOR SEQ ID NO:5199:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 161 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: protein
- (iii) HYPOTHETICAL: YES
- (vi) ORIGINAL SOURCE:
 - (A) ORGANISM: Streptococcus pneumoniae
- (ix) FEATURE:
 - (A) NAME/KEY: misc_feature
 - (B) LOCATION 1...161
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5199:

Gly	Gly	Asn	Ser	Arg	Gln	Asp	Pro	Tyr	His	Gly	Pro	Gly	Gln	Ala	Gln				
1			5				10				15								
Gly	Leu	Ser	Phe	Ser	Val	Pro	Asp	Ser	Ile	Pro	Ala	Pro	Pro	Ser	Leu				
			20				25				30								
Gln	Asn	Ile	Leu	Lys	Glu	Leu	Ser	Asp	Asp	Ile	Gly	Val	Lys	Lys	Ser				

(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...440

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5201:

```

Lys Asp Asn Ser Met Ile His Leu Ile Met Ile Ser Ala Ile Ala Leu
1      5      10      15
Ala Ile Gly Ile Gly Tyr Arg Thr Lys Ile Asn Ile Gly Leu Leu Ala
20      25      30
Ile Ala Phe Ser Tyr Leu Ile Ala Thr Thr Leu Met Gly Leu Ser Pro
35      40      45
Lys Glu Leu Leu His Phe Trp Pro Thr Ser Leu Phe Phe Thr Ile Phe
50      55      60
Ser Val Ser Leu Phe Tyr Asn Val Ala Thr Thr Asn Gly Thr Leu Asp
65      70      75      80
Val Leu Ala Gln His Ile Leu Tyr Arg Thr Arg Thr His Pro Asn Ala
85      90      95
Leu Tyr Met Ile Leu Tyr Leu Met Ala Thr Leu Leu Ser Ala Leu Gly
100     105     110
Ala Gly Phe Phe Thr Thr Met Ala Val Cys Cys Pro Leu Ala Ile Thr
115     120     125
Leu Cys Gln Lys Ala Asp Lys His Pro Leu Ile Gly Ala Gln Ala Val
130     135     140
Asn Trp Gly Ala Ser Gly Gly Ala Asn Leu Ile Thr Ser Ser Ser Gly
145     150     155     160
Ile Val Phe Gln Gly Leu Phe Lys Gln Met Gly Trp Glu Glu Gln Ala
165     170     175
Phe Ser Leu Gly Asn His Ile Phe Ile Val Ser Ile Ile Tyr Pro Leu
180     185     190
Ile Val Leu Leu Leu Leu Ser Cys Tyr Ser His Tyr Ser Lys Gly Arg
195     200     205
Thr Asn Ser Ser Leu Thr Ile Asp Gln Pro Pro Leu Leu Ser Lys Val
210     215     220
Gln Arg Gln Thr Thr Leu Leu Met Ile Ser Ser Met Val Leu Val Trp
225     230     235     240
Leu Phe Pro Leu Leu His Leu Ile Phe Pro Asn Ile Ala Trp Ile Ala
245     250     255
Thr Tyr Gln Lys Thr Phe Asp Ile Gly Phe Val Ser Ile Leu Met Val
260     265     270
Cys Leu Ala Leu Arg Leu Lys Leu Gly Lys Gln Glu Ala Ile Leu Ala
275     280     285
Lys Val Pro Trp Ala Thr Ile Ile Met Leu Cys Gly Met Ser Leu Leu
290     295     300
Met Ser Leu Ala Val Lys Ser Gly Leu Val Thr Leu Ile Gly His Leu
305     310     315     320
Met Thr Thr Thr Ile Pro His Phe Trp Leu Pro Leu Phe Phe Cys Val

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				325					330					335					
Ile	Ala	Gly	Val	Met	Ser	Leu	Phe	Ser	Ser	Thr	Leu	Ser	Val	Val	Ala				
				340					345					350					
Pro	Ala	Leu	Phe	Pro	Ile	Ile	Ala	Ile	Ile	Ser	Ala	Gln	Asn	Pro	Gln				
				355					360					365					
Ile	Asp	Ile	His	Leu	Leu	Thr	Thr	Ala	Thr	Val	Ile	Gly	Ala	Leu	Ser				
				370					375					380					
Thr	Asn	Ile	Ser	Pro	Phe	Ser	Ser	Ala	Gly	Ser	Leu	Ile	Gln	Leu	Ser				
385					390					395									
Leu	Pro	Asn	Ile	Glu	Glu	Arg	Gly	Leu	Ala	Phe	Lys	Lys	Gln	Ile	Ile				
				405					410					415					
Leu	Gly	Val	Pro	Ile	Ser	Leu	Ser	Leu	Gly	Leu	Leu	Thr	Thr	Trp	Ile				
				420					425					430					
Leu	Ile	Leu	Leu	Ala	Ser	Leu	Ser												
				435					440										

(2) INFORMATION FOR SEQ ID NO:5202:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 424 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...424

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5202:

Ile	Ile	Asn	Ser	His	Ser	Met	Cys	Arg	His	Lys	Glu	Lys	Ser	Met	Lys				
1				5					10					15					
Leu	Phe	Trp	Thr	Asn	Asn	Ile	Tyr	Arg	Gln	Leu	Leu	Leu	Asn	Ser	Cys				
				20				25					30						
Phe	Ser	Ser	Phe	Gly	Asp	Ser	Ile	Phe	Tyr	Leu	Ala	Ile	Ile	Asn	Tyr				
				35				40					45						
Val	Ala	Gln	Tyr	Asn	Phe	Ala	Pro	Leu	Ala	Ile	Leu	Leu	Ile	Ser	Ile				
				50				55				60							
Ser	Glu	Met	Val	Pro	Leu	Leu	Ser	Gln	Leu	Phe	Leu	Gly	Ile	Leu	Gly				
65					70				75						80				
Asp	Phe	Gln	Glu	Asn	Arg	Val	Lys	His	Ala	Leu	Trp	Ile	Ala	Lys	Ile				
				85					90					95					
Lys	Ile	Leu	Leu	Tyr	Ala	Ile	Leu	Thr	Val	Phe	Leu	Val	Leu	Ser	Pro				
				100				105					110						
Phe	Ser	Leu	Val	Ser	Val	Ile	Met	Ile	Val	Ile	Ile	Asn	Leu	Ile	Ser				
				115				120				125							
Asp	Thr	Leu	Ser	Tyr	Leu	Ser	Ala	Tyr	Met	Met	Asn	Ala	Leu	Tyr	Ile				
130					135				140										
Ser	Val	Ile	Lys	Asp	Asp	Leu	His	Asp	Ala	Met	Gly	Phe	Arg	Gln	Ser				
145					150				155					160					
Leu	Met	Arg	Val	Val	Arg	Ile	Val	Ala	Asn	Leu	Ala	Gly	Ala	Phe	Leu				

(2) INFORMATION FOR SEO ID NO:5204:

(A) LENGTH: 138 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(iii) HYPOTHETICAL: YES

(A) ORGANISM: *Streptococcus pneumoniae*

(A) NAME/KEY: misc_feature
(B) LOCATION 1...138

4054

			100					105					110				
Ala	Gln	Asp	Gly	Tyr	Glu	Ala	Lys	Trp	Tyr	Asn	Trp	Cys	Asp	Gly	Phe		
		115					120					125					
Asn	Gln	Ala	Ala	Thr	Leu	Leu	Leu	Lys	Arg								
	130					135											

(2) INFORMATION FOR SEQ ID NO:5205:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 361 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

- (A) NAME/KEY: misc_feature
- (B) LOCATION 1...361

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5205:

Glu	Asn	Asp	Ser	Leu	Ala	Val	Leu	Glu	Ile	Gly	Ile	Leu	Asn	Ser	Glu		
1				5				10					15				
Tyr	Val	Ile	Ile	Ser	Ile	Ser	Arg	Arg	Cys	Phe	Arg	Leu	Glu	Lys	Lys		
		20					25					30					
Leu	Thr	Ile	Lys	Asp	Ile	Ala	Glu	Met	Ala	Gln	Thr	Ser	Lys	Thr	Thr		
	35					40					45						
Val	Ser	Phe	Tyr	Leu	Asn	Gly	Lys	Tyr	Glu	Lys	Met	Ser	Gln	Glu	Thr		
	50				55				60								
Arg	Glu	Lys	Ile	Glu	Lys	Val	Ile	His	Glu	Thr	Asn	Tyr	Lys	Pro	Ser		
65				70				75						80			
Ile	Val	Ala	Arg	Ser	Leu	Asn	Ser	Lys	Arg	Thr	Lys	Leu	Ile	Gly	Val		
		85					90						95				
Leu	Ile	Gly	Asp	Ile	Thr	Asn	Ser	Phe	Ser	Asn	Gln	Ile	Val	Lys	Gly		
	100					105					110						
Ile	Glu	Asp	Ile	Ala	Ser	Gln	Asn	Gly	Tyr	Gln	Val	Met	Ile	Gly	Asn		
	115					120					125						
Ser	Asn	Tyr	Ser	Gln	Glu	Ser	Glu	Asp	Arg	Tyr	Ile	Glu	Ser	Met	Leu		
	130				135					140							
Leu	Leu	Gly	Val	Asp	Gly	Phe	Ile	Ile	Gln	Pro	Thr	Ser	Asn	Phe	Arg		
145				150					155						160		
Lys	Tyr	Ser	Arg	Ile	Ile	Asp	Glu	Lys	Lys	Lys	Lys	Met	Val	Phe	Phe		
		165				170								175			
Asp	Ser	Gln	Leu	Tyr	Glu	His	Arg	Thr	Ser	Trp	Val	Lys	Thr	Asn	Asn		
	180					185							190				
Tyr	Asp	Ala	Val	Tyr	Asp	Met	Thr	Gln	Ser	Cys	Ile	Glu	Lys	Gly	Tyr		
	195					200					205						
Glu	His	Phe	Leu	Leu	Ile	Thr	Ala	Asp	Thr	Ser	Arg	Leu	Ser	Thr	Arg		
	210				215						220						
Ile	Glu	Arg	Ala	Ser	Gly	Phe	Val	Asp	Ala	Leu	Thr	Asp	Ala	Asn	Met		
225					230				235					240			
Arg	His	Ala	Ser	Leu	Thr	Ile	Glu	Asp	Lys	His	Thr	Asn	Leu	Glu	Gln		

				245					250					255					
Ile	Lys	Glu	Phe	Leu	Gln	Lys	Glu	Ile	Asp	Pro	Asp	Glu	Lys	Thr	Leu				
			260					265					270						
Val	Phe	Ile	Pro	Asn	Cys	Trp	Ala	Leu	Pro	Leu	Val	Phe	Thr	Val	Ile				
		275					280					285							
Lys	Glu	Leu	Asn	Tyr	Asn	Leu	Pro	Gln	Val	Gly	Leu	Ile	Gly	Phe	Asp				
	290					295					300								
Asn	Thr	Glu	Trp	Thr	Cys	Phe	Ser	Ser	Pro	Ser	Val	Ser	Thr	Leu	Val				
305					310					315					320				
Gln	Pro	Ser	Phe	Glu	Glu	Gly	Gln	Gln	Ala	Thr	Lys	Ile	Leu	Ile	Asp				
			325						330					335					
Gln	Ile	Glu	Gly	Arg	Asn	Gln	Glu	Glu	Arg	Gln	Gln	Val	Leu	Asp	Cys				
		340					345					350							
Ser	Val	Asn	Trp	Lys	Glu	Ser	Thr	Phe											
		355				360													

(2) INFORMATION FOR SEQ ID NO:5206:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 352 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(iii) HYPOTHETICAL: YES

(vi) ORIGINAL SOURCE:

(A) ORGANISM: *Streptococcus pneumoniae*

(ix) FEATURE:

(A) NAME/KEY: misc_feature

(B) LOCATION 1...352

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5206:

Ala	Thr	Asp	Ser	Pro	Leu	Lys	Lys	Arg	Lys	Lys	Gln	Met	Thr	Asn	Lys				
1				5				10						15					
Asn	Ala	Tyr	Ala	Gln	Ser	Gly	Val	Asp	Val	Glu	Ala	Gly	Tyr	Glu	Val				
		20					25					30							
Val	Glu	Arg	Ile	Lys	Lys	His	Val	Ala	Arg	Thr	Glu	Arg	Ala	Gly	Val				
	35					40					45								
Met	Gly	Ala	Leu	Gly	Gly	Phe	Gly	Gly	Met	Phe	Asp	Leu	Ser	Lys	Thr				
	50				55					60									
Gly	Val	Lys	Glu	Pro	Val	Leu	Ile	Ser	Gly	Thr	Asp	Gly	Val	Gly	Thr				
65				70				75						80					
Lys	Leu	Met	Leu	Ala	Ile	Lys	Tyr	Asp	Lys	His	Asp	Thr	Ile	Gly	Gln				
			85				90						95						
Asp	Cys	Val	Ala	Met	Cys	Val	Asn	Asp	Ile	Ile	Ala	Ala	Gly	Ala	Glu				
		100					105					110							
Pro	Leu	Tyr	Phe	Leu	Asp	Tyr	Val	Ala	Thr	Gly	Lys	Asn	Glu	Pro	Ala				
	115					120						125							
Lys	Leu	Glu	Gln	Val	Val	Ala	Gly	Val	Ala	Glu	Gly	Cys	Val	Gln	Ala				
	130				135					140									
Gly	Ala	Ala	Leu	Ile	Gly	Gly	Glu	Thr	Ala	Glu	Met	Pro	Gly	Met	Tyr				
145				150			155					160							
Gly	Glu	Asp	Asp	Tyr	Asp	Leu	Ala	Gly	Phe	Ala	Val	Gly	Val	Ala	Glu				

				165					170					175			
Lys	Ser	Gln	Ile	Ile	Asp	Gly	Ser	Lys	Val	Val	Glu	Gly	Asp	Val	Leu		
			180					185					190				
Leu	Gly	Leu	Ala	Ser	Ser	Gly	Ile	His	Ser	Asn	Gly	Tyr	Ser	Leu	Val		
		195					200					205					
Arg	Arg	Val	Phe	Ala	Asp	Tyr	Thr	Gly	Glu	Glu	Val	Leu	Pro	Glu	Leu		
		210				215					220						
Glu	Gly	Lys	Lys	Leu	Lys	Glu	Val	Leu	Leu	Glu	Pro	Thr	Arg	Ile	Tyr		
225					230					235					240		
Val	Lys	Ala	Val	Leu	Pro	Leu	Ile	Lys	Glu	Glu	Leu	Val	Asn	Gly	Ile		
				245					250					255			
Ala	His	Ile	Thr	Gly	Gly	Gly	Phe	Ile	Glu	Asn	Val	Pro	Arg	Met	Phe		
			260				265						270				
Ala	Asp	Asp	Leu	Ala	Ala	Glu	Ile	Asp	Glu	Ser	Lys	Val	Pro	Val	Leu		
		275					280					285					
Pro	Ile	Phe	Lys	Ala	Leu	Glu	Lys	Tyr	Gly	Gln	Ile	Lys	His	Glu	Glu		
290						295					300						
Met	Phe	Glu	Ile	Phe	Asn	Met	Gly	Val	Gly	Leu	Met	Leu	Ala	Val	Ser		
305					310					315					320		
Pro	Glu	Asn	Val	Glu	Arg	Val	Lys	Glu	Leu	Leu	Asp	Glu	Ala	Val	Tyr		
				325					330					335			
Glu	Ile	Gly	Arg	Ile	Val	Lys	Lys	Glu	Asn	Glu	Ser	Val	Ile	Ile	Lys		
			340					345					350				